

Match length 99
% identity 45
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 296324
Seq. ID LIB3088-045-Q1-K1-H6
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 48
% identity 67
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 296325
Seq. ID LIB3088-046-Q1-K1-A7
Method BLASTN
NCBI GI g531828
BLAST score 41
E value 8.0e-14
Match length 73
% identity 89
NCBI Description Cloning vector pSport1, complete cds

Seq. No. 296326
Seq. ID LIB3088-046-Q1-K1-B1
Method BLASTN
NCBI GI g13904
BLAST score 73
E value 3.0e-33
Match length 165
% identity 87
NCBI Description Maize mitochondrial cytochrome b gene

Seq. No. 296327
Seq. ID LIB3088-046-Q1-K1-C11
Method BLASTN
NCBI GI g3925236
BLAST score 84
E value 1.0e-39
Match length 136
% identity 94
NCBI Description Zea mays 6-phosphogluconate dehydrogenase gene, partial cds

Seq. No. 296328
Seq. ID LIB3088-046-Q1-K1-E8
Method BLASTX
NCBI GI g3152605
BLAST score 202
E value 8.0e-20
Match length 76
% identity 64
NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 296329
Seq. ID LIB3088-046-Q1-K1-F11
Method BLASTX

NCBI GI g2842493
BLAST score 155
E value 3.0e-10
Match length 51
% identity 55
NCBI Description (AL021749) predicted protein [Arabidopsis thaliana]

Seq. No. 296330
Seq. ID LIB3088-046-Q1-K1-F2
Method BLASTX
NCBI GI g2062405
BLAST score 180
E value 3.0e-13
Match length 74
% identity 47
NCBI Description (U79011) cytochrome b5 [Borago officinalis]

Seq. No. 296331
Seq. ID LIB3088-046-Q1-K1-F9
Method BLASTN
NCBI GI g397395
BLAST score 152
E value 3.0e-80
Match length 164
% identity 98
NCBI Description Z.mays MNB1b mRNA for DNA-binding protein

Seq. No. 296332
Seq. ID LIB3088-046-Q1-K1-G5
Method BLASTX
NCBI GI g2736147
BLAST score 150
E value 8.0e-10
Match length 39
% identity 79
NCBI Description (AF021804) fatty acid hydroxylase Fah1p [Arabidopsis thaliana] >gi_3132481 (AC003096) fatty acid hydroxylase, FAH1 [Arabidopsis thaliana]

Seq. No. 296333
Seq. ID LIB3088-046-Q1-K1-H10
Method BLASTX
NCBI GI g2245036
BLAST score 272
E value 6.0e-24
Match length 111
% identity 60
NCBI Description (Z97342) triacylglycerol lipase homolog [Arabidopsis thaliana]

Seq. No. 296334
Seq. ID LIB3088-047-Q1-K1-D2
Method BLASTX
NCBI GI g1574938
BLAST score 235
E value 1.0e-19
Match length 57

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C
E
S
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N
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% identity 81
NCBI Description (U34726) superoxide dismutase 4 [Zea mays]

Seq. No. 296335
Seq. ID LIB3088-047-Q1-K1-D5
Method BLASTX
NCBI GI g927577
BLAST score 154
E value 3.0e-10
Match length 75
% identity 40
NCBI Description (U12927) alpha-galactosidase [Phaseolus vulgaris]

Seq. No. 296336
Seq. ID LIB3088-047-Q1-K1-E9
Method BLASTX
NCBI GI g3785995
BLAST score 510
E value 7.0e-52
Match length 114
% identity 80
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 296337
Seq. ID LIB3088-047-Q1-K1-F3
Method BLASTX
NCBI GI g2632105
BLAST score 405
E value 1.0e-39
Match length 96
% identity 78
NCBI Description (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]
>gi_4539426 emb CAB38959.1 (AL049171) arginyl-tRNA
synthetase [Arabidopsis thaliana]

Seq. No. 296338
Seq. ID LIB3088-047-Q1-K1-H9
Method BLASTX
NCBI GI g2827139
BLAST score 191
E value 6.0e-15
Match length 71
% identity 56
NCBI Description (AF027172) cellulose synthase catalytic subunit
[Arabidopsis thaliana] >gi_4049343 emb CAA22568 (AL034567)
cellulose synthase catalytic subunit (RSW1) [Arabidopsis
thaliana]

Seq. No. 296339
Seq. ID LIB3088-049-Q1-K1-C2
Method BLASTX
NCBI GI g2632252
BLAST score 176
E value 1.0e-12
Match length 52
% identity 63
NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]

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Seq. No.	296340
Seq. ID	LIB3088-049-Q1-K1-E1
Method	BLASTX
NCBI GI	g3927831
BLAST score	203
E value	8.0e-16
Match length	108
% identity	48
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]
Seq. No.	296341
Seq. ID	LIB3088-049-Q1-K1-F5
Method	BLASTX
NCBI GI	g1705585
BLAST score	305
E value	5.0e-28
Match length	96
% identity	69
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE) >gi_82710_pir_JH0667 phosphoenolpyruvate carboxylase (EC 4.1.1.31) C3-form - maize >gi_429149_emb_CAA43709_ (X61489) phosphoenolpyruvate carboxylase [Zea mays]
Seq. No.	296342
Seq. ID	LIB3088-049-Q1-K1-F7
Method	BLASTN
NCBI GI	g2668741
BLAST score	151
E value	1.0e-79
Match length	227
% identity	92
NCBI Description	Zea mays glycine-rich RNA binding protein (GRP) mRNA, complete cds
Seq. No.	296343
Seq. ID	LIB3088-050-Q1-K1-A7
Method	BLASTX
NCBI GI	g3309086
BLAST score	298
E value	4.0e-27
Match length	93
% identity	67
NCBI Description	(AF076253) calcineurin B-like protein 3 [Arabidopsis thaliana]
Seq. No.	296344
Seq. ID	LIB3088-050-Q1-K1-C2
Method	BLASTX
NCBI GI	g729671
BLAST score	200
E value	7.0e-16
Match length	66
% identity	70
NCBI Description	HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]

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Seq. No. 296345
Seq. ID LIB3088-050-Q1-K1-F4
Method BLASTN
NCBI GI g22484
BLAST score 73
E value 7.0e-33
Match length 213
% identity 84
NCBI Description Z.mays RNA for superoxide dismutase Sod4A

Seq. No. 296346
Seq. ID LIB3088-050-Q1-K1-F5
Method BLASTX
NCBI GI g538607
BLAST score 164
E value 3.0e-14
Match length 70
% identity 67
NCBI Description superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 4A - maize
>gi_1885354 (U34727) superoxide dismutase 4A [Zea mays]

Seq. No. 296347
Seq. ID LIB3088-050-Q1-K1-F6
Method BLASTX
NCBI GI g4586265
BLAST score 160
E value 6.0e-11
Match length 105
% identity 34
NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 296348
Seq. ID LIB3088-050-Q1-K1-G10
Method BLASTX
NCBI GI g663070
BLAST score 330
E value 8.0e-31
Match length 96
% identity 76
NCBI Description (X77806) histone H4 [Pyrenomonas salina]

Seq. No. 296349
Seq. ID LIB3088-058-Q1-K1-A2
Method BLASTN
NCBI GI g22356
BLAST score 86
E value 1.0e-40
Match length 186
% identity 87
NCBI Description Maize mRNA for light-harvesting chlorophyll a/b binding protein LHCP

Seq. No. 296350
Seq. ID LIB3088-058-Q1-K1-B4
Method BLASTX
NCBI GI g1346809
BLAST score 258

E value 1.0e-22
Match length 75
% identity 65
NCBI Description PATHOGEN-RELATED PROTEIN >gi_499074_emb_CAA34641_ (X16648)
pathogenesis related protein [Hordeum vulgare]

Seq. No. 296351
Seq. ID LIB3088-058-Q1-K1-B6
Method BLASTX
NCBI GI g3128209
BLAST score 228
E value 2.0e-19
Match length 117
% identity 54
NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]

Seq. No. 296352
Seq. ID LIB3115-001-Q1-K1-B8
Method BLASTX
NCBI GI g461999
BLAST score 156
E value 3.0e-10
Match length 39
% identity 79
NCBI Description ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)

Seq. No. 296353
Seq. ID LIB3115-001-Q1-K1-C8
Method BLASTX
NCBI GI g4504771
BLAST score 318
E value 2.0e-29
Match length 85
% identity 66
NCBI Description integrin beta 4 binding protein
>gi_3122258_sp_P56537_IF6 HUMAN EUKARYOTIC TRANSLATION
INITIATION FACTOR 6 (EIF-6) (B4 INTEGRIN INTERACTOR) (CAB)
>gi_2809383 (AF022229) translation initiation factor 6
[Homo sapiens] >gi_2910997_emb_CAA72243_ (Y11435) b4
integrin interactor [Homo sapiens] >gi_3335506 (AF047433)
b(2)gcn homolog [Homo sapiens]

Seq. No. 296354
Seq. ID LIB3115-001-Q1-K1-D7
Method BLASTN
NCBI GI g531828
BLAST score 43
E value 5.0e-15
Match length 79
% identity 89
NCBI Description Cloning vector pSport1, complete cds

Seq. No. 296355
Seq. ID LIB3115-001-Q1-K1-E3
Method BLASTX
NCBI GI g2827704
BLAST score 200

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E value 2.0e-15
Match length 63
% identity 57
NCBI Description (AL021684) LRR-like protein [Arabidopsis thaliana]

Seq. No. 296356
Seq. ID LIB3115-001-Q1-K1-E6
Method BLASTX
NCBI GI g141597
BLAST score 285
E value 3.0e-36
Match length 150
% identity 62
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 296357
Seq. ID LIB3115-001-Q1-K1-G9
Method BLASTX
NCBI GI g217909
BLAST score 272
E value 4.0e-24
Match length 107
% identity 56
NCBI Description (D14044) glycolate oxidase [Cucurbita sp.]

Seq. No. 296358
Seq. ID LIB3115-002-Q1-K1-A2
Method BLASTX
NCBI GI g2911076
BLAST score 151
E value 1.0e-09
Match length 45
% identity 62
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 296359
Seq. ID LIB3115-002-Q1-K1-B1
Method BLASTN
NCBI GI g2665839
BLAST score 92
E value 3.0e-44
Match length 367
% identity 82
NCBI Description Zea mays putative histone deacetylase RPD3 mRNA, complete cds

Seq. No. 296360
Seq. ID LIB3115-002-Q1-K1-B9
Method BLASTX
NCBI GI g3386621
BLAST score 241
E value 2.0e-20
Match length 62
% identity 71

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NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 296361
Seq. ID LIB3115-002-Q1-K1-F8
Method BLASTX
NCBI GI g2511574
BLAST score 181
E value 3.0e-13
Match length 108
% identity 47
NCBI Description (Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]

Seq. No. 296362
Seq. ID LIB3115-002-Q1-K1-G2
Method BLASTN
NCBI GI g3043528
BLAST score 292
E value 1.0e-163
Match length 353
% identity 98
NCBI Description Zea mays mRNA for flavin containing polyamine oxidase (PAO)

Seq. No. 296363
Seq. ID LIB3115-003-Q1-K1-F9
Method BLASTX
NCBI GI g445612
BLAST score 234
E value 8.0e-20
Match length 90
% identity 53
NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No. 296364
Seq. ID LIB3115-003-Q1-K1-G10
Method BLASTX
NCBI GI g3928150
BLAST score 222
E value 4.0e-18
Match length 66
% identity 61
NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 296365
Seq. ID LIB3115-005-Q1-K1-D12
Method BLASTX
NCBI GI g4185740
BLAST score 444
E value 4.0e-44
Match length 150
% identity 62
NCBI Description (AF079999) putative glutamate receptor [Arabidopsis thaliana]

Seq. No. 296366
Seq. ID LIB3115-005-Q1-K1-F2

Method BLASTX
NCBI GI g1122315
BLAST score 200
E value 8.0e-16
Match length 97
% identity 51
NCBI Description (X94191) heat shock protein 17.0 [Pennisetum glaucum]

Seq. No. 296367
Seq. ID LIB3115-005-Q1-K1-F9
Method BLASTN
NCBI GI g2623247
BLAST score 81
E value 1.0e-37
Match length 157
% identity 98
NCBI Description Zea mays SU1 isoamylase (sugary1) gene, complete cds

Seq. No. 296368
Seq. ID LIB3115-005-Q1-K1-H11
Method BLASTN
NCBI GI g22292
BLAST score 50
E value 2.0e-19
Match length 82
% identity 90
NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 296369
Seq. ID LIB3115-005-Q1-K1-H6
Method BLASTX
NCBI GI g2668742
BLAST score 422
E value 2.0e-41
Match length 86
% identity 95
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 296370
Seq. ID LIB3115-006-Q1-K1-C10
Method BLASTX
NCBI GI g2088647
BLAST score 195
E value 6.0e-20
Match length 98
% identity 54
NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]
>gi_3158394 (AF036340) LRR-containing F-box protein
[Arabidopsis thaliana]

Seq. No. 296371
Seq. ID LIB3115-006-Q1-K1-C2
Method BLASTX
NCBI GI g730588
BLAST score 187
E value 1.0e-14
Match length 64

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% identity 59
NCBI Description MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L5

Seq. No. 296372
Seq. ID LIB3115-006-Q1-K1-C4
Method BLASTX
NCBI GI g4510385
BLAST score 280
E value 7.0e-25
Match length 129
% identity 48
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 296373
Seq. ID LIB3115-006-Q1-K1-D2
Method BLASTX
NCBI GI g4510385
BLAST score 271
E value 7.0e-24
Match length 94
% identity 62
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 296374
Seq. ID LIB3115-006-Q1-K1-E1
Method BLASTX
NCBI GI g4512651
BLAST score 261
E value 1.0e-22
Match length 110
% identity 43
NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No. 296375
Seq. ID LIB3115-006-Q1-K1-F1
Method BLASTN
NCBI GI g1403523
BLAST score 42
E value 7.0e-15
Match length 66
% identity 91
NCBI Description Plasmid pIJ2581 tsr & glkA genes

Seq. No. 296376
Seq. ID LIB3115-006-Q1-K1-G3
Method BLASTN
NCBI GI g22537
BLAST score 86
E value 9.0e-41
Match length 229
% identity 88
NCBI Description Maize mRNA for zein polypeptide (clone M6)

Seq. No. 296377
Seq. ID LIB3115-006-Q1-K1-H3
Method BLASTN

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NCBI GI	g22445
BLAST score	109
E value	2.0e-54
Match length	232
% identity	88
NCBI Description	Zea mays ZMPMS1 gene for 19 kDa zein protein
Seq. No.	296378
Seq. ID	LIB3115-007-Q1-K1-A3
Method	BLASTX
NCBI GI	g4490706
BLAST score	320
E value	9.0e-30
Match length	81
% identity	81
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]
Seq. No.	296379
Seq. ID	LIB3115-007-Q1-K1-G5
Method	BLASTX
NCBI GI	g4455190
BLAST score	143
E value	5.0e-09
Match length	90
% identity	40
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]
Seq. No.	296380
Seq. ID	LIB3115-007-Q1-K1-H5
Method	BLASTN
NCBI GI	g1944204
BLAST score	40
E value	3.0e-13
Match length	56
% identity	93
NCBI Description	Oryza sativa mRNA for RicMT, complete cds
Seq. No.	296381
Seq. ID	LIB3115-008-Q1-K1-A9
Method	BLASTX
NCBI GI	g3860020
BLAST score	245
E value	6.0e-21
Match length	113
% identity	46
NCBI Description	(AF091091) unknown [Homo sapiens]
Seq. No.	296382
Seq. ID	LIB3115-008-Q1-K1-C8
Method	BLASTN
NCBI GI	g1377914
BLAST score	35
E value	9.0e-11
Match length	59
% identity	90
NCBI Description	Cloning vector pEGFP-C1, complete sequence, enhanced green fluorescent protein (egfp) and neomycin phosphotransferase

DRAFT Sequence

genes, complete cds

Seq. No. 296383
Seq. ID LIB3115-008-Q1-K1-D10
Method BLASTX
NCBI GI g3298540
BLAST score 167
E value 4.0e-12
Match length 64
% identity 55
NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]

Seq. No. 296384
Seq. ID LIB3115-008-Q1-K1-D2
Method BLASTX
NCBI GI g82696
BLAST score 238
E value 3.0e-20
Match length 51
% identity 88
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]

Seq. No. 296385
Seq. ID LIB3115-008-Q1-K1-G7
Method BLASTX
NCBI GI g1345881
BLAST score 280
E value 5.0e-25
Match length 98
% identity 56
NCBI Description CYTOCHROME B5 >gi_1076743_pir_S46307 cytochrome b5 - rice >gi_414705_emb_CAA53366_(X75670) cytochrome b5 [Oryza sativa]

Seq. No. 296386
Seq. ID LIB3115-008-Q1-K1-H9
Method BLASTX
NCBI GI g168701
BLAST score 150
E value 1.0e-20
Match length 68
% identity 82
NCBI Description (M60837) zein [Zea mays]

Seq. No. 296387
Seq. ID LIB3115-009-Q1-K1-B2
Method BLASTX
NCBI GI g517500
BLAST score 154
E value 2.0e-10
Match length 75
% identity 56
NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

D E S C R I P T I O N

Seq. No. 296388
Seq. ID LIB3115-009-Q1-K1-B7
Method BLASTX
NCBI GI g4539002
BLAST score 200
E value 1.0e-15
Match length 75
% identity 59
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 296389
Seq. ID LIB3115-009-Q1-K1-D3
Method BLASTN
NCBI GI g559535
BLAST score 207
E value 1.0e-113
Match length 307
% identity 92
NCBI Description Z.mays mRNA for metallothionein

Seq. No. 296390
Seq. ID LIB3115-009-Q1-K1-E12
Method BLASTN
NCBI GI g168704
BLAST score 72
E value 1.0e-32
Match length 128
% identity 89
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 296391
Seq. ID LIB3115-009-Q1-K1-F1
Method BLASTX
NCBI GI g2832243
BLAST score 222
E value 4.0e-18
Match length 106
% identity 55
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 296392
Seq. ID LIB3115-009-Q1-K1-F10
Method BLASTX
NCBI GI g520570
BLAST score 438
E value 2.0e-43
Match length 119
% identity 71
NCBI Description (U12315) peroxidase [Cenchrus ciliaris]

Seq. No. 296393
Seq. ID LIB3115-009-Q1-K1-G4
Method BLASTX
NCBI GI g531829
BLAST score 158
E value 1.0e-10
Match length 78

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% identity 40
NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No. 296394
Seq. ID LIB3115-010-Q1-K1-A1
Method BLASTN
NCBI GI g397395
BLAST score 97
E value 2.0e-47
Match length 157
% identity 90
NCBI Description Z.mays MNBlb mRNA for DNA-binding protein

Seq. No. 296395
Seq. ID LIB3115-010-Q1-K1-C1
Method BLASTX
NCBI GI g1173275
BLAST score 204
E value 1.0e-18
Match length 88
% identity 64
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
>gi_2119068_pir_S58630 ribosomal protein S7 - maize
chloroplast >gi_902274_emb_CAA60339 (X86563) ribosomal
protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563)
ribosomal protein S7 [Zea mays]

Seq. No. 296396
Seq. ID LIB3115-010-Q1-K1-C12
Method BLASTN
NCBI GI g998429
BLAST score 51
E value 3.0e-20
Match length 67
% identity 94
NCBI Description GRF1=general regulatory factor [Zea mays, XL80, Genomic,
5348 nt]

Seq. No. 296397
Seq. ID LIB3115-010-Q1-K1-C2
Method BLASTX
NCBI GI g2668742
BLAST score 284
E value 1.0e-25
Match length 81
% identity 73
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 296398
Seq. ID LIB3115-010-Q1-K1-E12
Method BLASTN
NCBI GI g998429
BLAST score 79
E value 1.0e-36
Match length 244
% identity 83

SEQUENCE DATA

NCBI Description GRF1=general regulatory factor [Zea mays, XL80, Genomic, 5348 nt]

Seq. No. 296399
Seq. ID LIB3115-010-Q1-K1-F4
Method BLASTX
NCBI GI g82733
BLAST score 330
E value 8.0e-31
Match length 102
% identity 70
NCBI Description ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937)
ubiquitin fusion protein [Zea mays] >gi_902527 (U29161)
ubiquitin fusion protein [Zea mays]
>gi_1589388_prf_2211240B ubiquitin fusion protein [Zea mays]

Seq. No. 296400
Seq. ID LIB3115-010-Q1-K1-G1
Method BLASTN
NCBI GI g454880
BLAST score 62
E value 3.0e-26
Match length 92
% identity 92
NCBI Description Rice mRNA for WSI724 protein induced by water stress, complete cds

Seq. No. 296401
Seq. ID LIB3115-010-Q1-K1-G12
Method BLASTX
NCBI GI g2947070
BLAST score 155
E value 9.0e-11
Match length 55
% identity 58
NCBI Description (AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 296402
Seq. ID LIB3115-010-Q1-K1-H11
Method BLASTN
NCBI GI g1673455
BLAST score 40
E value 1.0e-13
Match length 56
% identity 93
NCBI Description Z.mays rubisco small subunit gene

Seq. No. 296403
Seq. ID LIB3115-010-Q1-K1-H3
Method BLASTX
NCBI GI g141603
BLAST score 269
E value 9.0e-24
Match length 80
% identity 70

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NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 296404
Seq. ID LIB3115-011-Q1-K1-C7
Method BLASTN
NCBI GI g168579
BLAST score 219
E value 1.0e-120
Match length 275
% identity 95
NCBI Description Maize pyruvate,orthophosphate dikinase mRNA, complete cds

Seq. No. 296405
Seq. ID LIB3115-011-Q1-K1-E3
Method BLASTX
NCBI GI g551047
BLAST score 413
E value 8.0e-41
Match length 97
% identity 80
NCBI Description (X79277) type II LHCI [Lolium temulentum]

Seq. No. 296406
Seq. ID LIB3115-011-Q1-K1-H3
Method BLASTX
NCBI GI g1778141
BLAST score 275
E value 1.0e-24
Match length 99
% identity 55
NCBI Description (U66321) phosphate/phosphoenolpyruvate translocator precursor; PPT [Arabidopsis thaliana]

Seq. No. 296407
Seq. ID LIB3115-012-Q1-K1-C3
Method BLASTX
NCBI GI g1237250
BLAST score 222
E value 2.0e-18
Match length 82
% identity 50
NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum]

Seq. No. 296408
Seq. ID LIB3115-012-Q1-K1-C6
Method BLASTX
NCBI GI g2738248
BLAST score 298
E value 4.0e-27
Match length 95
% identity 63
NCBI Description (U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No. 296409

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Seq. ID	LIB3115-012-Q1-K1-D10
Method	BLASTN
NCBI GI	g3355716
BLAST score	154
E value	3.0e-81
Match length	191
% identity	95
NCBI Description	Zea mays mRNA for seryl-tRNA synthetase
Seq. No.	296410
Seq. ID	LIB3115-012-Q1-K1-F6
Method	BLASTX
NCBI GI	g629862
BLAST score	260
E value	1.0e-22
Match length	121
% identity	51
NCBI Description	zein Zd1, 19K - maize >gi_535021_emb_CAA47640_ (X67203) zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.	296411
Seq. ID	LIB3115-013-P1-K1-A4
Method	BLASTX
NCBI GI	g2832247
BLAST score	179
E value	3.0e-13
Match length	82
% identity	51
NCBI Description	(AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.	296412
Seq. ID	LIB3115-013-P1-K1-C11
Method	BLASTX
NCBI GI	g2564920
BLAST score	178
E value	4.0e-13
Match length	50
% identity	70
NCBI Description	(AF025951) heat-shock cognate protein 70; Hsc70 [Dictyostelium discoideum]
Seq. No.	296413
Seq. ID	LIB3115-013-P1-K1-D9
Method	BLASTX
NCBI GI	g4098880
BLAST score	312
E value	8.0e-29
Match length	72
% identity	85
NCBI Description	(U80970) heat shock protein 70B/SSB1 [Pneumocystis carinii f. sp. hominis]
Seq. No.	296414
Seq. ID	LIB3115-013-P1-K1-E5
Method	BLASTX
NCBI GI	g168586
BLAST score	226

E value 3.0e-19
Match length 56
% identity 80
NCBI Description (M58656) pyruvate,orthophosphate dikinase [Zea mays]

Seq. No. 296415
Seq. ID LIB3115-013-P1-K1-E9
Method BLASTX
NCBI GI g1723506
BLAST score 242
E value 2.0e-20
Match length 121
% identity 40
NCBI Description HYPOTHETICAL PROTEIN C19G10.16 IN CHROMOSOME I
>gi_1216256_emb_CAA93798_ (Z69909) hypothetical protein
[Schizosaccharomyces pombe]

Seq. No. 296416
Seq. ID LIB3115-013-P1-K1-F7
Method BLASTX
NCBI GI g4206306
BLAST score 590
E value 2.0e-61
Match length 119
% identity 94
NCBI Description (AF049110) prpol [Zea mays]

Seq. No. 296417
Seq. ID LIB3115-013-P1-K1-F8
Method BLASTX
NCBI GI g82660
BLAST score 211
E value 2.0e-17
Match length 62
% identity 68
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 296418
Seq. ID LIB3115-013-P1-K1-F9
Method BLASTX
NCBI GI g2506443
BLAST score 338
E value 1.0e-31
Match length 78
% identity 87
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
CHLOROPLAST >gi_2117520_pir_ JQ1285
glyceraldehyde-3-phosphate dehydrogenase (NADP+)
(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
3-phosphate dehydrogenase [Arabidopsis thaliana]
>gi_1402885_emb_CAA66816_ (X98130)
glyceraldehyde-3-phosphate dehydrogenase (NADP+)
(phosphorylating) [Arabidopsis thaliana]

Seq. No. 296419

DRAFT Sequence

Seq. ID LIB3115-014-P1-K1-B3
Method BLASTX
NCBI GI g115779
BLAST score 293
E value 4.0e-27
Match length 99
% identity 67
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_81772_pir_JA0179 chlorophyll a/b-binding protein precursor - soybean (fragment) >gi_169933 (M21396) chlorophyll a/b-binding protein precursor [Glycine max]

Seq. No. 296420
Seq. ID LIB3115-014-P1-K1-B5
Method BLASTX
NCBI GI g2832246
BLAST score 218
E value 1.0e-17
Match length 103
% identity 50
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 296421
Seq. ID LIB3115-014-P1-K1-B9
Method BLASTN
NCBI GI g236729
BLAST score 54
E value 1.0e-21
Match length 70
% identity 94
NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]

Seq. No. 296422
Seq. ID LIB3115-014-P1-K1-C12
Method BLASTX
NCBI GI g20733
BLAST score 226
E value 3.0e-19
Match length 66
% identity 73
NCBI Description (X15188) precursor C-terminal fragment (AA -80 to 367) [Pisum sativum]

Seq. No. 296423
Seq. ID LIB3115-014-P1-K1-C8
Method BLASTX
NCBI GI g4106577
BLAST score 206
E value 4.0e-16
Match length 76
% identity 57
NCBI Description (AL031866) ORF10, len: 268 aa, hutG, highly similar to N-formylglutamate amidohydrolase, from Pseudomonas putida AF032970_3, Fasta scores: opt: 1057, E(): 0, 59.6% identity in 260 aa overlap [Yersinia pestis]

Seq. No. 296424

DDBJ/EMBL/GenBank

Seq. ID	LIB3115-014-P1-K1-D10
Method	BLASTN
NCBI GI	g2645165
BLAST score	49
E value	1.0e-18
Match length	73
% identity	92
NCBI Description	Oryza sativa mRNA, similar to ribosomal protein
Seq. No.	296425
Seq. ID	LIB3115-014-P1-K1-D3
Method	BLASTX
NCBI GI	g1723177
BLAST score	215
E value	2.0e-17
Match length	82
% identity	50
NCBI Description	HYPOTHETICAL 13.8 KD PROTEIN SLR0709 >gi_1361332_pir_S56682 hypothetical protein 2 - Synechocystis sp >gi_1006602_dbj_BAA10755_ (D64005) hypothetical protein [Synechocystis sp.] >gi_1006750_emb_CAA54600_ (X77454) ORF2 [Synechocystis sp.]
Seq. No.	296426
Seq. ID	LIB3115-014-P1-K1-E5
Method	BLASTN
NCBI GI	g3819345
BLAST score	62
E value	3.0e-26
Match length	218
% identity	82
NCBI Description	Hordeum vulgare genomic DNA fragment; clone MWG0803
Seq. No.	296427
Seq. ID	LIB3115-015-P1-K1-C4
Method	BLASTN
NCBI GI	g532622
BLAST score	38
E value	6.0e-12
Match length	165
% identity	91
NCBI Description	Zea mays lipase (LIP) mRNA, complete cds
Seq. No.	296428
Seq. ID	LIB3115-015-P1-K1-F11
Method	BLASTN
NCBI GI	g22548
BLAST score	54
E value	4.0e-22
Match length	58
% identity	98
NCBI Description	Maize chimeric zein/beta-phaseolin gene 3'end region
Seq. No.	296429
Seq. ID	LIB3115-015-P1-K1-F4
Method	BLASTX
NCBI GI	g2262105

BLAST score 195
 E value 6.0e-15
 Match length 61
 % identity 61
 NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 296430
 Seq. ID LIB3115-015-P1-K1-F5
 Method BLASTX
 NCBI GI g542176
 BLAST score 252
 E value 1.0e-21
 Match length 111
 % identity 51
 NCBI Description probable finger protein WZF1 - wheat
 >gi_485814_dbj_BAA03901_ (D16415) WZF1 [Triticum aestivum]
 >gi_485816_dbj_BAA03902_ (D16416) WZF1 [Triticum aestivum]

Seq. No. 296431
 Seq. ID LIB3115-015-P1-K1-G1
 Method BLASTX
 NCBI GI g112994
 BLAST score 212
 E value 1.0e-17
 Match length 46
 % identity 91
 NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
 >gi_82685_pir_S04536 embryonic abundant protein,
 glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
 ABA-inducible gene protein [Zea mays]
 >gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 296432
 Seq. ID LIB3115-016-P1-K1-B4
 Method BLASTX
 NCBI GI g4455232
 BLAST score 236
 E value 3.0e-21
 Match length 88
 % identity 60
 NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 296433
 Seq. ID LIB3115-016-P1-K1-D12
 Method BLASTX
 NCBI GI g2145477
 BLAST score 229
 E value 1.0e-26
 Match length 123
 % identity 58
 NCBI Description (X91406) phosphoenolpyruvate carboxylase [Tillandsia usneoides]

Seq. No. 296434
 Seq. ID LIB3115-016-P1-K1-F5
 Method BLASTX

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NCBI GI	g2612826
BLAST score	181
E value	2.0e-13
Match length	57
% identity	68
NCBI Description	(AJ002731) ribosomal protein s30 [Schizosaccharomyces pombe] >gi_4581509_emb_CAA17057.2_ (AL021839) ribosomal protein s30 [Schizosaccharomyces pombe]
Seq. No.	296435
Seq. ID	LIB3115-017-P1-K1-A8
Method	BLASTN
NCBI GI	g168436
BLAST score	56
E value	6.0e-23
Match length	60
% identity	98
NCBI Description	Zea mays catalase (Cat3) gene, complete cds
Seq. No.	296436
Seq. ID	LIB3115-017-P1-K1-C1
Method	BLASTX
NCBI GI	g1710752
BLAST score	217
E value	1.0e-17
Match length	102
% identity	45
NCBI Description	PROBABLE 40S RIBOSOMAL PROTEIN S25 >gi_1118105 (U41558) coded for by C. elegans cDNA CEMSA31R; coded for by C. elegans cDNA yk116e4.5; coded for by C. elegans cDNA yk94b11.5; coded for by C. elegans cDNA yk90d1.5; coded for by C. elegans cDNA CEESK93F; coded for by C. elegans cDNA yk94b1
Seq. No.	296437
Seq. ID	LIB3115-017-P1-K1-D3
Method	BLASTX
NCBI GI	g4582468
BLAST score	188
E value	3.0e-14
Match length	65
% identity	58
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
Seq. No.	296438
Seq. ID	LIB3115-017-P1-K1-E11
Method	BLASTN
NCBI GI	g3550984
BLAST score	71
E value	1.0e-31
Match length	151
% identity	87
NCBI Description	Oryza sativa mRNA for OsS5a, complete cds
Seq. No.	296439
Seq. ID	LIB3115-017-P1-K1-E4

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Method	BLASTX
NCBI GI	g1835731
BLAST score	195
E value	6.0e-15
Match length	72
% identity	56
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.	296440
Seq. ID	LIB3115-017-P1-K1-E5
Method	BLASTX
NCBI GI	g1709619
BLAST score	214
E value	3.0e-17
Match length	75
% identity	64
NCBI Description	PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) / DOLICHYL-DIPHOSPHOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP) >gi_2146814_pir_S69181 protein disulfide isomerase (EC 5.3.4.1) precursor - maize >gi_625148 (L39014) protein disulfide isomerase [Zea mays]
Seq. No.	296441
Seq. ID	LIB3115-018-P1-K1-A6
Method	BLASTX
NCBI GI	g3522929
BLAST score	438
E value	1.0e-43
Match length	97
% identity	84
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No.	296442
Seq. ID	LIB3115-018-P1-K1-A7
Method	BLASTX
NCBI GI	g3522929
BLAST score	165
E value	1.0e-11
Match length	46
% identity	72
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No.	296443
Seq. ID	LIB3115-018-P1-K1-B7
Method	BLASTX
NCBI GI	g2827992
BLAST score	273
E value	4.0e-24
Match length	89
% identity	54
NCBI Description	(AF034743) UDP-glucuronosyltransferase [Pisum sativum]

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Seq. No.	296444
Seq. ID	LIB3115-018-P1-K1-F10
Method	BLASTN
NCBI GI	g3450892
BLAST score	55
E value	3.0e-22
Match length	75
% identity	93
NCBI Description	Avena fatua ras-like small monomeric GTP-binding protein (SAR1) mRNA, complete cds
Seq. No.	296445
Seq. ID	LIB3115-018-P1-K1-G8
Method	BLASTX
NCBI GI	g4455254
BLAST score	154
E value	3.0e-10
Match length	72
% identity	49
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]
Seq. No.	296446
Seq. ID	LIB3115-019-P1-K1-C8
Method	BLASTX
NCBI GI	g1750404
BLAST score	169
E value	6.0e-12
Match length	60
% identity	52
NCBI Description	(U80953) Similar to 40S ribosomal protein S29; coded for by C. elegans cDNA cm10c2; coded for by C. elegans cDNA yk61d8.5; coded for by C. elegans cDNA yk107e8.5; coded for by C. elegans cDNA CEESF55F; coded for by C. elegans cDNA yk107e8.3;
Seq. No.	296447
Seq. ID	LIB3115-020-P1-K1-A2
Method	BLASTX
NCBI GI	g551047
BLAST score	215
E value	8.0e-18
Match length	58
% identity	72
NCBI Description	(X79277) type II LHCI [Lolium temulentum]
Seq. No.	296448
Seq. ID	LIB3115-020-P1-K1-B7
Method	BLASTX
NCBI GI	g2149640
BLAST score	210
E value	3.0e-17
Match length	65
% identity	63
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No.	296449
Seq. ID	LIB3115-020-P1-K1-B8

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Method BLASTX
NCBI GI g730536
BLAST score 164
E value 2.0e-11
Match length 76
% identity 46
NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal protein subunit L17 [Nicotiana tabacum]

Seq. No. 296450
Seq. ID LIB3115-020-P1-K1-D5
Method BLASTX
NCBI GI g2494417
BLAST score 254
E value 4.0e-22
Match length 75
% identity 72
NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_1364071_pir_S57717 fructose-1, 6-bisphosphatase (EC 3.1.3.11) - sugarcane hybrid H65-7052 >gi_895909_emb_CAA61409.1 (X89006) fructose-1, 6-bisphosphatase [Saccharum hybrid cultivar H65-7052]

Seq. No. 296451
Seq. ID LIB3115-020-P1-K1-E5
Method BLASTN
NCBI GI g2431766
BLAST score 115
E value 7.0e-58
Match length 190
% identity 92
NCBI Description Zea mays acidic ribosomal protein P3a (rpp3a) mRNA, complete cds

Seq. No. 296452
Seq. ID LIB3115-021-P1-K1-C5
Method BLASTX
NCBI GI g266578
BLAST score 241
E value 2.0e-20
Match length 56
% identity 77
NCBI Description METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir_S17560 metallothionein-like protein - maize >gi_236730_bbs_57629 (S57628) metallothionein homologue [Zea mays, Peptide, 76 aa] [Zea mays] >gi_559536_emb_CAA57676 (X82186) metallothionein- like protein [Zea mays] >gi_228095_prf_1717215A metallothionein-like protein [Zea mays]

Seq. No. 296453
Seq. ID LIB3115-021-P1-K1-D9
Method BLASTX
NCBI GI g3080425
BLAST score 287
E value 6.0e-26

Match length 71
% identity 83
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 296454
Seq. ID LIB3115-021-P1-K1-G9
Method BLASTX
NCBI GI g3914465
BLAST score 187
E value 3.0e-14
Match length 83
% identity 54
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
(LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
>gi_2981207 (AF052076) photosystem I complex PsaH subunit
precursor [Zea mays]

Seq. No. 296455
Seq. ID LIB3115-021-P1-K1-H1
Method BLASTX
NCBI GI g115786
BLAST score 231
E value 2.0e-19
Match length 61
% identity 79
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
(CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding
protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
mays]

Seq. No. 296456
Seq. ID LIB3115-021-P1-K1-H3
Method BLASTX
NCBI GI g2827548
BLAST score 409
E value 4.0e-40
Match length 131
% identity 56
NCBI Description (AL021635) cytochrome P450 - like protein [Arabidopsis
thaliana]

Seq. No. 296457
Seq. ID LIB3115-022-P1-K1-C2
Method BLASTX
NCBI GI g2911043
BLAST score 176
E value 8.0e-13
Match length 75
% identity 43
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 296458
Seq. ID LIB3115-022-P1-K1-E9
Method BLASTX
NCBI GI g166410
BLAST score 379
E value 1.0e-36

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Match length	112
% identity	66
NCBI Description	(L07291) Alfin-1 [Medicago sativa]
Seq. No.	296459
Seq. ID	LIB3115-023-P1-K1-B8
Method	BLASTX
NCBI GI	g485518
BLAST score	312
E value	6.0e-29
Match length	60
% identity	100
NCBI Description	ubiquitin / ribosomal protein CEP52 - rice >gi_303857_dbj_BAA02154 (D12629) ubiquitin/ribosomal polyprotein [Oryza sativa]
Seq. No.	296460
Seq. ID	LIB3115-023-P1-K1-E10
Method	BLASTX
NCBI GI	g4115913
BLAST score	150
E value	3.0e-10
Match length	61
% identity	43
NCBI Description	(AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=307,1, E=2.2e-88, N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_(AL049524) putative flavanone 3-beta-hydroxylase [Arabidopsis thaliana]
Seq. No.	296461
Seq. ID	LIB3115-023-P1-K1-G2
Method	BLASTN
NCBI GI	g168436
BLAST score	61
E value	7.0e-26
Match length	111
% identity	90
NCBI Description	Zea mays catalase (Cat3) gene, complete cds
Seq. No.	296462
Seq. ID	LIB3115-023-P1-K1-H10
Method	BLASTX
NCBI GI	g4506621
BLAST score	157
E value	4.0e-11
Match length	49
% identity	63
NCBI Description	ribosomal protein L26 >gi_400990_sp_Q02877_RL26_HUMAN 60S RIBOSOMAL PROTEIN L26 >gi_423068_pir_S33713 ribosomal protein L26 - human >gi_1071990_pir_S48864 gene L26 protein - mouse >gi_36115_emb_CAA49189_(X69392) ribosomal protein L26 [Homo sapiens] >gi_565624_emb_CAA56716_(X80699) L26 [Mus musculus]
Seq. No.	296463
Seq. ID	LIB3115-024-P1-K1-A11

Method BLASTX
NCBI GI g3256035
BLAST score 151
E value 8.0e-10
Match length 53
% identity 51
NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No. 296464
Seq. ID LIB3115-024-P1-K1-A9
Method BLASTX
NCBI GI g3327033
BLAST score 284
E value 2.0e-25
Match length 79
% identity 71
NCBI Description (Z68198) 40S ribosomal protein [Schizosaccharomyces pombe]

Seq. No. 296465
Seq. ID LIB3115-024-P1-K1-E10
Method BLASTX
NCBI GI g544421
BLAST score 159
E value 1.0e-10
Match length 39
% identity 85
NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 1 >gi_485420_pir_S12311 glycine-rich RNA-binding protein (clone S1) - sorghum (fragment) >gi_21623_emb_CAA40863_ (X57663) glycine-rich RNA-binding protein [Sorghum bicolor]

Seq. No. 296466
Seq. ID LIB3115-025-P1-K1-B12
Method BLASTX
NCBI GI g4559358
BLAST score 176
E value 1.0e-12
Match length 50
% identity 68
NCBI Description (AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No. 296467
Seq. ID LIB3115-025-P1-K1-B3
Method BLASTN
NCBI GI g1272684
BLAST score 50
E value 4.0e-19
Match length 62
% identity 97
NCBI Description Z.mays mRNA for acetyl CoA carboxylase (partial)

Seq. No. 296468
Seq. ID LIB3115-025-P1-K1-B6
Method BLASTX
NCBI GI g4574320

Q9E3D0 E1 D0 C0

BLAST score	164
E value	3.0e-11
Match length	67
% identity	57
NCBI Description	(AF117224) wound-induced protein WI12 [Mesembryanthemum crystallinum]
Seq. No.	296469
Seq. ID	LIB3115-025-P1-K1-C8
Method	BLASTX
NCBI GI	g3122625
BLAST score	260
E value	6.0e-23
Match length	90
% identity	59
NCBI Description	PROBABLE 26S PROTEASE REGULATORY SUBUNIT S10B >gi_2394434 (AF024493) strong similarity to the AAA family of ATPases [Caenorhabditis elegans]
Seq. No.	296470
Seq. ID	LIB3115-025-P1-K1-F6
Method	BLASTX
NCBI GI	g466172
BLAST score	173
E value	2.0e-12
Match length	34
% identity	100
NCBI Description	GTP-BINDING PROTEIN YPTM2 >gi_283056_pir_B38202 ypt family - maize >gi_287835_emb_CAA44919_ (X63278) yptm2 [Zea mays]
Seq. No.	296471
Seq. ID	LIB3115-026-P1-K1-A11
Method	BLASTX
NCBI GI	g1352681
BLAST score	473
E value	1.0e-47
Match length	113
% identity	80
NCBI Description	PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir_S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi_633028_dbj_BAA07287_ (D38109) protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	296472
Seq. ID	LIB3115-026-P1-K1-A2
Method	BLASTN
NCBI GI	g1935910
BLAST score	175
E value	8.0e-94
Match length	247
% identity	93
NCBI Description	Zea mays lethal leaf-spot 1 (lls1) gene, partial cds
Seq. No.	296473
Seq. ID	LIB3115-026-P1-K1-H2
Method	BLASTN
NCBI GI	g170784

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BLAST score	35
E value	4.0e-10
Match length	59
% identity	90
NCBI Description	Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds
Seq. No.	296474
Seq. ID	LIB3115-026-P1-K1-H3
Method	BLASTX
NCBI GI	g548603
BLAST score	345
E value	1.0e-32
Match length	106
% identity	70
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir_JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.	296475
Seq. ID	LIB3115-028-P1-K1-A6
Method	BLASTN
NCBI GI	g22312
BLAST score	117
E value	3.0e-59
Match length	177
% identity	92
NCBI Description	Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)
Seq. No.	296476
Seq. ID	LIB3115-028-P1-K1-B10
Method	BLASTX
NCBI GI	g4099090
BLAST score	219
E value	3.0e-18
Match length	63
% identity	63
NCBI Description	(U83178) unknown [Arabidopsis thaliana]
Seq. No.	296477
Seq. ID	LIB3115-028-P1-K1-B4
Method	BLASTX
NCBI GI	g4335745
BLAST score	275
E value	2.0e-24
Match length	133
% identity	41
NCBI Description	(AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]
Seq. No.	296478
Seq. ID	LIB3115-028-P1-K1-D8
Method	BLASTX
NCBI GI	g1173071
BLAST score	303

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E value 1.0e-27
Match length 113
% identity 60
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P2 (MINOR ALLERGEN ALT A 6)
(ALT A VI) >gi_1085614_pir_S43109 acidic ribosomal protein
P2 - Alternaria alternata >gi_467617_emb_CAA55066_ (X78222)
minor allergen, ribosomal protein [Alternaria alternata]

Seq. No. 296479
Seq. ID LIB3115-028-P1-K1-E3
Method BLASTX
NCBI GI g2245138
BLAST score 542
E value 1.0e-55
Match length 136
% identity 71
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 296480
Seq. ID LIB3115-028-P1-K1-F12
Method BLASTX
NCBI GI g2507443
BLAST score 221
E value 2.0e-18
Match length 72
% identity 62
NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) (23
KD CALLUS PROTEIN) (P23) >gi_1675196 (L47968) callus
protein P23 [Pisum sativum]

Seq. No. 296481
Seq. ID LIB3115-028-P1-K1-G3
Method BLASTN
NCBI GI g2331140
BLAST score 43
E value 5.0e-15
Match length 109
% identity 85
NCBI Description Oryza sativa water-stress inducible protein (WSI) mRNA,
complete cds

Seq. No. 296482
Seq. ID LIB3115-028-P1-K1-H8
Method BLASTX
NCBI GI g141608
BLAST score 293
E value 1.0e-26
Match length 94
% identity 67
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19.kDa
zein [Zea mays]

Seq. No. 296483
Seq. ID LIB3115-029-P1-K1-F7
Method BLASTX
NCBI GI g2459430

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BLAST score 224
E value 2.0e-18
Match length 91
% identity 48
NCBI Description (AC002332) putative CUC2 protein [Arabidopsis thaliana]

Seq. No. 296484
Seq. ID LIB3115-030-P1-K1-A10
Method BLASTX
NCBI GI g4204265
BLAST score 168
E value 1.0e-11
Match length 66
% identity 47
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 296485
Seq. ID LIB3115-030-P1-K1-A12
Method BLASTX
NCBI GI g2245066
BLAST score 166
E value 8.0e-12
Match length 80
% identity 45
NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 296486
Seq. ID LIB3115-030-P1-K1-A4
Method BLASTX
NCBI GI g2982297
BLAST score 209
E value 1.0e-16
Match length 69
% identity 62
NCBI Description (AF051233) KIAA0107-like protein [Picea mariana]

Seq. No. 296487
Seq. ID LIB3115-030-P1-K1-B12
Method BLASTN
NCBI GI g2668739
BLAST score 64
E value 2.0e-27
Match length 152
% identity 86
NCBI Description Zea mays translation initiation factor GOS2 (TIF) mRNA, complete cds

Seq. No. 296488
Seq. ID LIB3115-030-P1-K1-B4
Method BLASTX
NCBI GI g2245066
BLAST score 203
E value 3.0e-16
Match length 85
% identity 44
NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

0953401101000

Seq. No.	296489
Seq. ID	LIB3115-030-P1-K1-C5
Method	BLASTX
NCBI GI	g2781345
BLAST score	245
E value	5.0e-21
Match length	80
% identity	55
NCBI Description	(AC003113) F24O1.2 [Arabidopsis thaliana]
Seq. No.	296490
Seq. ID	LIB3115-030-P1-K1-D6
Method	BLASTX
NCBI GI	g445612
BLAST score	192
E value	1.0e-14
Match length	73
% identity	53
NCBI Description	ribosomal protein S19 [Solanum tuberosum]
Seq. No.	296491
Seq. ID	LIB3115-030-P1-K1-E1
Method	BLASTX
NCBI GI	g120657
BLAST score	155
E value	3.0e-10
Match length	67
% identity	51
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_66024_pir_DEZMG3 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - maize >gi_168479 (M18976) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi_763035_emb_CAA33455 (X15408) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.	296492
Seq. ID	LIB3115-030-P1-K1-F10
Method	BLASTX
NCBI GI	g548774
BLAST score	220
E value	8.0e-18
Match length	118
% identity	65
NCBI Description	60S RIBOSOMAL PROTEIN L7A >gi_542158_pir_S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631) ribosomal protein L7A [Oryza sativa]
Seq. No.	296493
Seq. ID	LIB3115-030-P1-K1-F7
Method	BLASTX
NCBI GI	g68029
BLAST score	390
E value	1.0e-37
Match length	105
% identity	72
NCBI Description	phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize

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>gi_22408_emb_CAA33317_ (X15239) PEP carboxylase [Zea mays]
>gi_228619_prf_1807332A phosphoenolpyruvate carboxylase
[Zea mays]

Seq. No. 296494
Seq. ID LIB3115-030-P1-K1-H7
Method BLASTX
NCBI GI g2267595
BLAST score 181
E value 3.0e-13
Match length 52
% identity 65
NCBI Description (AF009412) plastocyanin precursor [Oryza sativa]

Seq. No. 296495
Seq. ID LIB3115-031-P1-K1-A12
Method BLASTX
NCBI GI g2944417
BLAST score 304
E value 1.0e-27
Match length 88
% identity 64
NCBI Description (AF049881) peroxidase FLXPER4 [Linum usitatissimum]

Seq. No. 296496
Seq. ID LIB3115-031-P1-K1-G2
Method BLASTX
NCBI GI g1171866
BLAST score 158
E value 9.0e-11
Match length 54
% identity 57
NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR
(COMPLEX I-20KD) (CI-20KD) >gi_629601_pir_S48826 NADH
dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild
cabbage >gi_562282_emb_CAA57725_ (X82274) PSST subunit of
NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No. 296497
Seq. ID LIB3115-031-P1-K1-G3
Method BLASTX
NCBI GI g3059131
BLAST score 259
E value 2.0e-22
Match length 94
% identity 50
NCBI Description (AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No. 296498
Seq. ID LIB3115-032-P1-K1-D11
Method BLASTN
NCBI GI g2326946
BLAST score 65
E value 5.0e-28
Match length 125
% identity 88
NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29

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Seq. No. 296499
Seq. ID LIB3115-032-P1-K1-D5
Method BLASTX
NCBI GI g4220594
BLAST score 229
E value 6.0e-19
Match length 96
% identity 47
NCBI Description (AB011264) nicochianamine synthase 3 [Hordeum vulgare]

Seq. No. 296500
Seq. ID LIB3115-034-P1-K2-A1
Method BLASTX
NCBI GI g168701
BLAST score 369
E value 2.0e-35
Match length 100
% identity 80
NCBI Description (M60837) zein [Zea mays]

Seq. No. 296501
Seq. ID LIB3115-034-P1-K2-A2
Method BLASTN
NCBI GI g168700
BLAST score 62
E value 2.0e-26
Match length 152
% identity 85
NCBI Description Z.mays zein mRNA, complete cds

Seq. No. 296502
Seq. ID LIB3115-034-P1-K2-C5
Method BLASTN
NCBI GI g168521
BLAST score 44
E value 1.0e-15
Match length 84
% identity 88
NCBI Description Maize glyceraldehyde-3-phosphate dehydrogenase, 3' end

Seq. No. 296503
Seq. ID LIB3115-034-P1-K2-D5
Method BLASTX
NCBI GI g100907
BLAST score 285
E value 1.0e-25
Match length 91
% identity 63
NCBI Description pathogenesis-related protein 1 - maize
>gi_228409_prf_1803521A pathogenesis-related protein 1
[Zea mays]

Seq. No. 296504
Seq. ID LIB3115-034-P1-K2-D7
Method BLASTX
NCBI GI g3928519

BIOLOGICAL ASPECTS

BLAST score	154
E value	1.0e-10
Match length	45
% identity	69
NCBI Description	(AB011670) wpk4 protein kinase [Triticum aestivum]
Seq. No.	296505
Seq. ID	LIB3115-034-P1-K2-E4
Method	BLASTN
NCBI GI	g248336
BLAST score	99
E value	2.0e-48
Match length	247
% identity	89
NCBI Description	polyubiquitin [maize, Genomic, 3841 nt]
Seq. No.	296506
Seq. ID	LIB3115-034-P1-K2-G7
Method	BLASTX
NCBI GI	g1350930
BLAST score	375
E value	3.0e-36
Match length	96
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN S13
Seq. No.	296507
Seq. ID	LIB3115-036-P1-K2-B3
Method	BLASTX
NCBI GI	g2708745
BLAST score	458
E value	6.0e-46
Match length	114
% identity	79
NCBI Description	(AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]
Seq. No.	296508
Seq. ID	LIB3115-036-P1-K2-C1
Method	BLASTX
NCBI GI	g3820648
BLAST score	143
E value	2.0e-09
Match length	56
% identity	55
NCBI Description	(Y12636) allene oxide synthase [Arabidopsis thaliana]
Seq. No.	296509
Seq. ID	LIB3115-036-P1-K2-C12
Method	BLASTN
NCBI GI	g606814
BLAST score	195
E value	1.0e-105
Match length	319
% identity	91
NCBI Description	Zea mays Golden Bantam carbonic anhydrase mRNA, complete cds

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Seq. No.	296510
Seq. ID	LIB3115-038-P1-K2-G5
Method	BLASTX
NCBI GI	g2739387
BLAST score	202
E value	8.0e-16
Match length	125
% identity	36
NCBI Description	(AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.	296511
Seq. ID	LIB3115-038-P1-K2-H10
Method	BLASTX
NCBI GI	g131147
BLAST score	337
E value	8.0e-32
Match length	99
% identity	64
NCBI Description	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 >gi_72675_pir_A2LVP7 photosystem I P700 apoprotein A2 - liverwort (<i>Marchantia polymorpha</i>) chloroplast >gi_11671_emb_CAA28084_ (X04465) psaB [<i>Marchantia polymorpha</i>]
Seq. No.	296512
Seq. ID	LIB3115-039-P1-K2-B1
Method	BLASTX
NCBI GI	g1076653
BLAST score	144
E value	5.0e-09
Match length	62
% identity	45
NCBI Description	water-stress-inducible protein DS2 - Chaco potato >gi_607905 (U12439) abscisic stress ripening protein [<i>Solanum chacoense</i>]
Seq. No.	296513
Seq. ID	LIB3115-039-P1-K2-D5
Method	BLASTN
NCBI GI	g2331300
BLAST score	105
E value	3.0e-52
Match length	177
% identity	92
NCBI Description	Zea mays ribosomal protein S4 type I (rps4) mRNA, complete cds
Seq. No.	296514
Seq. ID	LIB3115-039-P1-K2-G11
Method	BLASTN
NCBI GI	g12429
BLAST score	299
E value	1.0e-167
Match length	363
% identity	96
NCBI Description	Maize chloroplast ORF170 and psaA gene

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Seq. No.	296515
Seq. ID	LIB3116-001-Q1-K1-B12
Method	BLASTX
NCBI GI	g729304
BLAST score	149
E value	6.0e-22
Match length	87
% identity	58
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi_479730_pir_S35258 pyruvate decarboxylase (EC 4.1.1.1) 2 - maize (fragment) >gi_22763_emb_CAA79818 (Z21721) pyruvate decarboxylase [Zea mays] >gi_217970_dbj_BAA03353_ (D14456) Pyruvate Decarboxylase [Zea mays]
Seq. No.	296516
Seq. ID	LIB3116-001-Q1-K1-E8
Method	BLASTX
NCBI GI	g1850968
BLAST score	165
E value	1.0e-11
Match length	101
% identity	38
NCBI Description	(U79733) Hs1pro-1 [Beta procumbens]
Seq. No.	296517
Seq. ID	LIB3116-001-Q1-K1-G1
Method	BLASTN
NCBI GI	g4538990
BLAST score	55
E value	3.0e-22
Match length	83
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)
Seq. No.	296518
Seq. ID	LIB3116-001-Q1-K1-G2
Method	BLASTX
NCBI GI	g3334376
BLAST score	401
E value	4.0e-39
Match length	121
% identity	67
NCBI Description	THIOREDOXIN M-TYPE PRECURSOR (TRX-M) >gi_725276 (L40957) thioredoxin M [Zea mays]
Seq. No.	296519
Seq. ID	LIB3116-001-Q1-K1-G7
Method	BLASTX
NCBI GI	g4455232
BLAST score	184
E value	1.0e-13
Match length	142
% identity	36
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 296520
Seq. ID LIB3116-002-Q1-K1-B1
Method BLASTN
NCBI GI g1944204
BLAST score 40
E value 3.0e-13
Match length 56
% identity 93
NCBI Description Oryza sativa mRNA for RicMT, complete cds

Seq. No. 296521
Seq. ID LIB3116-004-Q1-K1-A10
Method BLASTN
NCBI GI g450504
BLAST score 65
E value 4.0e-28
Match length 97
% identity 93
NCBI Description G.hirsutum rbcS gene for ribulose-1,5-bisphosphate carboxylase, small subunit

Seq. No. 296522
Seq. ID LIB3116-004-Q1-K1-G11
Method BLASTX
NCBI GI g2244919
BLAST score 157
E value 1.0e-10
Match length 62
% identity 42
NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 296523
Seq. ID LIB3116-004-Q1-K2-A1
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 48
% identity 67
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 296524
Seq. ID LIB3116-004-Q1-K2-B2
Method BLASTN
NCBI GI g22292
BLAST score 36
E value 4.0e-11
Match length 48
% identity 94
NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 296525
Seq. ID LIB3116-004-Q1-K2-E3
Method BLASTX
NCBI GI g4098250
BLAST score 270
E value 6.0e-24

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Match length 72
% identity 65
NCBI Description (U76611) similar to Solanum tuberosum ci21A gene product encoded by the sequence presented in GenBank Accession Number U76610 [Solanum tuberosum]

Seq. No. 296526
Seq. ID LIB3116-004-Q1-K2-F7
Method BLASTX
NCBI GI g4218535
BLAST score 352
E value 2.0e-33
Match length 76
% identity 84
NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

Seq. No. 296527
Seq. ID LIB3116-004-Q1-K2-H8
Method BLASTX
NCBI GI g2245028
BLAST score 148
E value 2.0e-09
Match length 97
% identity 34
NCBI Description (Z97341) limonene cyclase [Arabidopsis thaliana]

Seq. No. 296528
Seq. ID LIB3116-005-Q1-K1-C4
Method BLASTN
NCBI GI g454880
BLAST score 58
E value 8.0e-24
Match length 92
% identity 91
NCBI Description Rice mRNA for WSI724 protein induced by water stress, complete cds

Seq. No. 296529
Seq. ID LIB3116-005-Q1-K1-F6
Method BLASTX
NCBI GI g2880051
BLAST score 179
E value 3.0e-13
Match length 113
% identity 35
NCBI Description (AC002340) putative protein kinase [Arabidopsis thaliana]

Seq. No. 296530
Seq. ID LIB3116-005-Q1-K1-H6
Method BLASTX
NCBI GI g2058498
BLAST score 199
E value 5.0e-27
Match length 100
% identity 69
NCBI Description (U76029) hemoglobin 1 [Oryza sativa] >gi_2058500 (U76030) hemoglobin 1 [Oryza sativa]

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Seq. No. 296531
Seq. ID LIB3116-006-Q1-K1-A1
Method BLASTX
NCBI GI g1495804
BLAST score 319
E value 1.0e-29
Match length 97
% identity 60
NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No. 296532
Seq. ID LIB3116-006-Q1-K1-A12
Method BLASTX
NCBI GI g4567250
BLAST score 212
E value 6.0e-17
Match length 85
% identity 49
NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No. 296533
Seq. ID LIB3116-006-Q1-K1-B2
Method BLASTN
NCBI GI g2446997
BLAST score 151
E value 2.0e-79
Match length 284
% identity 89
NCBI Description Zea mays FAD7 gene for fatty acid desaturase, complete cds

Seq. No. 296534
Seq. ID LIB3116-006-Q1-K1-C9
Method BLASTX
NCBI GI g2245012
BLAST score 196
E value 4.0e-15
Match length 50
% identity 68
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 296535
Seq. ID LIB3116-006-Q1-K1-D6
Method BLASTX
NCBI GI g4056477
BLAST score 229
E value 6.0e-19
Match length 103
% identity 48
NCBI Description (AC005896) putative RNA binding protein [Arabidopsis thaliana]

Seq. No. 296536
Seq. ID LIB3116-006-Q1-K1-F4
Method BLASTX
NCBI GI g730904
BLAST score 703

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E value 2.0e-74
Match length 161
% identity 87
NCBI Description 26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING HOMOLOG 5) >gi_626989_pir_S46613 YTA5 protein - yeast (Saccharomyces cerevisiae) >gi_531758_emb_CAA56957 (X81070) probable regulatory subunit of 26S proteasome; homologue to S4 subunit of human 26S proteasome [Saccharomyces cerevisiae] >gi_683690_emb_CAA88352 (Z48432) homolog to S4 subunit of human 26S proteasome (X81070) [Saccharomyces cerevisiae]
>gi_1430967_emb_CAA98563 (Z74055) ORF YDL007w [Saccharomyces cerevisiae]

Seq. No. 296537
Seq. ID LIB3116-006-Q1-K1-F5
Method BLASTX
NCBI GI g462193
BLAST score 150
E value 9.0e-10
Match length 47
% identity 51
NCBI Description GOLIATH PROTEIN (G1 PROTEIN) >gi_483296_pir_JC1495 regulatory protein G1 - fruit fly (Drosophila melanogaster)
>gi_157535 (M97204) goliath protein [Drosophila melanogaster]

Seq. No. 296538
Seq. ID LIB3116-007-Q1-K1-A7
Method BLASTX
NCBI GI g2293568
BLAST score 250
E value 1.0e-21
Match length 83
% identity 60
NCBI Description (AF012897) HvB12D homolog [Oryza sativa]

Seq. No. 296539
Seq. ID LIB3116-007-Q1-K1-D5
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 296540
Seq. ID LIB3116-007-Q1-K1-F11
Method BLASTN
NCBI GI g606814
BLAST score 186
E value 1.0e-100
Match length 235
% identity 95
NCBI Description Zea mays Golden Bantam carbonic anhydrase mRNA, complete cds

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Seq. No. 296541
Seq. ID LIB3116-008-Q1-K1-G10
Method BLASTX
NCBI GI g3913018
BLAST score 372
E value 8.0e-36
Match length 102
% identity 73
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No. 296542
Seq. ID LIB3116-008-Q1-K1-H9
Method BLASTX
NCBI GI g4154352
BLAST score 228
E value 6.0e-19
Match length 93
% identity 51
NCBI Description (AF110333) PrMC3 [Pinus radiata]

Seq. No. 296543
Seq. ID LIB3116-009-Q1-K1-A11
Method BLASTN
NCBI GI g22223
BLAST score 49
E value 2.0e-18
Match length 165
% identity 83
NCBI Description Maize cab-1 gene for chlorophyll a/b-binding protein

Seq. No. 296544
Seq. ID LIB3116-009-Q1-K1-D2
Method BLASTX
NCBI GI g2501578
BLAST score 363
E value 1.0e-34
Match length 98
% identity 74
NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir_S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No. 296545
Seq. ID LIB3116-009-Q1-K1-D5
Method BLASTX
NCBI GI g128388
BLAST score 214
E value 3.0e-17
Match length 71
% identity 63
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP) >gi_82711_pir_A31779 phospholipid transfer protein 9C2

precursor - maize >gi_168576 (J04176) phospholipid transfer protein precursor [Zea mays]

Seq. No. 296546
Seq. ID LIB3116-009-Q1-K1-H11
Method BLASTX
NCBI GI g115771
BLAST score 335
E value 2.0e-31
Match length 100
% identity 69
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCPI) >gi_82682_pir_S04453 chlorophyll a/b-binding protein precursor - maize >gi_22224_emb_CAA32900 (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

Seq. No. 296547
Seq. ID LIB3116-010-Q1-K1-B10
Method BLASTX
NCBI GI g416731
BLAST score 229
E value 5.0e-19
Match length 66
% identity 68
NCBI Description POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi_82655_pir_JQ1107 18.3K protein precursor, pollen - maize >gi_255569_bbs_113677 (S44171) pollen specific protein [Zea mays=corn, Peptide, 170 aa] [Zea mays]
>gi_1588669_prf_2209273A Zm13 [Zea mays]

Seq. No. 296548
Seq. ID LIB3116-010-Q1-K1-C8
Method BLASTN
NCBI GI g1698669
BLAST score 57
E value 1.0e-23
Match length 77
% identity 94
NCBI Description Zea mays S-like RNase (kin1) mRNA, complete cds

Seq. No. 296549
Seq. ID LIB3116-010-Q1-K1-D5
Method BLASTN
NCBI GI g22528
BLAST score 117
E value 4.0e-59
Match length 245
% identity 89
NCBI Description Zea mays mRNA encoding a zein (clone A20)

Seq. No. 296550
Seq. ID LIB3116-010-Q1-K1-E12
Method BLASTN
NCBI GI g902200
BLAST score 50
E value 2.0e-19

Match length 106
% identity 87
NCBI Description Z.mays complete chloroplast genome

Seq. No. 296551
Seq. ID LIB3116-010-Q1-K1-E9
Method BLASTX
NCBI GI g1171161
BLAST score 337
E value 9.0e-32
Match length 108
% identity 55
NCBI Description (U41472) pectate lyase homolog [Medicago sativa]

Seq. No. 296552
Seq. ID LIB3116-010-Q1-K1-F1
Method BLASTX
NCBI GI g141602
BLAST score 152
E value 5.0e-17
Match length 99
% identity 59
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
>gi_82658_pir_A22831 19K zein precursor (clone M6) - maize
>gi_22538_emb_CAA26294_ (X02450) zein precursor [Zea mays]

Seq. No. 296553
Seq. ID LIB3116-010-Q1-K1-F3
Method BLASTX
NCBI GI g141604
BLAST score 450
E value 7.0e-45
Match length 108
% identity 86
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
>gi_72310_pir_ZIZM91 19K zein precursor (clone cz19C1) - maize
>gi_168678 (M12146) 19 kDa zein protein [Zea mays]

Seq. No. 296554
Seq. ID LIB3116-010-Q1-K1-G1
Method BLASTX
NCBI GI g4539660
BLAST score 482
E value 9.0e-49
Match length 107
% identity 83
NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 296555
Seq. ID LIB3116-010-Q1-K1-G11
Method BLASTX
NCBI GI g3293559
BLAST score 166
E value 1.0e-11
Match length 74
% identity 49
NCBI Description (AF072694) germin-like protein 7 [Oryza sativa]

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Seq. No. 296556
Seq. ID LIB3116-011-Q1-K1-A12
Method BLASTX
NCBI GI g3451411
BLAST score 227
E value 5.0e-19
Match length 79
% identity 57
NCBI Description (Z98761) seryl-tRNA synthetase [Helianthus annuus]

Seq. No. 296557
Seq. ID LIB3116-011-Q1-K1-B7
Method BLASTN
NCBI GI g397395
BLAST score 126
E value 1.0e-64
Match length 154
% identity 95
NCBI Description Z.mays MNBlb mRNA for DNA-binding protein

Seq. No. 296558
Seq. ID LIB3116-011-Q1-K1-C5
Method BLASTX
NCBI GI g397396
BLAST score 189
E value 2.0e-14
Match length 66
% identity 65
NCBI Description (X66077) DNA-binding protein [Zea mays]

Seq. No. 296559
Seq. ID LIB3116-011-Q1-K1-D5
Method BLASTX
NCBI GI g141600
BLAST score 283
E value 2.0e-25
Match length 70
% identity 86
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) -
maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 296560
Seq. ID LIB3116-011-Q1-K1-D9
Method BLASTX
NCBI GI g3075395
BLAST score 344
E value 3.0e-32
Match length 100
% identity 64
NCBI Description (AC004484) nodulin-35 homologue [Arabidopsis thaliana]

Seq. No. 296561
Seq. ID LIB3116-011-Q1-K1-F10
Method BLASTX
NCBI GI g4539417

BLAST score 268
E value 4.0e-34
Match length 119
% identity 59
NCBI Description (AL049171) putative protein [Arabidopsis thaliana]

Seq. No. 296562
Seq. ID LIB3116-011-Q1-K1-G1
Method BLASTX
NCBI GI g3169116
BLAST score 200
E value 4.0e-16
Match length 55
% identity 71
NCBI Description (AL021366) cICK0721Q.2 (60S Ribosomal Protein L12 LIKE protein) [Homo sapiens]

Seq. No. 296563
Seq. ID LIB3116-011-Q1-K1-G11
Method BLASTX
NCBI GI g1706260
BLAST score 151
E value 2.0e-10
Match length 35
% identity 80
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir_S59597
cysteine proteinase 1 precursor - maize
>gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays]

Seq. No. 296564
Seq. ID LIB3116-012-Q1-K1-B3
Method BLASTN
NCBI GI g3452290
BLAST score 191
E value 1.0e-103
Match length 338
% identity 89
NCBI Description Zea mays retrotransposon Huck-1 5' LTR, partial sequence

Seq. No. 296565
Seq. ID LIB3116-012-Q1-K1-B6
Method BLASTX
NCBI GI g112994
BLAST score 210
E value 4.0e-19
Match length 67
% identity 84
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
>gi_82685_pir_S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 296566
Seq. ID LIB3116-012-Q1-K1-C8

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Method BLASTN
NCBI GI g167086
BLAST score 45
E value 3.0e-16
Match length 153
% identity 90
NCBI Description Hordeum vulgare photosystem I protein (PSI-L) mRNA, complete cds

Seq. No. 296567
Seq. ID LIB3116-012-Q1-K1-H7
Method BLASTX
NCBI GI g4249416
BLAST score 242
E value 1.0e-20
Match length 66
% identity 64
NCBI Description (AC006072) putative exoribonuclease (also contains zinc-finger C2H2-type domain) [Arabidopsis thaliana]

Seq. No. 296568
Seq. ID LIB3116-013-Q1-K1-A11
Method BLASTN
NCBI GI g470670
BLAST score 60
E value 4.0e-25
Match length 103
% identity 89
NCBI Description Zea mays transposable element ILS-1

Seq. No. 296569
Seq. ID LIB3116-013-Q1-K1-B9
Method BLASTX
NCBI GI g3877951
BLAST score 168
E value 5.0e-12
Match length 58
% identity 47
NCBI Description (Z81555) predicted using Genefinder [Caenorhabditis elegans]

Seq. No. 296570
Seq. ID LIB3116-013-Q1-K1-C8
Method BLASTN
NCBI GI g208277
BLAST score 34
E value 1.0e-09
Match length 82
% identity 85
NCBI Description rous sarcoma virus gag gene ligated to e.coli lacZ gene

Seq. No. 296571
Seq. ID LIB3116-014-Q1-K1-B2
Method BLASTN
NCBI GI g433041
BLAST score 106
E value 1.0e-52

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Match length 189
% identity 90
NCBI Description Zea mays W-22 clone PREM-1B retroelement PREM-1, partial sequence

Seq. No. 296572
Seq. ID LIB3116-014-Q1-K1-E4
Method BLASTX
NCBI GI g168697
BLAST score 262
E value 5.0e-23
Match length 101
% identity 57
NCBI Description (M60835) zein [Zea mays]

Seq. No. 296573
Seq. ID LIB3116-014-Q1-K1-H12
Method BLASTX
NCBI GI g481190
BLAST score 172
E value 1.0e-12
Match length 56
% identity 64
NCBI Description plastocyanin precursor - barley >gi_22705_emb_CAA68696_(Y00704) plastocyanin precursor [Hordeum vulgare]>gi_431920_emb_CAA82201_(Z28347) plastocyanin [Hordeum vulgare]

Seq. No. 296574
Seq. ID LIB3116-014-Q1-K1-H6
Method BLASTN
NCBI GI g3885895
BLAST score 41
E value 4.0e-14
Match length 65
% identity 91
NCBI Description Oryza sativa plastocyanin precursor, mRNA, complete cds

Seq. No. 296575
Seq. ID LIB3116-015-P1-K1-A4
Method BLASTX
NCBI GI g4204277
BLAST score 207
E value 2.0e-16
Match length 70
% identity 57
NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 296576
Seq. ID LIB3116-015-P1-K1-C5
Method BLASTX
NCBI GI g2246625
BLAST score 142
E value 8.0e-09
Match length 44
% identity 50
NCBI Description (AF004947) protein kinase [Oryza sativa]

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Seq. No. 296577
Seq. ID LIB3116-015-P1-K1-E1
Method BLASTN
NCBI GI g2695930
BLAST score 45
E value 4.0e-16
Match length 77
% identity 90
NCBI Description Hordeum vulgare mRNA for hypothetical protein, clone RG49

Seq. No. 296578
Seq. ID LIB3116-015-P1-K1-H1
Method BLASTX
NCBI GI g4455350
BLAST score 305
E value 2.0e-28
Match length 70
% identity 81
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 296579
Seq. ID LIB3116-016-P1-K1-A4
Method BLASTX
NCBI GI g3345477
BLAST score 239
E value 1.0e-20
Match length 56
% identity 82
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

Seq. No. 296580
Seq. ID LIB3116-016-P1-K1-C10
Method BLASTN
NCBI GI g2065239
BLAST score 33
E value 3.0e-09
Match length 37
% identity 97
NCBI Description M.musculus mRNA for coxsackie and adenovirus receptor homologue

Seq. No. 296581
Seq. ID LIB3116-016-P1-K1-E6
Method BLASTX
NCBI GI g2982453
BLAST score 293
E value 2.0e-46
Match length 121
% identity 80
NCBI Description (AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No. 296582
Seq. ID LIB3116-016-P1-K1-G4
Method BLASTX
NCBI GI g2688822

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BLAST score	473
E value	9.0e-48
Match length	102
% identity	87
NCBI Description	(U93272) pyrophosphate-dependent phosphofructo-1-kinase [Prunus armeniaca]
Seq. No.	296583
Seq. ID	LIB3116-017-P1-K1-A5
Method	BLASTX
NCBI GI	g687677
BLAST score	200
E value	2.0e-15
Match length	71
% identity	54
NCBI Description	(U19925) unknown [Arabidopsis thaliana]
Seq. No.	296584
Seq. ID	LIB3116-017-P1-K1-C4
Method	BLASTN
NCBI GI	g3290003
BLAST score	85
E value	4.0e-40
Match length	101
% identity	96
NCBI Description	Zea mays pathogenesis related protein-1 (PR-1) mRNA, complete cds
Seq. No.	296585
Seq. ID	LIB3116-017-P1-K1-D2
Method	BLASTN
NCBI GI	g2065239
BLAST score	36
E value	9.0e-11
Match length	40
% identity	97
NCBI Description	M.musculus mRNA for coxsackie and adenovirus receptor homologue
Seq. No.	296586
Seq. ID	LIB3116-017-P1-K1-E9
Method	BLASTX
NCBI GI	g4510373
BLAST score	157
E value	2.0e-10
Match length	101
% identity	35
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]
Seq. No.	296587
Seq. ID	LIB3116-017-P1-K1-F6
Method	BLASTX
NCBI GI	g3757521
BLAST score	441
E value	1.0e-43
Match length	134

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% identity	59
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]
Seq. No.	296588
Seq. ID	LIB3116-017-P1-K1-G11
Method	BLASTX
NCBI GI	g399334
BLAST score	246
E value	2.0e-38
Match length	131
% identity	66
NCBI Description	CYSTATIN I PRECURSOR (CORN KERNEL CYSTEINE PROTEINASE INHIBITOR) >gi_322868_pir_S27239 cysteine proteinase inhibitor - maize >gi_217962_dbj_BAA01472_ (D10622) corn cystatin I [Zea mays]
Seq. No.	296589
Seq. ID	LIB3116-017-P1-K1-H3
Method	BLASTX
NCBI GI	g141598
BLAST score	256
E value	2.0e-22
Match length	77
% identity	71
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99) >gi_72313_pir_ZIZM99 19K zein precursor (clone ZG99) - maize >gi_22519_emb_CAA24717_ (V01470) zein [Zea mays] >gi_22534_emb_CAA24726_ (V01479) zein [Zea mays]
Seq. No.	296590
Seq. ID	LIB3116-018-P1-K1-B3
Method	BLASTN
NCBI GI	g2062705
BLAST score	38
E value	5.0e-12
Match length	42
% identity	98
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.	296591
Seq. ID	LIB3116-018-P1-K1-H4
Method	BLASTX
NCBI GI	g3024018
BLAST score	169
E value	2.0e-12
Match length	44
% identity	80
NCBI Description	INITIATION FACTOR 5A (EIF-5A) (EIF-4D) >gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation initiation factor 5A [Zea mays]
Seq. No.	296592
Seq. ID	LIB3116-020-P1-K1-A4
Method	BLASTX
NCBI GI	g2245098
BLAST score	319

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E value	2.0e-29
Match length	96
% identity	61
NCBI Description	(Z97343) ribosomal protein [Arabidopsis thaliana]
Seq. No.	296593
Seq. ID	LIB3116-020-P1-K1-B7
Method	BLASTX
NCBI GI	g4544445
BLAST score	246
E value	5.0e-21
Match length	105
% identity	50
NCBI Description	(AC006592) putative pyrophosphate--fructose 6-phosphate 1-phosphotransferase [Arabidopsis thaliana]
Seq. No.	296594
Seq. ID	LIB3116-020-P1-K1-C10
Method	BLASTX
NCBI GI	g4263509
BLAST score	292
E value	3.0e-26
Match length	126
% identity	51
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]
Seq. No.	296595
Seq. ID	LIB3116-020-P1-K1-C11
Method	BLASTX
NCBI GI	g4093169
BLAST score	332
E value	6.0e-31
Match length	132
% identity	53
NCBI Description	(AF095933) p20-Arc [Dictyostelium discoideum]
Seq. No.	296596
Seq. ID	LIB3116-020-P1-K1-D12
Method	BLASTX
NCBI GI	g1076758
BLAST score	190
E value	2.0e-14
Match length	77
% identity	49
NCBI Description	heat-shock protein precursor - rye >gi_2130093_pir_S65776 heat-shock protein, 82K, precursor - rye >gi_556673_emb_CAA82945_ (Z30243) heat-shock protein [Secale cereale]
Seq. No.	296597
Seq. ID	LIB3116-020-P1-K1-E3
Method	BLASTX
NCBI GI	g3096931
BLAST score	140
E value	9.0e-09
Match length	54
% identity	46

NCBI Description (AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]

Seq. No. 296598
Seq. ID LIB3116-020-P1-K1-F10
Method BLASTX
NCBI GI g3024657
BLAST score 150
E value 9.0e-21
Match length 97
% identity 62
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
>gi_2668740 (AF034944) translation initiation factor; GOS2
[Zea mays]

Seq. No. 296599
Seq. ID LIB3116-020-P1-K1-H4
Method BLASTX
NCBI GI g1001355
BLAST score 172
E value 3.0e-12
Match length 119
% identity 38
NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]

Seq. No. 296600
Seq. ID LIB3116-021-P1-K1-B1
Method BLASTX
NCBI GI g1805254
BLAST score 229
E value 4.0e-26
Match length 99
% identity 65
NCBI Description (U62622) monogalactosyldiacylglycerol synthase [Cucumis sativus]

Seq. No. 296601
Seq. ID LIB3116-021-P1-K1-B7
Method BLASTX
NCBI GI g141600
BLAST score 277
E value 1.0e-24
Match length 109
% identity 60
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) -
maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 296602
Seq. ID LIB3116-021-P1-K1-C7
Method BLASTX
NCBI GI g1332579
BLAST score 420
E value 2.0e-41
Match length 108
% identity 8
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 296603
Seq. ID LIB3116-021-P1-K1-D5
Method BLASTX
NCBI GI g4584852
BLAST score 145
E value 4.0e-09
Match length 78
% identity 41
NCBI Description (AF014810) proline transporter 3 [Lycopersicon esculentum]

Seq. No. 296604
Seq. ID LIB3116-021-P1-K1-D8
Method BLASTX
NCBI GI g3800853
BLAST score 352
E value 2.0e-33
Match length 111
% identity 60
NCBI Description (AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase activase precursor [Zea mays]

Seq. No. 296605
Seq. ID LIB3116-021-P1-K1-E3
Method BLASTX
NCBI GI g168586
BLAST score 217
E value 6.0e-18
Match length 67
% identity 67
NCBI Description (M58656) pyruvate,orthophosphate dikinase [Zea mays]

Seq. No. 296606
Seq. ID LIB3116-021-P1-K1-E6
Method BLASTX
NCBI GI g4587681
BLAST score 225
E value 1.0e-18
Match length 74
% identity 53
NCBI Description (AC007197) hypothetical protein [Arabidopsis thaliana]

Seq. No. 296607
Seq. ID LIB3116-021-P1-K1-E9
Method BLASTX
NCBI GI g141602
BLAST score 273
E value 4.0e-24
Match length 106
% identity 60
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
>gi_82658_pir_A22831 19K zein precursor (clone M6) - maize
>gi_22538_emb_CAA26294_ (X02450) zein precursor [Zea mays]

Seq. No. 296608
Seq. ID LIB3116-021-P1-K1-F11
Method BLASTX

NCBI GI g99487
 BLAST score 333
 E value 3.0e-31
 Match length 112
 % identity 59
 NCBI Description chlorophyll a/b-binding protein (clone pINEab 43) - Scotch pine >gi_20794_emb_CAA41407_ (X58517) Type III chlorophyll a /b-binding protein [Pinus sylvestris]

 Seq. No. 296609
 Seq. ID LIB3116-021-P1-K1-G9
 Method BLASTX
 NCBI GI g1619300
 BLAST score 159
 E value 9.0e-11
 Match length 46
 % identity 65
 NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

 Seq. No. 296610
 Seq. ID LIB3116-021-P1-K1-H1
 Method BLASTX
 NCBI GI g1352200
 BLAST score 293
 E value 1.0e-26
 Match length 78
 % identity 78
 NCBI Description CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
>gi_480909_pir_S37497 triose
phosphate/3-phosphoglycerate/phosphate translocator - maize
>gi_405635_emb_CAA81349_ (Z26595) triose
phosphate/phosphate translocator [Zea mays]

 Seq. No. 296611
 Seq. ID LIB3116-022-P1-K1-A12
 Method BLASTX
 NCBI GI g141597
 BLAST score 188
 E value 3.0e-14
 Match length 71
 % identity 58
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

 Seq. No. 296612
 Seq. ID LIB3116-022-P1-K1-A4
 Method BLASTX
 NCBI GI g170354
 BLAST score 452
 E value 4.0e-45
 Match length 124
 % identity 16
 NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]

 Seq. No. 296613

DRAFT Sequence Database

Seq. ID	LIB3116-022-P1-K1-A6
Method	BLASTX
NCBI GI	g4049341
BLAST score	245
E value	6.0e-21
Match length	99
% identity	54
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]
Seq. No.	296614
Seq. ID	LIB3116-022-P1-K1-C2
Method	BLASTN
NCBI GI	g3821780
BLAST score	33
E value	5.0e-09
Match length	37
% identity	97
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	296615
Seq. ID	LIB3116-022-P1-K1-D3
Method	BLASTX
NCBI GI	g2760334
BLAST score	169
E value	6.0e-12
Match length	93
% identity	41
NCBI Description	(AC002130) F1N21.5 [Arabidopsis thaliana]
Seq. No.	296616
Seq. ID	LIB3116-022-P1-K1-D7
Method	BLASTX
NCBI GI	g1351014
BLAST score	249
E value	2.0e-21
Match length	101
% identity	57
NCBI Description	40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]
Seq. No.	296617
Seq. ID	LIB3116-022-P1-K1-D9
Method	BLASTX
NCBI GI	g2499488
BLAST score	195
E value	5.0e-15
Match length	74
% identity	49
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]
Seq. No.	296618
Seq. ID	LIB3116-022-P1-K1-E3

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Method	BLASTX
NCBI GI	g1871195
BLAST score	163
E value	2.0e-11
Match length	91
% identity	37
NCBI Description	(U90439) Ca++ dependent protein kinase isolog [Arabidopsis thaliana] >gi_2335093 (AC002339) putative calcium-dependent protein kinase [Arabidopsis thaliana]
Seq. No.	296619
Seq. ID	LIB3116-022-P1-K1-E6
Method	BLASTX
NCBI GI	g3402684
BLAST score	293
E value	2.0e-26
Match length	108
% identity	58
NCBI Description	(AC004697) hypothetical protein [Arabidopsis thaliana]
Seq. No.	296620
Seq. ID	LIB3116-022-P1-K1-E7
Method	BLASTN
NCBI GI	g758354
BLAST score	38
E value	5.0e-12
Match length	190
% identity	81
NCBI Description	Z.mays mRNA for plasma membrane H+ ATPase
Seq. No.	296621
Seq. ID	LIB3116-022-P1-K1-E9
Method	BLASTX
NCBI GI	g531829
BLAST score	189
E value	1.0e-14
Match length	74
% identity	54
NCBI Description	(U12390) beta-galactosidase alpha peptide [cloning vector pSport1]
Seq. No.	296622
Seq. ID	LIB3116-022-P1-K1-F12
Method	BLASTX
NCBI GI	g2246378
BLAST score	152
E value	8.0e-10
Match length	76
% identity	46
NCBI Description	(Z86094) plastid protein [Arabidopsis thaliana]
Seq. No.	296623
Seq. ID	LIB3116-022-P1-K1-F2
Method	BLASTX
NCBI GI	g70772
BLAST score	265
E value	4.0e-23

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Match length 81
% identity 65
NCBI Description histone H4 - wheat >gi_70773_pir_HSPM4 histone H4 - garden pea

Seq. No. 296624
Seq. ID LIB3116-022-P1-K1-F6
Method BLASTX
NCBI GI g168699
BLAST score 335
E value 3.0e-31
Match length 122
% identity 57
NCBI Description (M60836) zein [Zea mays]

Seq. No. 296625
Seq. ID LIB3116-022-P1-K1-G6
Method BLASTN
NCBI GI g12474
BLAST score 52
E value 3.0e-20
Match length 80
% identity 91
NCBI Description Zea mays chloroplast tV-UAC gene for transfer RNA-Val (UAC)

Seq. No. 296626
Seq. ID LIB3116-025-P1-K1-A11
Method BLASTX
NCBI GI g1352427
BLAST score 306
E value 6.0e-28
Match length 105
% identity 58
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
(EIF-4C)

Seq. No. 296627
Seq. ID LIB3116-025-P1-K1-B10
Method BLASTX
NCBI GI g4581203
BLAST score 352
E value 3.0e-33
Match length 132
% identity 54
NCBI Description (Y17912) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No. 296628
Seq. ID LIB3116-025-P1-K1-B3
Method BLASTX
NCBI GI g825756
BLAST score 170
E value 6.0e-12
Match length 69
% identity 57
NCBI Description (U12391) beta-galactosidase alpha peptide [Cloning vector pSport2]

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Seq. No.	296629
Seq. ID	LIB3116-025-P1-K1-B6
Method	BLASTX
NCBI GI	g939785
BLAST score	363
E value	1.0e-34
Match length	120
% identity	66
NCBI Description	(L46400) MADS box protein [Zea mays]
Seq. No.	296630
Seq. ID	LIB3116-025-P1-K1-B8
Method	BLASTX
NCBI GI	g2668744
BLAST score	325
E value	4.0e-30
Match length	100
% identity	66
NCBI Description	(AF034946) ubiquitin conjugating enzyme [Zea mays]
Seq. No.	296631
Seq. ID	LIB3116-025-P1-K1-C11
Method	BLASTX
NCBI GI	g3024018
BLAST score	179
E value	3.0e-13
Match length	53
% identity	70
NCBI Description	INITIATION FACTOR 5A (EIF-5A) (EIF-4D) >gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation initiation factor 5A [Zea mays]
Seq. No.	296632
Seq. ID	LIB3116-025-P1-K1-C3
Method	BLASTX
NCBI GI	g629861
BLAST score	215
E value	3.0e-17
Match length	119
% identity	48
NCBI Description	zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203) zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.	296633
Seq. ID	LIB3116-025-P1-K1-C4
Method	BLASTX
NCBI GI	g3913427
BLAST score	206
E value	3.0e-16
Match length	98
% identity	50
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]

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Seq. No.	296634
Seq. ID	LIB3116-025-P1-K1-C6
Method	BLASTX
NCBI GI	g2224733
BLAST score	183
E value	1.0e-13
Match length	125
% identity	38
NCBI Description	(AB004933) Aux22e [Vigna radiata]
Seq. No.	296635
Seq. ID	LIB3116-025-P1-K1-C7
Method	BLASTX
NCBI GI	g548770
BLAST score	346
E value	1.0e-32
Match length	116
% identity	61
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]
Seq. No.	296636
Seq. ID	LIB3116-025-P1-K1-C8
Method	BLASTX
NCBI GI	g464987
BLAST score	274
E value	3.0e-24
Match length	77
% identity	68
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir_S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]
Seq. No.	296637
Seq. ID	LIB3116-025-P1-K1-D4
Method	BLASTX
NCBI GI	g3915131
BLAST score	171
E value	2.0e-12
Match length	89
% identity	42
NCBI Description	THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1) >gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza sativa]
Seq. No.	296638
Seq. ID	LIB3116-025-P1-K1-D5
Method	BLASTX
NCBI GI	g168701
BLAST score	233

E value 2.0e-19
Match length 139
% identity 45
NCBI Description (M60837) zein [Zea mays]

Seq. No. 296639
Seq. ID LIB3116-025-P1-K1-D9
Method BLASTX
NCBI GI g567893
BLAST score 155
E value 7.0e-11
Match length 55
% identity 62
NCBI Description (L37382) beta-galactosidase-complementation protein [Cloning vector]

Seq. No. 296640
Seq. ID LIB3116-025-P1-K1-E10
Method BLASTX
NCBI GI g3913427
BLAST score 325
E value 3.0e-30
Match length 125
% identity 54
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
(SAMDC) >gi_1532073_emb_CAA69075 (Y07767)
S-adenosylmethionine decarboxylase [Zea mays]

Seq. No. 296641
Seq. ID LIB3116-025-P1-K1-F8
Method BLASTX
NCBI GI g1053047
BLAST score 273
E value 2.0e-24
Match length 85
% identity 68
NCBI Description (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No. 296642
Seq. ID LIB3116-025-P1-K1-H12
Method BLASTX
NCBI GI g128388
BLAST score 317
E value 3.0e-29
Match length 107
% identity 64
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
(PHOSPHOLIPID TRANSFER PROTEIN) (PLTP)
>gi_82711_pir_A31779 phospholipid transfer protein 9C2
precursor - maize >gi_168576 (J04176) phospholipid transfer
protein precursor [Zea mays]

Seq. No. 296643
Seq. ID LIB3116-025-P1-K2-C6
Method BLASTX

NCBI GI g2224731
 BLAST score 165
 E value 6.0e-22
 Match length 108
 % identity 57
 NCBI Description (AB004932) Aux22d [Vigna radiata]

Seq. No. 296644
 Seq. ID LIB3116-025-P1-K2-F1
 Method BLASTX
 NCBI GI g1216391
 BLAST score 174
 E value 1.0e-12
 Match length 90
 % identity 48
 NCBI Description (U39319) myrosinase-associated protein [Brassica napus]
 >gi_1589010_prf_2209432B myrosinase-associated
 protein:ISOTYPE=4 [Brassica napus]

Seq. No. 296645
 Seq. ID LIB3116-025-P1-K2-F8
 Method BLASTX
 NCBI GI g417103
 BLAST score 219
 E value 2.0e-20
 Match length 69
 % identity 84
 NCBI Description HISTONE H3.2, MINOR >gi_282871_pir_S24346 histone
 H3.3-like protein - Arabidopsis thaliana
 >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
 [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
 histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460)
 histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
 H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2
 [Medicago sativa] >gi_488577 (U09465) histone H3.2
 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone
 H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422)
 histone H3 variant H3.3 [Lycopersicon esculentum]
 >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]
 >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana
 tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
 >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porterlesia
 coarctata] >gi_4490754_emb CAB38916.1. (AL035708) histone
 H3.3 [Arabidopsis thaliana] >gi_4490755_emb CAB38917.1_
 (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 296646
 Seq. ID LIB3116-025-P1-K2-H4
 Method BLASTX
 NCBI GI g130274
 BLAST score 182
 E value 7.0e-14
 Match length 57
 % identity 63
 NCBI Description PLASTOCYANIN >gi_82500_pir_S06105 plastocyanin - rice

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Seq. No.	296647
Seq. ID	LIB3116-026-P1-K2-A11
Method	BLASTN
NCBI GI	g168579
BLAST score	52
E value	2.0e-20
Match length	60
% identity	97
NCBI Description	Maize pyruvate,orthophosphate dikinase mRNA, complete cds
Seq. No.	296648
Seq. ID	LIB3116-026-P1-K2-A4
Method	BLASTX
NCBI GI	g82080
BLAST score	212
E value	4.0e-17
Match length	51
% identity	80
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]
Seq. No.	296649
Seq. ID	LIB3116-026-P1-K2-B10
Method	BLASTX
NCBI GI	g4581203
BLAST score	142
E value	2.0e-11
Match length	70
% identity	59
NCBI Description	(Y17912) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]
Seq. No.	296650
Seq. ID	LIB3116-026-P1-K2-E1
Method	BLASTN
NCBI GI	g22312
BLAST score	50
E value	3.0e-19
Match length	62
% identity	95
NCBI Description	Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)
Seq. No.	296651
Seq. ID	LIB3116-026-P1-K2-F11
Method	BLASTX
NCBI GI	g168701
BLAST score	290
E value	3.0e-45
Match length	132
% identity	58
NCBI Description	(M60837) zein [Zea mays]
Seq. No.	296652
Seq. ID	LIB3116-026-P1-K2-F6
Method	BLASTX

SEQUENCE DATA

NCBI GI	g115786
BLAST score	148
E value	6.0e-10
Match length	53
% identity	64
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays]
Seq. No.	296653
Seq. ID	LIB3116-026-P1-K2-G6
Method	BLASTX
NCBI GI	g1173189
BLAST score	170
E value	7.0e-12
Match length	117
% identity	48
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi_2119091_pir_S58629 ribosomal protein S12 - maize chloroplast >gi_342619 (M17841) ribosomal protein S12 [Zea mays] >gi_1216141_emb_CAA60309_ (X86563) ribosomal protein S12 [Zea mays]
Seq. No.	296654
Seq. ID	LIB3116-027-P1-K1-B12
Method	BLASTX
NCBI GI	g3287696
BLAST score	172
E value	2.0e-12
Match length	72
% identity	51
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
Seq. No.	296655
Seq. ID	LIB3116-027-P1-K1-B2
Method	BLASTX
NCBI GI	g266398
BLAST score	474
E value	1.0e-47
Match length	120
% identity	76
NCBI Description	TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR INHIBITOR) (CHFI) >gi_68849_pir_TIZM1 trypsin/factor XIIa inhibitor precursor - maize >gi_22327_emb_CAA37998_ (X54064) corn Hageman factor inhibitor [Zea mays]
Seq. No.	296656
Seq. ID	LIB3116-027-P1-K1-B8
Method	BLASTN
NCBI GI	g2522426
BLAST score	63
E value	5.0e-27
Match length	195

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% identity 83
NCBI Description Cloning vector pWSK29, complete sequence

Seq. No. 296657
Seq. ID LIB3116-027-P1-K1-C1
Method BLASTX
NCBI GI g485744
BLAST score 250
E value 2.0e-21
Match length 96
% identity 55
NCBI Description (L32792) pyrophosphatase [Beta vulgaris]

Seq. No. 296658
Seq. ID LIB3116-027-P1-K1-C10
Method BLASTX
NCBI GI g1835731
BLAST score 181
E value 3.0e-13
Match length 83
% identity 46
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 296659
Seq. ID LIB3116-027-P1-K1-C5
Method BLASTX
NCBI GI g2407279
BLAST score 428
E value 3.0e-42
Match length 129
% identity 67
NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 296660
Seq. ID LIB3116-027-P1-K1-E7
Method BLASTX
NCBI GI g2493852
BLAST score 189
E value 3.0e-14
Match length 63
% identity 56
NCBI Description CYTOCHROME C OXIDASE POLYPEPTIDE VC
>gi_1070356_emb_CAA92107 (Z68091) cytochrome c oxidase, Vc
subunit [Hordeum vulgare]

Seq. No. 296661
Seq. ID LIB3116-027-P1-K1-G11
Method BLASTX
NCBI GI g3337356
BLAST score 230
E value 4.0e-19
Match length 115
% identity 48
NCBI Description (AC004481) putative protein transport protein SEC61 alpha
subunit [Arabidopsis thaliana]

Seq. No. 296662

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Seq. No.	LIB3116-028-P1-K1-A10
Method	BLASTX
NCBI GI	g4371282
BLAST score	345
E value	2.0e-32
Match length	115
% identity	61
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]
Seq. No.	296663
Seq. ID	LIB3116-028-P1-K1-A11
Method	BLASTX
NCBI GI	g2130024
BLAST score	180
E value	3.0e-13
Match length	64
% identity	58
NCBI Description	DNA-binding protein ABF2 - wild oat >gi_1159879_emb_CAA88331_ (Z48431) DNA-binding protein [Avena fatua]
Seq. No.	296664
Seq. ID	LIB3116-028-P1-K1-B1
Method	BLASTX
NCBI GI	g293093
BLAST score	203
E value	5.0e-16
Match length	79
% identity	57
NCBI Description	(L01931) ribulose 1,5-bisphosphate carboxylase [Lobelia sp.]
Seq. No.	296665
Seq. ID	LIB3116-028-P1-K1-B4
Method	BLASTX
NCBI GI	g2262100
BLAST score	350
E value	3.0e-33
Match length	106
% identity	61
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.	296666
Seq. ID	LIB3116-028-P1-K1-B5
Method	BLASTX
NCBI GI	g3184282
BLAST score	160
E value	7.0e-11
Match length	116
% identity	38
NCBI Description	(AC004136) hypothetical protein [Arabidopsis thaliana]
Seq. No.	296667
Seq. ID	LIB3116-028-P1-K1-B7
Method	BLASTX
NCBI GI	g1673456

BLAST score 270
 E value 5.0e-27
 Match length 77
 % identity 80
 NCBI Description (Y09214) rubisco small subunit [Zea mays]

Seq. No. 296668
 Seq. ID LIB3116-028-P1-K1-B9
 Method BLASTX
 NCBI GI g1711036
 BLAST score 177
 E value 7.0e-13
 Match length 90
 % identity 44
 NCBI Description (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]

Seq. No. 296669
 Seq. ID LIB3116-028-P1-K1-C1
 Method BLASTX
 NCBI GI g99487
 BLAST score 275
 E value 2.0e-24
 Match length 130
 % identity 46
 NCBI Description chlorophyll a/b-binding protein (clone pINEab 43) - Scotch pine >gi_20794_emb_CAA41407_ (X58517) Type III chlorophyll a /b-binding protein [Pinus sylvestris]

Seq. No. 296670
 Seq. ID LIB3116-028-P1-K1-C8
 Method BLASTX
 NCBI GI g417103
 BLAST score 360
 E value 2.0e-34
 Match length 96
 % identity 78
 NCBI Description HISTONE H3.2, MINOR >gi_282871_pir_S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563_ (U09458) histone H3.2 [Medicago sativa] >gi_488567_ (U09460) histone H3.2 [Medicago sativa] >gi_488569_ (U09461) histone H3.2 [Medicago sativa] >gi_488575_ (U09464) histone H3.2 [Medicago sativa] >gi_488577_ (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944_ (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890_ (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

BIOLOGICAL SEQUENCES

Seq. No.	296671
Seq. ID	LIB3116-028-P1-K1-D11
Method	BLASTX
NCBI GI	g224550
BLAST score	265
E value	4.0e-23
Match length	90
% identity	61
NCBI Description	synthase CF0I,ATP [Triticum aestivum]
Seq. No.	296672
Seq. ID	LIB3116-028-P1-K1-D2
Method	BLASTX
NCBI GI	g121472
BLAST score	218
E value	1.0e-17
Match length	109
% identity	47
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]
Seq. No.	296673
Seq. ID	LIB3116-028-P1-K1-D5
Method	BLASTX
NCBI GI	g112994
BLAST score	252
E value	5.0e-22
Match length	57
% identity	84
NCBI Description	GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN >gi_82685_pir_S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077 (X12564) ABA-inducible gene protein [Zea mays] >gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]
Seq. No.	296674
Seq. ID	LIB3116-028-P1-K1-D7
Method	BLASTX
NCBI GI	g1710551
BLAST score	194
E value	7.0e-15
Match length	51
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728_ (X95458) ribosomal protein L39 [Zea mays]
Seq. No.	296675
Seq. ID	LIB3116-028-P1-K1-F12
Method	BLASTX
NCBI GI	g2668742
BLAST score	286
E value	1.0e-25

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Match length 84
% identity 67
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 296676
Seq. ID LIB3116-028-P1-K1-F2
Method BLASTX
NCBI GI g82040
BLAST score 460
E value 4.0e-46
Match length 119
% identity 20
NCBI Description ubiquitin precursor - flax (fragment) >gi_168304 (M57895)
ubiquitin [Linum usitatissimum]

Seq. No. 296677
Seq. ID LIB3116-028-P1-K1-F4
Method BLASTX
NCBI GI g1835731
BLAST score 209
E value 9.0e-17
Match length 71
% identity 62
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 296678
Seq. ID LIB3116-028-P1-K1-F5
Method BLASTX
NCBI GI g1698670
BLAST score 521
E value 4.0e-53
Match length 136
% identity 68
NCBI Description (U66241) S-like RNase [Zea mays]

Seq. No. 296679
Seq. ID LIB3116-028-P1-K1-F8
Method BLASTN
NCBI GI g559535
BLAST score 68
E value 4.0e-30
Match length 136
% identity 88
NCBI Description Z.mays mRNA for metallothionein

Seq. No. 296680
Seq. ID LIB3116-028-P1-K1-G3
Method BLASTX
NCBI GI g3337352
BLAST score 303
E value 1.0e-27
Match length 122
% identity 47
NCBI Description (AC004481) putative chromatin structural protein Supt5hp
[Arabidopsis thaliana]

Seq. No. 296681

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Seq. ID	LIB3116-028-P1-K1-G9
Method	BLASTX
NCBI GI	g4204761
BLAST score	166
E value	8.0e-12
Match length	57
% identity	54
NCBI Description	(U51192) peroxidase precursor [Glycine max]
Seq. No.	296682
Seq. ID	LIB3116-028-P1-K1-H2
Method	BLASTX
NCBI GI	g3096910
BLAST score	168
E value	7.0e-12
Match length	65
% identity	55
NCBI Description	(AJ005813) neoxanthin cleavage enzyme [Arabidopsis thaliana]
Seq. No.	296683
Seq. ID	LIB3116-028-P1-K1-H9
Method	BLASTX
NCBI GI	g417544
BLAST score	275
E value	3.0e-24
Match length	85
% identity	61
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD PROTEIN) (PSI-D) (PS I SUBUNIT 5) >gi_320209_pir_A60695 photosystem I chain II precursor - cucumber >gi_625966_pir_JQ2132 photosystem I complex 20K protein precursor - cucumber >gi_227772_prf_1710320A photosystem I 20kD protein [Cucumis sativus]
Seq. No.	296684
Seq. ID	LIB3116-030-P1-K1-A10
Method	BLASTX
NCBI GI	g417154
BLAST score	362
E value	1.0e-34
Match length	110
% identity	70
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]
Seq. No.	296685
Seq. ID	LIB3116-030-P1-K1-A6
Method	BLASTX
NCBI GI	g113456
BLAST score	266
E value	2.0e-23
Match length	100
% identity	60
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
 >gi_22162_emb_CAA40781_ (X57556) adenine nucleotide
 translocator [Zea mays]

Seq. No. 296686
 Seq. ID LIB3116-030-P1-K1-B12
 Method BLASTX
 NCBI GI g531829
 BLAST score 175
 E value 5.0e-13
 Match length 77
 % identity 53
 NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No. 296687
 Seq. ID LIB3116-030-P1-K1-C5
 Method BLASTX
 NCBI GI g224509
 BLAST score 193
 E value 1.0e-14
 Match length 65
 % identity 65
 NCBI Description zein E19 [Zea mays]

Seq. No. 296688
 Seq. ID LIB3116-030-P1-K1-D3
 Method BLASTX
 NCBI GI g4039153
 BLAST score 151
 E value 8.0e-10
 Match length 35
 % identity 71
 NCBI Description (AF104221) low temperature and salt responsive protein LTI6A [Arabidopsis thaliana] >gi_4325217_gb_AAD17302 (AF122005) hydrophobic protein [Arabidopsis thaliana]

Seq. No. 296689
 Seq. ID LIB3116-030-P1-K1-E10
 Method BLASTN
 NCBI GI g2981206
 BLAST score 65
 E value 4.0e-28
 Match length 145
 % identity 86
 NCBI Description Zea mays photosystem I complex PsaH subunit precursor (psaH) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 296690
 Seq. ID LIB3116-030-P1-K1-E12
 Method BLASTX
 NCBI GI g1853970
 BLAST score 143
 E value 3.0e-09
 Match length 66
 % identity 45

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NCBI Description (D88122) CPRD46 protein [Vigna unguiculata]

Seq. No. 296691
Seq. ID LIB3116-031-P1-K1-C12
Method BLASTX
NCBI GI g115782
BLAST score 214
E value 1.0e-17
Match length 49
% identity 82
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_72747_pir_CDWT chlorophyll a/b-binding protein precursor - wheat >gi_170674 (M10144) chlorophyll a/b-binding protein precursor [Triticum aestivum]

Seq. No. 296692
Seq. ID LIB3116-032-P1-K1-E10
Method BLASTX
NCBI GI g82040
BLAST score 354
E value 7.0e-34
Match length 96
% identity 21
NCBI Description ubiquitin precursor - flax (fragment) >gi_168304 (M57895) ubiquitin [Linum usitatissimum]

Seq. No. 296693
Seq. ID LIB3116-032-P1-K1-F4
Method BLASTX
NCBI GI g1931645
BLAST score 185
E value 6.0e-14
Match length 83
% identity 49
NCBI Description (U95973) Fe(II) transporter isolog [Arabidopsis thaliana]

Seq. No. 296694
Seq. ID LIB3116-033-P1-K1-A12
Method BLASTN
NCBI GI g559535
BLAST score 152
E value 3.0e-80
Match length 192
% identity 95
NCBI Description Z.mays mRNA for metallothionein

Seq. No. 296695
Seq. ID LIB3116-034-P1-K1-B5
Method BLASTX
NCBI GI g123537
BLAST score 191
E value 2.0e-14
Match length 93
% identity 45
NCBI Description 12 KD HEAT SHOCK PROTEIN (GLUCOSE AND LIPID-REGULATED PROTEIN) >gi_72231_pir_HHBY12 heat shock protein 12 - yeast (Saccharomyces cerevisiae) >gi_3800_emb_CAA39306_

(X55785) hsp12 [Saccharomyces cerevisiae] >gi_171607
(M60827) 15 kD glucose and lipid regulated protein
[Saccharomyces cerevisiae] >gi_559934_emb_CAA86349
(Z46255) hsp12, glp1, len: 109, CAI: 0.65, HS12_YEAST
P22943 12 KD HEAT SHOCK PROTEIN [Saccharomyces cerevisiae]
>gi_836740_dbj_BAA09224.1 (D50617) 12KD heat shock protein
[Saccharomyces cerevisiae] >gi_1100790_dbj_BAA08003
(D44596) 15kD glucose and lipid regulated protein
[Saccharomyces cerevisiae] >gi_1742028_dbj_BAA14033
(D89864) Sc-Hsp12p [Saccharomyces pastorianus]

Seq. No. 296696
Seq. ID LIB3117-001-Q1-K1-A6
Method BLASTN
NCBI GI g168681
BLAST score 41
E value 8.0e-14
Match length 137
% identity 82
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333 Sequence 8 from Patent US

Seq. No. 296697
Seq. ID LIB3117-001-Q1-K1-B5
Method BLASTX
NCBI GI g3659995
BLAST score 309
E value 2.0e-28
Match length 62
% identity 85
NCBI Description Bifunctional Hageman Factor AMYLASE INHIBITOR FROM MAIZE

Seq. No. 296698
Seq. ID LIB3117-001-Q1-K1-B9
Method BLASTX
NCBI GI g1655424
BLAST score 147
E value 2.0e-09
Match length 39
% identity 77
NCBI Description (D83531) GDP dissociation inhibitor [Arabidopsis thaliana]
>gi_3212878 (AC004005) GDP dissociation inhibitor
[Arabidopsis thaliana]

Seq. No. 296699
Seq. ID LIB3117-001-Q1-K1-C10
Method BLASTX
NCBI GI g419803
BLAST score 280
E value 6.0e-25
Match length 111
% identity 52
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 296700
Seq. ID LIB3117-001-Q1-K1-C4

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Method	BLASTX
NCBI GI	g3402754
BLAST score	189
E value	3.0e-14
Match length	121
% identity	35
NCBI Description	(AL031187) putative protein [Arabidopsis thaliana]
Seq. No.	296701
Seq. ID	LIB3117-001-Q1-K1-C9
Method	BLASTX
NCBI GI	g419803
BLAST score	353
E value	2.0e-33
Match length	140
% identity	54
NCBI Description	zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
Seq. No.	296702
Seq. ID	LIB3117-001-Q1-K1-F5
Method	BLASTX
NCBI GI	g2832243
BLAST score	167
E value	5.0e-12
Match length	88
% identity	47
NCBI Description	(AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.	296703
Seq. ID	LIB3117-001-Q1-K1-G3
Method	BLASTN
NCBI GI	g4140643
BLAST score	68
E value	6.0e-30
Match length	96
% identity	93
NCBI Description	Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	296704
Seq. ID	LIB3117-001-Q1-K1-H12
Method	BLASTN
NCBI GI	g312180
BLAST score	41
E value	6.0e-14
Match length	105
% identity	85
NCBI Description	Z.mays GapC4 gene
Seq. No.	296705
Seq. ID	LIB3117-002-Q1-K1-B2
Method	BLASTX
NCBI GI	g3776011
BLAST score	141
E value	6.0e-09
Match length	63

% identity 51
NCBI Description (AJ010469) RNA helicase [Arabidopsis thaliana]

Seq. No. 296706
Seq. ID LIB3117-002-Q1-K1-C1
Method BLASTN
NCBI GI g2832242
BLAST score 105
E value 4.0e-52
Match length 161
% identity 91
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 296707
Seq. ID LIB3117-002-Q1-K1-C11
Method BLASTX
NCBI GI g1173187
BLAST score 343
E value 1.0e-32
Match length 71
% identity 90
NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir_S56673
ribosomal protein S23.e, cytosolic (clone RJ3) - garden
strawberry >gi_643074 (U19940) putative 40S ribosomal
protein s12 [Fragaria x ananassa]

Seq. No. 296708
Seq. ID LIB3117-002-Q1-K1-C12
Method BLASTX
NCBI GI g1173187
BLAST score 488
E value 2.0e-49
Match length 104
% identity 88
NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir_S56673
ribosomal protein S23.e, cytosolic (clone RJ3) - garden
strawberry >gi_643074 (U19940) putative 40S ribosomal
protein s12 [Fragaria x ananassa]

Seq. No. 296709
Seq. ID LIB3117-002-Q1-K1-E7
Method BLASTN
NCBI GI g2832242
BLAST score 36
E value 6.0e-11
Match length 48
% identity 94
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 296710
Seq. ID LIB3117-002-Q1-K1-F12
Method BLASTX
NCBI GI g3914423
BLAST score 208
E value 1.0e-20
Match length 85
% identity 67

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NCBI Description PROFILIN 4 >gi_2642324 (AF032370) profilin [Zea mays]
Seq. No. 296711
Seq. ID LIB3117-002-Q1-K1-F2
Method BLASTX
NCBI GI g141613
BLAST score 210
E value 7.0e-17
Match length 77
% identity 55
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
>gi_72305_pir_ZIZM21_22K zein precursor (clone pZ22.1) -
maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]

Seq. No. 296712
Seq. ID LIB3117-002-Q1-K1-F7
Method BLASTX
NCBI GI g4185308
BLAST score 162
E value 3.0e-11
Match length 72
% identity 49
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]

Seq. No. 296713
Seq. ID LIB3117-002-Q1-K1-F8
Method BLASTN
NCBI GI g4185305
BLAST score 88
E value 9.0e-42
Match length 233
% identity 86
NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
(sz22-21) gene, complete cds; retrotransposon Opie-2 gag
protein, polyprotein, and copia protein genes, complete
cds; and unknown genes

Seq. No. 296714
Seq. ID LIB3117-002-Q1-K1-G12
Method BLASTN
NCBI GI g1848280
BLAST score 33
E value 4.0e-09
Match length 41
% identity 95
NCBI Description Sorghum bicolor membrane intrinsic protein (Mip1) mRNA,
partial cds

Seq. No. 296715
Seq. ID LIB3117-002-Q1-K1-G4
Method BLASTN
NCBI GI g168581
BLAST score 111
E value 1.0e-55
Match length 155
% identity 94
NCBI Description Z.mays pyruvate,orthophosphate dikinase (PPDK2) gene, 3'

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Seq. No. 296716
Seq. ID LIB3117-002-Q1-K1-H10
Method BLASTX
NCBI GI g168489
BLAST score 403
E value 1.0e-39
Match length 78
% identity 99
NCBI Description (M16902) glutathione S-transferase I [Zea mays] >gi_168491
(M16901) glutathione S-transferase I [Zea mays]
>gi_225458_prf_1303351A transferase,glutathione S [Zea mays]

Seq. No. 296717
Seq. ID LIB3117-002-Q1-K1-H5
Method BLASTX
NCBI GI g22216
BLAST score 152
E value 3.0e-10
Match length 44
% identity 64
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 296718
Seq. ID LIB3117-002-Q1-K1-H7
Method BLASTX
NCBI GI g585202
BLAST score 246
E value 4.0e-21
Match length 97
% identity 53
NCBI Description GLUTAMINE SYNTHETASE ROOT ISOZYME 2 (GLUTAMATE--AMMONIA LIGASE) >gi_481807_pir_S39478 glutamate--ammonia ligase (EC 6.3.1.2) 1-2, cytosolic - maize
>gi_434326_emb_CAA46720_ (X65927) glutamine synthetase [Zea mays]

Seq. No. 296719
Seq. ID LIB3117-002-Q1-K1-H8
Method BLASTX
NCBI GI g463152
BLAST score 253
E value 2.0e-22
Match length 66
% identity 74
NCBI Description (L29505) zein [Zea mays] >gi_1094858_prf_2106415A Met-rich seed storage protein [Zea mays]

Seq. No. 296720
Seq. ID LIB3117-003-Q1-K1-A10
Method BLASTX
NCBI GI g508545
BLAST score 144
E value 3.0e-09
Match length 41

% identity 71
NCBI Description (L34340) zein [Zea mays]

Seq. No. 296721
Seq. ID LIB3117-003-Q1-K1-A12
Method BLASTX
NCBI GI g141613
BLAST score 241
E value 2.0e-20
Match length 111
% identity 46
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
>gi_72305_pir_ZIZM21_22K zein precursor (clone pZ22.1) -
maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]

Seq. No. 296722
Seq. ID LIB3117-003-Q1-K1-B12
Method BLASTX
NCBI GI g224509
BLAST score 222
E value 2.0e-20
Match length 105
% identity 57
NCBI Description zein E19 [Zea mays]

Seq. No. 296723
Seq. ID LIB3117-003-Q1-K1-B5
Method BLASTN
NCBI GI g168484
BLAST score 84
E value 2.0e-39
Match length 208
% identity 85
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 296724
Seq. ID LIB3117-003-Q1-K1-D11
Method BLASTX
NCBI GI g2828280
BLAST score 348
E value 7.0e-33
Match length 76
% identity 83
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]
>gi_2832633_emb_CAA16762_ (AL021711) putative protein
[Arabidopsis thaliana]

Seq. No. 296725
Seq. ID LIB3117-003-Q1-K1-D6
Method BLASTN
NCBI GI g483443
BLAST score 40
E value 3.0e-13
Match length 48
% identity 96
NCBI Description Z.mays IBP2 mRNA for initiator-binding protein

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Seq. No.	296726
Seq. ID	LIB3117-003-Q1-K1-D8
Method	BLASTN
NCBI GI	g22292
BLAST score	49
E value	8.0e-19
Match length	101
% identity	87
NCBI Description	Z.mays mRNA for glycine-rich protein
Seq. No.	296727
Seq. ID	LIB3117-003-Q1-K1-E8
Method	BLASTX
NCBI GI	g82696
BLAST score	160
E value	4.0e-12
Match length	73
% identity	64
NCBI Description	glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]
Seq. No.	296728
Seq. ID	LIB3117-003-Q1-K1-F6
Method	BLASTX
NCBI GI	g224507
BLAST score	398
E value	7.0e-39
Match length	117
% identity	74
NCBI Description	zein A1 [Zea mays]
Seq. No.	296729
Seq. ID	LIB3117-003-Q1-K1-G8
Method	BLASTN
NCBI GI	g2832242
BLAST score	40
E value	4.0e-13
Match length	45
% identity	25
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	296730
Seq. ID	LIB3117-003-Q1-K1-H11
Method	BLASTX
NCBI GI	g141597
BLAST score	351
E value	3.0e-33
Match length	95
% identity	83
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2] [Zea mays]
Seq. No.	296731
Seq. ID	LIB3117-003-Q1-K1-H6
Method	BLASTX

Q5E3D6 E1C0D0

NCBI GI	g2832247
BLAST score	230
E value	7.0e-23
Match length	122
% identity	57
NCBI Description	(AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.	296732
Seq. ID	LIB3117-004-Q1-K1-E10
Method	BLASTX
NCBI GI	g22220
BLAST score	244
E value	1.0e-20
Match length	114
% identity	53
NCBI Description	(X55723) 22 kD zein [Zea mays]
Seq. No.	296733
Seq. ID	LIB3117-004-Q1-K1-G5
Method	BLASTX
NCBI GI	g2245037
BLAST score	163
E value	2.0e-11
Match length	61
% identity	59
NCBI Description	(Z97342) nuclear antigen homolog [Arabidopsis thaliana]
Seq. No.	296734
Seq. ID	LIB3117-005-Q1-K1-A2
Method	BLASTX
NCBI GI	g1321924
BLAST score	176
E value	3.0e-13
Match length	50
% identity	60
NCBI Description	(X92205) NAM [Petunia x hybrida]
Seq. No.	296735
Seq. ID	LIB3117-005-Q1-K1-A8
Method	BLASTX
NCBI GI	g544421
BLAST score	218
E value	6.0e-18
Match length	52
% identity	87
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 1 >gi_485420_pir_S12311 glycine-rich RNA-binding protein (clone S1) - sorghum (fragment) >gi_21623_emb_CAA40863_ (X57663) glycine-rich RNA-binding protein [Sorghum bicolor]
Seq. No.	296736
Seq. ID	LIB3117-005-Q1-K1-H3
Method	BLASTX
NCBI GI	g224508
BLAST score	209
E value	8.0e-17
Match length	71

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% identity 65
NCBI Description zein A20 [Zea mays]

Seq. No. 296737
Seq. ID LIB3117-006-Q1-K1-B10
Method BLASTN
NCBI GI g535019
BLAST score 36
E value 3.0e-11
Match length 77
% identity 87
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)

Seq. No. 296738
Seq. ID LIB3117-006-Q1-K1-D4
Method BLASTX
NCBI GI g100939
BLAST score 354
E value 1.0e-33
Match length 140
% identity 58
NCBI Description zein precursor - maize

Seq. No. 296739
Seq. ID LIB3117-006-Q1-K1-D8
Method BLASTX
NCBI GI g1172977
BLAST score 167
E value 9.0e-12
Match length 84
% identity 46
NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 296740
Seq. ID LIB3117-006-Q1-K1-D9
Method BLASTX
NCBI GI g3851333
BLAST score 317
E value 1.0e-29
Match length 79
% identity 76
NCBI Description (Y09302) putative MADS-domain transcription factor [Zea mays]

Seq. No. 296741
Seq. ID LIB3117-006-Q1-K1-E2
Method BLASTX
NCBI GI g2832243
BLAST score 227
E value 8.0e-19
Match length 114
% identity 48
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 296742
Seq. ID LIB3117-006-Q1-K1-G5

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Method	BLASTX
NCBI GI	g3283912
BLAST score	184
E value	9.0e-14
Match length	89
% identity	37
NCBI Description	(AF070639) unknown [Homo sapiens]
Seq. No.	296743
Seq. ID	LIB3117-007-Q1-K1-A12
Method	BLASTN
NCBI GI	g168669
BLAST score	45
E value	2.0e-16
Match length	45
% identity	100
NCBI Description	Maize 19 kDa zein mRNA, clone cZ19A2, partial cds
Seq. No.	296744
Seq. ID	LIB3117-007-Q1-K1-D11
Method	BLASTN
NCBI GI	g2832242
BLAST score	133
E value	8.0e-69
Match length	188
% identity	15
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	296745
Seq. ID	LIB3117-007-Q1-K1-D12
Method	BLASTN
NCBI GI	g2832242
BLAST score	60
E value	3.0e-25
Match length	208
% identity	17
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	296746
Seq. ID	LIB3117-007-Q1-K1-D8
Method	BLASTX
NCBI GI	g141617
BLAST score	391
E value	6.0e-38
Match length	111
% identity	68
NCBI Description	ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) >gi_100941_pir_S12140 zein Zc1 - maize >gi_100945_pir_B29017 zein 2 - maize >gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays] >gi_168666_(M16460) 16-kDa zein protein [Zea mays]
Seq. No.	296747
Seq. ID	LIB3117-007-Q1-K1-F2
Method	BLASTN
NCBI GI	g2832242
BLAST score	49

E value 1.0e-18
Match length 262
% identity 35
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 296748
Seq. ID LIB3117-008-Q1-K1-B10
Method BLASTX
NCBI GI g2668742
BLAST score 371
E value 1.0e-35
Match length 85
% identity 86
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 296749
Seq. ID LIB3117-008-Q1-K1-D8
Method BLASTX
NCBI GI g3860273
BLAST score 187
E value 2.0e-15
Match length 74
% identity 59
NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]
>gi_4314398_gb_AAD15608_(AC006232) hypothetical protein
[Arabidopsis thaliana]

Seq. No. 296750
Seq. ID LIB3117-008-Q1-K1-E5
Method BLASTX
NCBI GI g82654
BLAST score 219
E value 8.0e-18
Match length 41
% identity 98
NCBI Description 10K zein precursor - maize >gi_22541_emb_CAA30409_ (X07535)
10kDa zein (AA 1 - 150) [Zea mays]

Seq. No. 296751
Seq. ID LIB3117-009-Q1-K1-A4
Method BLASTX
NCBI GI g1346109
BLAST score 248
E value 2.0e-21
Match length 73
% identity 64
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231)
RWD [Oryza sativa]

Seq. No. 296752
Seq. ID LIB3117-009-Q1-K1-C6
Method BLASTN
NCBI GI g22540
BLAST score 154
E value 3.0e-81
Match length 190

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% identity 96
NCBI Description Maize mRNA for 10kDa zein

Seq. No. 296753
Seq. ID LIB3117-009-Q1-K1-F11
Method BLASTN
NCBI GI g22326
BLAST score 96
E value 7.0e-47
Match length 168
% identity 89
NCBI Description Z.mays gene for Hageman factor inhibitor

Seq. No. 296754
Seq. ID LIB3117-009-Q1-K1-G5
Method BLASTX
NCBI GI g4105697
BLAST score 198
E value 7.0e-16
Match length 64
% identity 67
NCBI Description (AF049870) thaumatin-like protein [Arabidopsis thaliana]

Seq. No. 296755
Seq. ID LIB3117-009-Q1-K1-G6
Method BLASTX
NCBI GI g3915847
BLAST score 282
E value 2.0e-25
Match length 108
% identity 61
NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 296756
Seq. ID LIB3117-010-Q1-K1-D2
Method BLASTN
NCBI GI g22530
BLAST score 68
E value 6.0e-30
Match length 252
% identity 81
NCBI Description Zea mays mRNA fragment encoding a zein (clone B49)

Seq. No. 296757
Seq. ID LIB3117-010-Q1-K1-E4
Method BLASTX
NCBI GI g467996
BLAST score 392
E value 4.0e-38
Match length 95
% identity 84
NCBI Description (U04434) flavanone 3-beta-hydroxylase [Zea mays]

Seq. No. 296758
Seq. ID LIB3117-010-Q1-K1-E5
Method BLASTN

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NCBI GI	g22292
BLAST score	57
E value	2.0e-23
Match length	117
% identity	88
NCBI Description	Z.mays mRNA for glycine-rich protein
Seq. No.	296759
Seq. ID	LIB3117-010-Q1-K1-G6
Method	BLASTX
NCBI GI	g3043428
BLAST score	163
E value	1.0e-11
Match length	40
% identity	70
NCBI Description	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
Seq. No.	296760
Seq. ID	LIB3117-011-Q1-K1-B2
Method	BLASTX
NCBI GI	g112994
BLAST score	352
E value	2.0e-33
Match length	92
% identity	77
NCBI Description	GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN >gi_82685_pir_S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564) ABA-inducible gene protein [Zea mays] >gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]
Seq. No.	296761
Seq. ID	LIB3117-011-Q1-K1-D6
Method	BLASTN
NCBI GI	g2832242
BLAST score	425
E value	0.0e+00
Match length	433
% identity	26
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	296762
Seq. ID	LIB3117-011-Q1-K1-E11
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	3.0e-11
Match length	49
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	296763
Seq. ID	LIB3117-011-Q1-K1-E8
Method	BLASTX
NCBI GI	g2832638
BLAST score	287

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E value	7.0e-26
Match length	73
% identity	73
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]
Seq. No.	296764
Seq. ID	LIB3117-011-Q1-K1-F3
Method	BLASTX
NCBI GI	g1184776
BLAST score	189
E value	7.0e-15
Match length	54
% identity	72
NCBI Description	(U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]
Seq. No.	296765
Seq. ID	LIB3117-011-Q1-K1-F7
Method	BLASTX
NCBI GI	g468516
BLAST score	189
E value	2.0e-14
Match length	88
% identity	48
NCBI Description	(X55724) zein [Zea mays]
Seq. No.	296766
Seq. ID	LIB3117-011-Q1-K1-G6
Method	BLASTX
NCBI GI	g548770
BLAST score	166
E value	1.0e-11
Match length	32
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]
Seq. No.	296767
Seq. ID	LIB3117-012-Q1-K1-A3
Method	BLASTN
NCBI GI	g22524
BLAST score	63
E value	5.0e-27
Match length	191
% identity	83
NCBI Description	Zea mays mRNA encoding a zein (clone ZG31A)
Seq. No.	296768
Seq. ID	LIB3117-012-Q1-K1-F5
Method	BLASTX
NCBI GI	g82660
BLAST score	261
E value	7.0e-23
Match length	76
% identity	70
NCBI Description	19K zein precursor (clone ZG31A) - maize (fragment)

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>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 296769
Seq. ID LIB3117-012-Q1-K1-F6
Method BLASTN
NCBI GI g22524
BLAST score 119
E value 2.0e-60
Match length 211
% identity 89
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)

Seq. No. 296770
Seq. ID LIB3117-012-Q1-K1-G6
Method BLASTX
NCBI GI g141605
BLAST score 381
E value 6.0e-37
Match length 89
% identity 87
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize
>gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 296771
Seq. ID LIB3117-013-Q1-K1-A12
Method BLASTX
NCBI GI g1707924
BLAST score 197
E value 5.0e-15
Match length 100
% identity 59
NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 1 PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) (SHRUNKEN-2) >gi_1947182 (M81603) shrunken-2 [Zea mays] >gi_444329_prf_1906378A ADP glucose pyrophosphorylase [Zea mays]

Seq. No. 296772
Seq. ID LIB3117-013-Q1-K1-A6
Method BLASTX
NCBI GI g3980254
BLAST score 297
E value 5.0e-27
Match length 103
% identity 60
NCBI Description (AJ006053) peroxisomal membrane protein [Arabidopsis thaliana]

Seq. No. 296773
Seq. ID LIB3117-013-Q1-K1-A7
Method BLASTX
NCBI GI g3980254
BLAST score 347
E value 9.0e-33
Match length 129

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% identity 51
NCBI Description (AJ006053) peroxisomal membrane protein [Arabidopsis thaliana]

Seq. No. 296774
Seq. ID LIB3117-013-Q1-K1-C11
Method BLASTN
NCBI GI g22516
BLAST score 109
E value 2.0e-54
Match length 265
% identity 85
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 296775
Seq. ID LIB3117-013-Q1-K1-E9
Method BLASTX
NCBI GI g141600
BLAST score 196
E value 3.0e-15
Match length 66
% identity 61
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) -
maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 296776
Seq. ID LIB3117-013-Q1-K1-G9
Method BLASTN
NCBI GI g22537
BLAST score 122
E value 4.0e-62
Match length 162
% identity 66
NCBI Description Maize mRNA for zein polypeptide (clone M6)

Seq. No. 296777
Seq. ID LIB3117-013-Q1-K1-H10
Method BLASTX
NCBI GI g2245098
BLAST score 371
E value 1.0e-35
Match length 84
% identity 77
NCBI Description (Z97343) ribosomal protein [Arabidopsis thaliana]

Seq. No. 296778
Seq. ID LIB3117-014-Q1-K1-B10
Method BLASTX
NCBI GI g141600
BLAST score 176
E value 7.0e-13
Match length 93
% identity 46
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) -
maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 296779
Seq. ID LIB3117-014-Q1-K1-C1
Method BLASTX
NCBI GI g82696
BLAST score 150
E value 9.0e-19
Match length 56
% identity 88
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]

Seq. No. 296780
Seq. ID LIB3117-014-Q1-K1-H4
Method BLASTN
NCBI GI g22544
BLAST score 236
E value 1.0e-130
Match length 330
% identity 83
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 296781
Seq. ID LIB3117-015-Q1-K1-A6
Method BLASTX
NCBI GI g3212852
BLAST score 155
E value 3.0e-10
Match length 109
% identity 36
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 296782
Seq. ID LIB3117-015-Q1-K1-C7
Method BLASTX
NCBI GI g468516
BLAST score 407
E value 8.0e-40
Match length 106
% identity 80
NCBI Description (X55724) zein [Zea mays]

Seq. No. 296783
Seq. ID LIB3117-015-Q1-K1-D4
Method BLASTN
NCBI GI g22544
BLAST score 70
E value 3.0e-31
Match length 237
% identity 82
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 296784
Seq. ID LIB3117-015-Q1-K1-D6
Method BLASTX
NCBI GI g2832243
BLAST score 166

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E value 4.0e-12
Match length 39
% identity 82
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 296785
Seq. ID LIB3117-015-Q1-K1-D7
Method BLASTX
NCBI GI g3450889
BLAST score 162
E value 4.0e-11
Match length 63
% identity 57
NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No. 296786
Seq. ID LIB3117-015-Q1-K1-E6
Method BLASTX
NCBI GI g224513
BLAST score 149
E value 7.0e-11
Match length 57
% identity 68
NCBI Description zein M6 [Zea mays]

Seq. No. 296787
Seq. ID LIB3117-015-Q1-K1-E9
Method BLASTX
NCBI GI g2961378
BLAST score 295
E value 1.0e-26
Match length 115
% identity 34
NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No. 296788
Seq. ID LIB3117-015-Q1-K1-F4
Method BLASTN
NCBI GI g1060934
BLAST score 102
E value 2.0e-50
Match length 194
% identity 88
NCBI Description Maize mRNA for mLIP15 (DNA-binding factor), complete cds

Seq. No. 296789
Seq. ID LIB3118-001-Q1-K1-D12
Method BLASTX
NCBI GI g4454464
BLAST score 147
E value 5.0e-12
Match length 46
% identity 80
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 296790
Seq. ID LIB3118-001-Q1-K1-E10

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Method	BLASTX
NCBI GI	g2144583
BLAST score	201
E value	5.0e-16
Match length	59
% identity	64
NCBI Description	proteinase inhibitor (Bowman-Birk) D-II precursor - soybean >gi_18572_emb_CAA48657_(X68706) Bowman-Birk proteinase isoinhibitor D-II [Glycine max] >gi_288619_emb_CAA48658 (X68707) Soybean Bowman-Birk proteinase iso-inhibitor D-II [Glycine max] >gi_743636_prf_2013215A Bowman-Birk protease inhibitor [Glycine max]
Seq. No.	296791
Seq. ID	LIB3118-001-Q1-K1-H10
Method	BLASTX
NCBI GI	g2144584
BLAST score	145
E value	1.0e-09
Match length	72
% identity	50
NCBI Description	trypsin inhibitor A (Kunitz) precursor - soybean >gi_18770_emb_CAA45777_(X64447) trypsin inhibitor subtype A [Glycine max]
Seq. No.	296792
Seq. ID	LIB3118-001-Q1-K1-H12
Method	BLASTX
NCBI GI	g2144584
BLAST score	153
E value	1.0e-10
Match length	45
% identity	73
NCBI Description	trypsin inhibitor A (Kunitz) precursor - soybean >gi_18770_emb_CAA45777_(X64447) trypsin inhibitor subtype A [Glycine max]
Seq. No.	296793
Seq. ID	LIB3118-002-Q1-K1-B2
Method	BLASTN
NCBI GI	g662367
BLAST score	76
E value	7.0e-35
Match length	125
% identity	100
NCBI Description	Zea mays farnesyl pyrophosphate synthetase (fps) mRNA, complete cds
Seq. No.	296794
Seq. ID	LIB3118-002-Q1-K1-B4
Method	BLASTN
NCBI GI	g2828011
BLAST score	54
E value	1.0e-21
Match length	194
% identity	84
NCBI Description	Zea mays starch synthase I precursor (Ss1) mRNA, nuclear

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gene encoding plastid protein, complete cds

Seq. No. 296795
Seq. ID LIB3118-002-Q1-K1-B8
Method BLASTX
NCBI GI g141605
BLAST score 511
E value 6.0e-52
Match length 129
% identity 81
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 296796
Seq. ID LIB3118-002-Q1-K1-D11
Method BLASTX
NCBI GI g82696
BLAST score 277
E value 8.0e-29
Match length 83
% identity 86
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_
(X61121) glycine-rich protein [Zea mays]

Seq. No. 296797
Seq. ID LIB3118-002-Q1-K1-D5
Method BLASTN
NCBI GI g2832242
BLAST score 94
E value 1.0e-45
Match length 233
% identity 11
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 296798
Seq. ID LIB3118-002-Q1-K1-E11
Method BLASTX
NCBI GI g4206306
BLAST score 240
E value 3.0e-20
Match length 65
% identity 68
NCBI Description (AF049110) prpol [Zea mays]

Seq. No. 296799
Seq. ID LIB3118-002-Q1-K1-E6
Method BLASTX
NCBI GI g130172
BLAST score 145
E value 2.0e-09
Match length 58
% identity 50
NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME PRECURSOR (STARCH
PHOSPHORYLASE L) >gi_168276 (M64362) starch phosphorylase
[Ipomoea batatas]

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Seq. No.	296800
Seq. ID	LIB3118-002-Q1-K1-H11
Method	BLASTX
NCBI GI	g72307
BLAST score	379
E value	1.0e-36
Match length	111
% identity	75
NCBI Description	22K zein precursor (clone pZ22.3) - maize >gi_168686 (J01246) 26.99 kd zein protein [Zea mays]
Seq. No.	296801
Seq. ID	LIB3118-002-Q1-K1-H4
Method	BLASTX
NCBI GI	g168586
BLAST score	243
E value	2.0e-20
Match length	69
% identity	72
NCBI Description	(M58656) pyruvate,orthophosphate dikinase [Zea mays]
Seq. No.	296802
Seq. ID	LIB3118-002-Q1-K1-H5
Method	BLASTX
NCBI GI	g1710530
BLAST score	291
E value	3.0e-26
Match length	102
% identity	54
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir_S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]
Seq. No.	296803
Seq. ID	LIB3118-003-Q1-K1-A4
Method	BLASTX
NCBI GI	g141605
BLAST score	152
E value	7.0e-10
Match length	144
% identity	33
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) >gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.	296804
Seq. ID	LIB3118-003-Q1-K1-B1
Method	BLASTX
NCBI GI	g141599
BLAST score	218
E value	8.0e-18
Match length	79
% identity	59
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2) >gi_72316_pir_ZIZMA2 19K zein precursor (clone cZ19A2) - maize (fragment) >gi_168670 (M12142) 19 kDa zein protein

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[Zea mays]

Seq. No. 296805
Seq. ID LIB3118-003-Q1-K1-B6
Method BLASTX
NCBI GI g3492806
BLAST score 246
E value 7.0e-21
Match length 115
% identity 44
NCBI Description (AJ225045) adventitious rooting related oxygenase [Malus domestica]

Seq. No. 296806
Seq. ID LIB3118-003-Q1-K1-B7
Method BLASTX
NCBI GI g141605
BLAST score 297
E value 6.0e-27
Match length 109
% identity 61
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 296807
Seq. ID LIB3118-003-Q1-K1-D10
Method BLASTX
NCBI GI g141598
BLAST score 227
E value 4.0e-19
Match length 84
% identity 60
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
>gi_72313_pir_ZIZM99 19K zein precursor (clone ZG99) - maize >gi_22519_emb_CAA24717_ (V01470) zein [Zea mays]
>gi_22534_emb_CAA24726_ (V01479) zein [Zea mays]

Seq. No. 296808
Seq. ID LIB3118-003-Q1-K1-D11
Method BLASTN
NCBI GI g602252
BLAST score 43
E value 4.0e-15
Match length 71
% identity 90
NCBI Description Zea mays enolase (eno2) mRNA, complete cds

Seq. No. 296809
Seq. ID LIB3118-003-Q1-K1-D4
Method BLASTX
NCBI GI g82696
BLAST score 451
E value 5.0e-45
Match length 94
% identity 93
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_

(X61121) glycine-rich protein [Zea mays]

Seq. No. 296810
Seq. ID LIB3118-003-Q1-K1-E4
Method BLASTX
NCBI GI g232161
BLAST score 176
E value 9.0e-13
Match length 77
% identity 55
NCBI Description 19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN)
>gi_68857_pir_WMRZ19 19K globulin precursor - rice
>gi_20159_emb_CAA45400_ (X63990) 19 kDa globulin precursor
[Oryza sativa]

Seq. No. 296811
Seq. ID LIB3118-003-Q1-K1-E7
Method BLASTN
NCBI GI g21794
BLAST score 50
E value 3.0e-19
Match length 98
% identity 88
NCBI Description Wheat histone H4 gene

Seq. No. 296812
Seq. ID LIB3118-003-Q1-K1-F11
Method BLASTN
NCBI GI g22292
BLAST score 35
E value 2.0e-10
Match length 59
% identity 90
NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 296813
Seq. ID LIB3118-003-Q1-K1-G3
Method BLASTX
NCBI GI g168697
BLAST score 405
E value 2.0e-49
Match length 132
% identity 86
NCBI Description (M60835) zein [Zea mays]

Seq. No. 296814
Seq. ID LIB3118-003-Q1-K1-G4
Method BLASTX
NCBI GI g141604
BLAST score 292
E value 4.0e-43
Match length 147
% identity 61
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
>gi_72310_pir_ZIZM91 19K zein precursor (clone cZ19C1) -
maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]

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Seq. No.	296815
Seq. ID	LIB3118-005-Q1-K1-A11
Method	BLASTX
NCBI GI	g2266992
BLAST score	201
E value	5.0e-16
Match length	73
% identity	55
NCBI Description	(U77412) O-linked GlcNAc transferase [Caenorhabditis elegans]
Seq. No.	296816
Seq. ID	LIB3118-005-Q1-K1-A5
Method	BLASTX
NCBI GI	g730461
BLAST score	205
E value	4.0e-16
Match length	56
% identity	64
NCBI Description	40S RIBOSOMAL PROTEIN YS29A >gi_626904_pir_S48503 ribosomal protein S29.e.A, cytosolic - yeast (Saccharomyces cerevisiae) >gi_287628_dbj_BAA03507 (D14676) ribosomal protein YS29 [Saccharomyces cerevisiae] >gi_625108 (U19729) Ylr388wp [Saccharomyces cerevisiae]
Seq. No.	296817
Seq. ID	LIB3118-005-Q1-K1-B11
Method	BLASTN
NCBI GI	g22312
BLAST score	153
E value	1.0e-80
Match length	200
% identity	95
NCBI Description	Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)
Seq. No.	296818
Seq. ID	LIB3118-005-Q1-K1-B3
Method	BLASTX
NCBI GI	g168699
BLAST score	293
E value	2.0e-26
Match length	79
% identity	78
NCBI Description	(M60836) zein [Zea mays]
Seq. No.	296819
Seq. ID	LIB3118-005-Q1-K1-B5
Method	BLASTX
NCBI GI	g168699
BLAST score	270
E value	6.0e-24
Match length	78
% identity	73
NCBI Description	(M60836) zein [Zea mays]
Seq. No.	296820

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Seq. ID	LIB3118-005-Q1-K1-C3
Method	BLASTN
NCBI GI	g22544
BLAST score	112
E value	2.0e-56
Match length	167
% identity	92
NCBI Description	Maize mRNA (clone A30) for zein (a plant storage protein)
Seq. No.	296821
Seq. ID	LIB3118-005-Q1-K1-E3
Method	BLASTX
NCBI GI	g168699
BLAST score	227
E value	7.0e-19
Match length	108
% identity	36
NCBI Description	(M60836) zein [Zea mays]
Seq. No.	296822
Seq. ID	LIB3118-005-Q1-K1-F12
Method	BLASTN
NCBI GI	g535019
BLAST score	66
E value	5.0e-29
Match length	145
% identity	44
NCBI Description	Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
Seq. No.	296823
Seq. ID	LIB3118-005-Q1-K1-H5
Method	BLASTX
NCBI GI	g82696
BLAST score	389
E value	1.0e-37
Match length	86
% identity	90
NCBI Description	glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]
Seq. No.	296824
Seq. ID	LIB3118-006-Q1-K1-A5
Method	BLASTX
NCBI GI	g1705844
BLAST score	263
E value	8.0e-23
Match length	85
% identity	62
NCBI Description	CHALCONE SYNTHASE RJ5 (NARINGENIN-CHALCONE SYNTHASE) >gi_1362040_pir_S56675 naringenin-chalcone synthase homolog RJ5 - garden strawberry (fragment) >gi_643078 (U19942) chalcone synthase [Fragaria x ananassa]
Seq. No.	296825
Seq. ID	LIB3118-006-Q1-K1-A6
Method	BLASTX
NCBI GI	g2911057

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BLAST score 189
E value 2.0e-14
Match length 52
% identity 73
NCBI Description (AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No. 296826
Seq. ID LIB3118-006-Q1-K1-A8
Method BLASTN
NCBI GI g5091496
BLAST score 35
E value 3.0e-10
Match length 71
% identity 87
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No. 296827
Seq. ID LIB3118-006-Q1-K1-B10
Method BLASTX
NCBI GI g168586
BLAST score 238
E value 3.0e-20
Match length 72
% identity 68
NCBI Description (M58656) pyruvate,orthophosphate dikinase [Zea mays]

Seq. No. 296828
Seq. ID LIB3118-006-Q1-K1-B7
Method BLASTX
NCBI GI g2944417
BLAST score 278
E value 1.0e-24
Match length 112
% identity 57
NCBI Description (AF049881) peroxidase FLXPER4 [Linum usitatissimum]

Seq. No. 296829
Seq. ID LIB3118-006-Q1-K1-E12
Method BLASTX
NCBI GI g2832243
BLAST score 179
E value 2.0e-13
Match length 76
% identity 55
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 296830
Seq. ID LIB3118-006-Q1-K1-H3
Method BLASTX
NCBI GI g122106
BLAST score 227
E value 7.0e-19
Match length 53
% identity 91
NCBI Description HISTONE H4 >gi_70771_pir_HSZM4 histone H4 - maize

D E G E N E R A T I O N

>gi_81642_pir_S06904 histone H4 - Arabidopsis thaliana
>gi_2119028_pir_S60475 histone H4 - garden pea
>gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]
>gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata]
>gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
>gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_225838_prf_1314298A histone H4 [Arabidopsis thaliana]

Seq. No. 296831
Seq. ID LIB3118-007-Q1-K1-A5
Method BLASTN
NCBI GI g1184773
BLAST score 35
E value 2.0e-10
Match length 35
% identity 100
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3 (gpc3) mRNA, complete cds

Seq. No. 296832
Seq. ID LIB3118-007-Q1-K1-A7
Method BLASTX
NCBI GI g168586
BLAST score 235
E value 5.0e-20
Match length 79
% identity 63
NCBI Description (M58656) pyruvate,orthophosphate dikinase [Zea mays]

Seq. No. 296833
Seq. ID LIB3118-007-Q1-K1-C1
Method BLASTX
NCBI GI g2832243
BLAST score 165
E value 1.0e-11
Match length 64
% identity 55
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 296834
Seq. ID LIB3118-007-Q1-K1-C3
Method BLASTX
NCBI GI g466160
BLAST score 336
E value 1.0e-31
Match length 81
% identity 80
NCBI Description HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
>gi_630771_pir_S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis

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Seq. No. 296835
Seq. ID LIB3118-007-Q1-K1-C6
Method BLASTX
NCBI GI g141613
BLAST score 195
E value 3.0e-15
Match length 90
% identity 49
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
>gi_72305_pir_ZIZM21_22K zein precursor (clone pZ22.1) -
maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]

Seq. No. 296836
Seq. ID LIB3118-007-Q1-K1-F6
Method BLASTX
NCBI GI g82696
BLAST score 259
E value 8.0e-23
Match length 87
% identity 62
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_
(X61121) glycine-rich protein [Zea mays]

Seq. No. 296837
Seq. ID LIB3118-008-Q1-K1-A4
Method BLASTN
NCBI GI g463151
BLAST score 185
E value 1.0e-99
Match length 409
% identity 86
NCBI Description Zea mays high sulfur zein gene, complete cds

Seq. No. 296838
Seq. ID LIB3118-008-Q1-K1-B2
Method BLASTN
NCBI GI g463151
BLAST score 68
E value 7.0e-30
Match length 148
% identity 86
NCBI Description Zea mays high sulfur zein gene, complete cds

Seq. No. 296839
Seq. ID LIB3118-008-Q1-K1-B5
Method BLASTX
NCBI GI g550434
BLAST score 322
E value 8.0e-30
Match length 110
% identity 56
NCBI Description (X81828) cytochrome P450 [Zea mays]

Seq. No. 296840
Seq. ID LIB3118-008-Q1-K1-B7

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Method	BLASTX
NCBI GI	g266398
BLAST score	254
E value	4.0e-22
Match length	61
% identity	79
NCBI Description	TRYPSIN/FACTOR XIII A INHIBITOR PRECURSOR (HAGEMAN FACTOR INHIBITOR) (CHFI) >gi_68849_pir_TIZM1 trypsin/factor XIIIa inhibitor precursor - maize >gi_22327_emb_CAA37998_(X54064) corn Hageman factor inhibitor [Zea mays]
Seq. No.	296841
Seq. ID	LIB3118-008-Q1-K1-C6
Method	BLASTX
NCBI GI	g82696
BLAST score	164
E value	9.0e-25
Match length	86
% identity	71
NCBI Description	glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]
Seq. No.	296842
Seq. ID	LIB3118-008-Q1-K1-D10
Method	BLASTN
NCBI GI	g168675
BLAST score	52
E value	1.0e-20
Match length	121
% identity	84
NCBI Description	Maize mutant zein (zE19) gene, complete cds
Seq. No.	296843
Seq. ID	LIB3118-008-Q1-K1-D9
Method	BLASTN
NCBI GI	g168675
BLAST score	62
E value	2.0e-26
Match length	150
% identity	87
NCBI Description	Maize mutant zein (zE19) gene, complete cds
Seq. No.	296844
Seq. ID	LIB3118-008-Q1-K1-E8
Method	BLASTX
NCBI GI	g4432814
BLAST score	188
E value	2.0e-14
Match length	93
% identity	45
NCBI Description	(AC006593) unknown protein [Arabidopsis thaliana]
Seq. No.	296845
Seq. ID	LIB3118-008-Q1-K1-G6
Method	BLASTX
NCBI GI	g129916
BLAST score	203

E value 1.0e-21
Match length 118
% identity 57
NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir_TVWTGY
phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
>gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
(AA 1 - 401) [Triticum aestivum]

Seq. No. 296846
Seq. ID LIB3118-008-Q1-K1-G9
Method BLASTN
NCBI GI g22516
BLAST score 141
E value 1.0e-73
Match length 161
% identity 97
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 296847
Seq. ID LIB3118-009-Q1-K1-A8
Method BLASTX
NCBI GI g100547
BLAST score 156
E value 2.0e-10
Match length 60
% identity 55
NCBI Description globulin precursor - oat

Seq. No. 296848
Seq. ID LIB3118-009-Q1-K1-B3
Method BLASTX
NCBI GI g141600
BLAST score 241
E value 4.0e-29
Match length 104
% identity 69
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) -
maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 296849
Seq. ID LIB3118-009-Q1-K1-B7
Method BLASTN
NCBI GI g22544
BLAST score 70
E value 4.0e-31
Match length 226
% identity 84
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 296850
Seq. ID LIB3118-009-Q1-K1-C6
Method BLASTX
NCBI GI g2982245
BLAST score 162
E value 2.0e-11
Match length 73

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% identity 47
NCBI Description (AF051205) hypothetical protein [Picea mariana]

Seq. No. 296851
Seq. ID LIB3118-009-Q1-K1-C7
Method BLASTX
NCBI GI g3377797
BLAST score 236
E value 7.0e-20
Match length 86
% identity 63
NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara]

Seq. No. 296852
Seq. ID LIB3118-009-Q1-K1-E3
Method BLASTN
NCBI GI g2811133
BLAST score 214
E value 1.0e-117
Match length 277
% identity 95
NCBI Description Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA, partial cds

Seq. No. 296853
Seq. ID LIB3118-010-Q1-K1-A2
Method BLASTX
NCBI GI g141597
BLAST score 166
E value 7.0e-24
Match length 109
% identity 66
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 296854
Seq. ID LIB3118-010-Q1-K1-B7
Method BLASTN
NCBI GI g22312
BLAST score 78
E value 6.0e-36
Match length 191
% identity 92
NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)

Seq. No. 296855
Seq. ID LIB3118-010-Q1-K1-C8
Method BLASTX
NCBI GI g112994
BLAST score 319

E value 1.0e-29
Match length 71
% identity 86
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
>gi_82685_pir_S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 296856
Seq. ID LIB3118-010-Q1-K1-D12
Method BLASTX
NCBI GI g22216
BLAST score 236
E value 7.0e-20
Match length 66
% identity 76
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 296857
Seq. ID LIB3118-010-Q1-K1-H10
Method BLASTN
NCBI GI g2062705
BLAST score 36
E value 5.0e-11
Match length 36
% identity 100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 296858
Seq. ID LIB3118-011-Q1-K1-A6
Method BLASTN
NCBI GI g1314428
BLAST score 150
E value 6.0e-79
Match length 150
% identity 100
NCBI Description Zea mays ssp. huehuetenangensis Doebley M031 ITS1, 5.8S
ribosomal RNA, ITS2

Seq. No. 296859
Seq. ID LIB3118-011-Q1-K1-B1
Method BLASTX
NCBI GI g3264767
BLAST score 269
E value 1.0e-23
Match length 68
% identity 74
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 296860
Seq. ID LIB3118-011-Q1-K1-C10
Method BLASTN
NCBI GI g498774
BLAST score 42
E value 9.0e-15

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Match length 70
% identity 90
NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein

Seq. No. 296861
Seq. ID LIB3118-011-Q1-K1-C4
Method BLASTX
NCBI GI g2119936
BLAST score 171
E value 3.0e-12
Match length 106
% identity 40
NCBI Description translation initiation factor eIF-4A.6 - common tobacco (fragment)

Seq. No. 296862
Seq. ID LIB3118-011-Q1-K1-C6
Method BLASTX
NCBI GI g224507
BLAST score 522
E value 3.0e-53
Match length 152
% identity 74
NCBI Description zein A1 [Zea mays]

Seq. No. 296863
Seq. ID LIB3118-011-Q1-K1-D7
Method BLASTX
NCBI GI g224508
BLAST score 170
E value 3.0e-12
Match length 70
% identity 61
NCBI Description zein A20 [Zea mays]

Seq. No. 296864
Seq. ID LIB3118-011-Q1-K1-E1
Method BLASTN
NCBI GI g168677
BLAST score 55
E value 3.0e-22
Match length 162
% identity 83
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C1, complete cds

Seq. No. 296865
Seq. ID LIB3118-011-Q1-K1-H3
Method BLASTX
NCBI GI g4335745
BLAST score 240
E value 1.0e-20
Match length 99
% identity 43
NCBI Description (AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

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Seq. No. 296866
Seq. ID LIB3118-012-Q1-K1-A3
Method BLASTN
NCBI GI g22514
BLAST score 124
E value 2.0e-63
Match length 232
% identity 88
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 296867
Seq. ID LIB3118-012-Q1-K1-A5
Method BLASTX
NCBI GI g3080400
BLAST score 192
E value 8.0e-15
Match length 48
% identity 73
NCBI Description (AL022603) putative protein [Arabidopsis thaliana]
>gi_4455264_emb_CAB36800.1_ (AL035527) putative protein
[Arabidopsis thaliana]

Seq. No. 296868
Seq. ID LIB3118-012-Q1-K1-B12
Method BLASTX
NCBI GI g141603
BLAST score 154
E value 1.0e-22
Match length 82
% identity 73
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 296869
Seq. ID LIB3118-012-Q1-K1-C9
Method BLASTX
NCBI GI g2832243
BLAST score 190
E value 1.0e-14
Match length 81
% identity 57
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 296870
Seq. ID LIB3118-012-Q1-K1-D6
Method BLASTN
NCBI GI g168702
BLAST score 48
E value 3.0e-18
Match length 116
% identity 86
NCBI Description Corn 22 kDa zein protein gene, complete cds

Seq. No. 296871
Seq. ID LIB3118-012-Q1-K1-E1
Method BLASTX

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NCBI GI g82660
BLAST score 342
E value 3.0e-32
Match length 100
% identity 70
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 296872
Seq. ID LIB3118-012-Q1-K1-E5
Method BLASTX
NCBI GI g82660
BLAST score 339
E value 7.0e-32
Match length 104
% identity 67
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 296873
Seq. ID LIB3118-012-Q1-K1-F10
Method BLASTX
NCBI GI g141598
BLAST score 313
E value 9.0e-29
Match length 120
% identity 58
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
>gi_72313_pir_ZIZM99 19K zein precursor (clone ZG99) - maize
>gi_22519_emb_CAA24717_ (V01470) zein [Zea mays]
>gi_22534_emb_CAA24726_ (V01479) zein [Zea mays]

Seq. No. 296874
Seq. ID LIB3118-012-Q1-K1-F6
Method BLASTX
NCBI GI g4559381
BLAST score 242
E value 1.0e-20
Match length 103
% identity 45
NCBI Description (AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No. 296875
Seq. ID LIB3118-012-Q1-K1-G5
Method BLASTX
NCBI GI g141608
BLAST score 325
E value 2.0e-30
Match length 99
% identity 72
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 296876
Seq. ID LIB3118-012-Q1-K1-G9
Method BLASTN

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NCBI GI	g168681
BLAST score	56
E value	8.0e-23
Match length	144
% identity	85
NCBI Description	Maize 19 kDa zein mRNA, clone cZ19D1, complete cds. >gi_270686_gb_I03333_Sequence 8 from Patent US
Seq. No.	296877
Seq. ID	LIB3118-013-Q1-K1-A1
Method	BLASTX
NCBI GI	g266398
BLAST score	369
E value	2.0e-35
Match length	86
% identity	73
NCBI Description	TRYPSIN/FACTOR XIII A INHIBITOR PRECURSOR (HAGEMAN FACTOR INHIBITOR) (CHFI) >gi_68849_pir_TIZM1 trypsin/factor XIIIa inhibitor precursor - maize >gi_22327_emb_CAA37998_(X54064) corn Hageman factor inhibitor [Zea mays]
Seq. No.	296878
Seq. ID	LIB3118-013-Q1-K1-A11
Method	BLASTX
NCBI GI	g629861
BLAST score	222
E value	2.0e-18
Match length	71
% identity	63
NCBI Description	zein Zd1, 19K - maize >gi_535020_emb_CAA47639_(X67203) zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.	296879
Seq. ID	LIB3118-013-Q1-K1-A4
Method	BLASTX
NCBI GI	g2618701
BLAST score	252
E value	1.0e-21
Match length	93
% identity	60
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]
Seq. No.	296880
Seq. ID	LIB3118-013-Q1-K1-A7
Method	BLASTX
NCBI GI	g266398
BLAST score	196
E value	4.0e-15
Match length	90
% identity	52
NCBI Description	TRYPSIN/FACTOR XIII A INHIBITOR PRECURSOR (HAGEMAN FACTOR INHIBITOR) (CHFI) >gi_68849_pir_TIZM1 trypsin/factor XIIIa inhibitor precursor - maize >gi_22327_emb_CAA37998_(X54064) corn Hageman factor inhibitor [Zea mays]
Seq. No.	296881
Seq. ID	LIB3118-013-Q1-K1-D10

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Method	BLASTX
NCBI GI	g419803
BLAST score	267
E value	1.0e-23
Match length	80
% identity	65
NCBI Description	zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
Seq. No.	296882
Seq. ID	LIB3118-013-Q1-K1-E7
Method	BLASTX
NCBI GI	g585202
BLAST score	214
E value	2.0e-17
Match length	76
% identity	63
NCBI Description	GLUTAMINE SYNTHETASE ROOT ISOZYME 2 (GLUTAMATE--AMMONIA LIGASE) >gi_481807_pir_S39478 glutamate--ammonia ligase (EC 6.3.1.2) 1-2, cytosolic - maize >gi_434326_emb_CAA46720_ (X65927) glutamine synthetase [Zea mays]
Seq. No.	296883
Seq. ID	LIB3118-013-Q1-K1-G5
Method	BLASTX
NCBI GI	g129916
BLAST score	151
E value	4.0e-10
Match length	90
% identity	41
NCBI Description	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir_TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum]
Seq. No.	296884
Seq. ID	LIB3118-013-Q1-K1-H10
Method	BLASTX
NCBI GI	g224507
BLAST score	164
E value	2.0e-11
Match length	50
% identity	64
NCBI Description	zein A1 [Zea mays]
Seq. No.	296885
Seq. ID	LIB3118-014-Q1-K1-A9
Method	BLASTX
NCBI GI	g4158230
BLAST score	290
E value	2.0e-26
Match length	85
% identity	71
NCBI Description	(Y18625) amylogenin [Triticum aestivum]
Seq. No.	296886

Seq. ID LIB3118-014-Q1-K1-B1
Method BLASTX
NCBI GI g129081
BLAST score 224
E value 2.0e-18
Match length 75
% identity 63
NCBI Description OLEOSIN ZM-II (OLEOSIN 18 KD) (LIPID BODY-ASSOCIATED PROTEIN L2) >gi_100904_pir_A35040 oleosin 18 - maize >gi_168509 (J05212) oleosin KD18 (L2) [Zea mays]

Seq. No. 296887
Seq. ID LIB3118-014-Q1-K1-B11
Method BLASTX
NCBI GI g3328122
BLAST score 167
E value 4.0e-12
Match length 53
% identity 66
NCBI Description (AF073473) phosphoglycerate kinase precursor [Solanum tuberosum]

Seq. No. 296888
Seq. ID LIB3118-014-Q1-K1-B6
Method BLASTX
NCBI GI g2829924
BLAST score 143
E value 6.0e-09
Match length 58
% identity 48
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 296889
Seq. ID LIB3118-014-Q1-K1-C10
Method BLASTX
NCBI GI g629862
BLAST score 469
E value 4.0e-47
Match length 108
% identity 86
NCBI Description zein Zd1, 19K - maize >gi_535021_emb_CAA47640_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 296890
Seq. ID LIB3118-014-Q1-K1-D3
Method BLASTX
NCBI GI g282881
BLAST score 218
E value 1.0e-17
Match length 109
% identity 43
NCBI Description receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 296891
Seq. ID LIB3118-014-Q1-K1-E10

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Method	BLASTX
NCBI GI	g944842
BLAST score	140
E value	4.0e-09
Match length	65
% identity	54
NCBI Description	(X80023) ATP/ADP carrier protein [Triticum turgidum]
Seq. No.	296892
Seq. ID	LIB3118-014-Q1-K1-E12
Method	BLASTX
NCBI GI	g141614
BLAST score	325
E value	3.0e-30
Match length	123
% identity	60
NCBI Description	ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1) >gi_82662_pir_B22831 22K zein precursor (clone M1) - maize >gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea mays] >gi_224510_prf_1107201D zein M1 [Zea mays]
Seq. No.	296893
Seq. ID	LIB3118-014-Q1-K1-E4
Method	BLASTX
NCBI GI	g629861
BLAST score	331
E value	6.0e-31
Match length	98
% identity	70
NCBI Description	zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203) zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.	296894
Seq. ID	LIB3136-001-P1-K1-A7
Method	BLASTX
NCBI GI	g4337179
BLAST score	152
E value	4.0e-10
Match length	63
% identity	49
NCBI Description	(AC006416) This gene is continued on the 5' end of BAC T12M14. [Arabidopsis thaliana]
Seq. No.	296895
Seq. ID	LIB3136-001-P1-K1-C9
Method	BLASTX
NCBI GI	g2511531
BLAST score	220
E value	6.0e-18
Match length	95
% identity	58
NCBI Description	(AF008120) alpha tubulin 1 [Eleusine indica] >gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1 [Eleusine indica]
Seq. No.	296896
Seq. ID	LIB3136-002-P1-K1-B11

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Method	BLASTX
NCBI GI	g4056469
BLAST score	192
E value	2.0e-24
Match length	84
% identity	74
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from <i>Arabidopsis thaliana</i> . ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t
Seq. No.	296897
Seq. ID	LIB3136-002-P1-K1-C1
Method	BLASTX
NCBI GI	g2827143
BLAST score	175
E value	9.0e-13
Match length	107
% identity	40
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]
Seq. No.	296898
Seq. ID	LIB3136-002-P1-K1-D2
Method	BLASTX
NCBI GI	g136745
BLAST score	712
E value	2.0e-75
Match length	151
% identity	89
NCBI Description	FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE) (BRONZE-1) (BZ-W22 ALLELE) >gi_82690_pir_S01037 flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (allele Bz-W22) - maize >gi_22210_emb_CAA30760_(X07937) UDPglucose flavonoid glycosyl transferase [Zea mays] >gi_22506_emb_CAA31857_ (X13502) UFGT (AA 1 - 471) [Zea mays]
Seq. No.	296899
Seq. ID	LIB3136-002-P1-K1-E8
Method	BLASTX
NCBI GI	g1350969
BLAST score	207
E value	1.0e-16
Match length	62
% identity	66
NCBI Description	40S RIBOSOMAL PROTEIN S26 (S31) >gi_971284_dbj_BAA07208_(D38011) ribosomal protein S31 [<i>Oryza sativa</i>]
Seq. No..	296900
Seq. ID	LIB3136-002-P1-K1-G9
Method	BLASTX
NCBI GI	g4582787
BLAST score	221
E value	1.0e-18
Match length	54

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% identity 83
NCBI Description (AJ012281) adenosine kinase [Zea mays]

Seq. No. 296901
Seq. ID LIB3136-002-P1-K1-H11
Method BLASTX
NCBI GI g3334115
BLAST score 213
E value 3.0e-17
Match length 74
% identity 64
NCBI Description ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664
(AF006489) adenine nucleotide translocator 1 [Gossypium
hirsutum].

Seq. No. 296902
Seq. ID LIB3136-003-Q1-K1-A10
Method BLASTX
NCBI GI g3935148
BLAST score 172
E value 4.0e-23
Match length 110
% identity 55
NCBI Description (AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No. 296903
Seq. ID LIB3136-003-Q1-K1-A4
Method BLASTX
NCBI GI g584893
BLAST score 164
E value 1.0e-11
Match length 80
% identity 47
NCBI Description SERINE CARBOXYPEPTIDASE III PRECURSOR
>gi_283002_pir_S22530 carboxypeptidase III (EC 3.4.16.-) -
rice >gi_218153_dbj_BAA01757_ (D10985) serine
carboxypeptidase III [Oryza sativa]

Seq. No. 296904
Seq. ID LIB3136-003-Q1-K1-B8
Method BLASTX
NCBI GI g2827534
BLAST score 264
E value 3.0e-23
Match length 92
% identity 63
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 296905
Seq. ID LIB3136-003-Q1-K1-C1
Method BLASTX
NCBI GI g2492636
BLAST score 457
E value 9.0e-46
Match length 95
% identity 94

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NCBI Description ACONITASE (ACONITATE HYDRATASE) (CITRATE HYDRO-LYASE)
>gi_1084317_pir_S49849 aconitase hydratase (EC 4.2.1.3) -
muskmelon (fragment) >gi_599723_emb_CAA58047_ (X82840)
aconitase [Cucumis melo]

Seq. No. 296906
Seq. ID LIB3136-003-Q1-K1-E11
Method BLASTX
NCBI GI g3236259
BLAST score 245
E value 7.0e-21
Match length 102
% identity 52
NCBI Description (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 296907
Seq. ID LIB3136-004-Q1-K1-C4
Method BLASTN
NCBI GI g2431768
BLAST score 104
E value 1.0e-51
Match length 180
% identity 89
NCBI Description Zea mays acidic ribosomal protein Pla (rppla) mRNA,
complete cds

Seq. No. 296908
Seq. ID LIB3136-004-Q1-K1-D1
Method BLASTX
NCBI GI g1931647
BLAST score 325
E value 3.0e-30
Match length 77
% identity 81
NCBI Description (U95973) endomembrane protein EMP70 precursor isolog
[Arabidopsis thaliana]

Seq. No. 296909
Seq. ID LIB3136-004-Q1-K1-F2
Method BLASTX
NCBI GI g2062167
BLAST score 391
E value 6.0e-38
Match length 123
% identity 58
NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No. 296910
Seq. ID LIB3136-004-Q1-K1-F9
Method BLASTN
NCBI GI g551482
BLAST score 40
E value 4.0e-13
Match length 126
% identity 83

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NCBI Description Zea mays ABA- and ripening-inducible-like protein mRNA, complete cds

Seq. No. 296911
Seq. ID LIB3136-004-Q1-K1-G1
Method BLASTX
NCBI GI g2262099
BLAST score 177
E value 4.0e-13
Match length 74
% identity 46
NCBI Description (AC002343) thaumatin isolog [Arabidopsis thaliana]

Seq. No. 296912
Seq. ID LIB3136-004-Q1-K1-G9
Method BLASTX
NCBI GI g2108252
BLAST score 271
E value 5.0e-24
Match length 112
% identity 56
NCBI Description (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
>gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
[Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1
(AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No. 296913
Seq. ID LIB3136-004-Q1-K1-H1
Method BLASTX
NCBI GI g1839188
BLAST score 150
E value 1.0e-09
Match length 56
% identity 55
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 296914
Seq. ID LIB3136-005-Q1-K1-A11
Method BLASTX
NCBI GI g2244888
BLAST score 144
E value 3.0e-09
Match length 46
% identity 48
NCBI Description (Z97338) similarity to cytochrome P450 [Arabidopsis thaliana]

Seq. No. 296915
Seq. ID LIB3136-005-Q1-K1-B4
Method BLASTN
NCBI GI g1845194
BLAST score 184
E value 4.0e-99
Match length 271
% identity 93
NCBI Description Z.mays mRNA for HMGcl protein

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Seq. No. 296916
Seq. ID LIB3136-005-Q1-K1-C11
Method BLASTX
NCBI GI g2495171
BLAST score 468
E value 4.0e-47
Match length 96
% identity 93
NCBI Description DELTA-AMINOLEVULINIC ACID DEHYDRATASE PRECURSOR
(PORPHOBILINOGEN SYNTHASE) (ALADH)
>gi_1041423_emb_CAA63139_(X92402) aminolevulinate
dehydratase [Hordeum vulgare]

Seq. No. 296917
Seq. ID LIB3136-005-Q1-K1-D3
Method BLASTX
NCBI GI g3451067
BLAST score 154
E value 1.0e-10
Match length 64
% identity 50
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 296918
Seq. ID LIB3136-005-Q1-K1-E2
Method BLASTX
NCBI GI g2326947
BLAST score 288
E value 4.0e-26
Match length 91
% identity 64
NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor
[Zea mays]

Seq. No. 296919
Seq. ID LIB3136-005-Q1-K1-F10
Method BLASTX
NCBI GI g893294
BLAST score 183
E value 7.0e-14
Match length 86
% identity 50
NCBI Description (L43362) 4-coumarate:CoA ligase isoform 2 [Oryza sativa]

Seq. No. 296920
Seq. ID LIB3136-005-Q1-K1-F11
Method BLASTX
NCBI GI g2511531
BLAST score 258
E value 6.0e-29
Match length 86
% identity 76
NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]
>gi_3163944_emb_CAA06618_(AJ005598) alpha-tubulin 1
[Eleusine indica]

Seq. No. 296921

Seq. ID LIB3136-005-Q1-K1-H1
Method BLASTX
NCBI GI g1076421
BLAST score 185
E value 8.0e-14
Match length 46
% identity 80
NCBI Description transcription factor TGA3 - Arabidopsis thaliana >gi_304113 (L10209) transcription factor [Arabidopsis thaliana]

Seq. No. 296922
Seq. ID LIB3136-006-Q1-K1-A10
Method BLASTX
NCBI GI g2911059
BLAST score 459
E value 5.0e-46
Match length 99
% identity 84
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 296923
Seq. ID LIB3136-006-Q1-K1-B10
Method BLASTX
NCBI GI g2980806
BLAST score 207
E value 2.0e-16
Match length 60
% identity 58
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 296924
Seq. ID LIB3136-006-Q1-K1-B3
Method BLASTX
NCBI GI g2109457
BLAST score 244
E value 6.0e-21
Match length 84
% identity 61
NCBI Description (AF001501) chitinase [Oryza sativa]

Seq. No. 296925
Seq. ID LIB3136-006-Q1-K1-B7
Method BLASTX
NCBI GI g2702280
BLAST score 668
E value 2.0e-70
Match length 140
% identity 89
NCBI Description (AC003033) photomorphogenesis repressor COP1 [Arabidopsis thaliana]

Seq. No. 296926
Seq. ID LIB3136-006-Q1-K1-D7
Method BLASTX
NCBI GI g642134
BLAST score 157
E value 2.0e-15

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Match length 69
% identity 68
NCBI Description (D45355) protein kinase [Arabidopsis thaliana]
>gi_3063704_emb_CAA18595.1_ (AL022537) protein kinase AME3
[Arabidopsis thaliana]

Seq. No. 296927
Seq. ID LIB3136-007-Q1-K1-E6
Method BLASTX
NCBI GI g3043428
BLAST score 355
E value 9.0e-34
Match length 89
% identity 75
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No. 296928
Seq. ID LIB3136-007-Q1-K1-H9
Method BLASTX
NCBI GI g2921304
BLAST score 309
E value 9.0e-55
Match length 129
% identity 86
NCBI Description (AF033496) herbicide safener binding protein [Zea mays]

Seq. No. 296929
Seq. ID LIB3136-008-Q1-K1-A12
Method BLASTX
NCBI GI g2829910
BLAST score 581
E value 3.0e-60
Match length 136
% identity 28
NCBI Description (AC002291) Unknown protein, contains regulator of
chromosome condensation motifs [Arabidopsis thaliana]

Seq. No. 296930
Seq. ID LIB3136-008-Q1-K1-B8
Method BLASTX
NCBI GI g3928543
BLAST score 146
E value 1.0e-09
Match length 42
% identity 55
NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
thaliana]

Seq. No. 296931
Seq. ID LIB3136-008-Q1-K1-C7
Method BLASTX
NCBI GI g3548802
BLAST score 337
E value 1.0e-31
Match length 132
% identity 52
NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi_4335769_gb_AAD17446_ (AC006284) putative axil protein
[Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 296932
Seq. ID LIB3136-008-Q1-K1-F12
Method BLASTX
NCBI GI g1076781
BLAST score 300
E value 3.0e-27
Match length 66
% identity 92
NCBI Description transcription factor HBP-1a(c14) - wheat
>gi_497895_dbj_BAA02304_ (D12920) transcription factor
HBP-1a(c14) [Triticum aestivum]

Seq. No. 296933
Seq. ID LIB3136-008-Q1-K1-F5
Method BLASTX
NCBI GI g4566505
BLAST score 152
E value 5.0e-10
Match length 45
% identity 67
NCBI Description (AF102868) beta-D-glucan exohydrolase isoenzyme ExoI
[Hordeum vulgare]

Seq. No. 296934
Seq. ID LIB3136-008-Q1-K1-H1
Method BLASTN
NCBI GI g22484
BLAST score 54
E value 7.0e-22
Match length 86
% identity 93
NCBI Description Z.mays RNA for superoxide dismutase Sod4A

Seq. No. 296935
Seq. ID LIB3136-008-Q1-K1-H11
Method BLASTX
NCBI GI g3163946
BLAST score 162
E value 1.0e-11
Match length 65
% identity 58
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No. 296936
Seq. ID LIB3136-009-Q1-K1-F12
Method BLASTX
NCBI GI g2984709
BLAST score 286
E value 7.0e-32
Match length 121
% identity 66
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 296937

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Seq. ID LIB3136-010-Q1-K1-A11
Method BLASTN
NCBI GI g2773153
BLAST score 122
E value 4.0e-62
Match length 158
% identity 94
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asrl) mRNA, complete cds

Seq. No. 296938
Seq. ID LIB3136-010-Q1-K1-A7
Method BLASTX
NCBI GI g2425066
BLAST score 226
E value 2.0e-18
Match length 50
% identity 94
NCBI Description (AF019147) cysteine proteinase Mir3 [Zea mays]

Seq. No. 296939
Seq. ID LIB3136-010-Q1-K1-C5
Method BLASTN
NCBI GI g2773153
BLAST score 67
E value 3.0e-29
Match length 158
% identity 87
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asrl) mRNA, complete cds

Seq. No. 296940
Seq. ID LIB3136-010-Q1-K1-C6
Method BLASTX
NCBI GI g1699023
BLAST score 346
E value 1.0e-32
Match length 99
% identity 70
NCBI Description (U78866) putative arginine-aspartate-rich RNA binding protein [Arabidopsis thaliana] >gi_1699051 (U78867) putative aspartate-arginine-rich mRNA binding protein [Arabidopsis thaliana]

Seq. No. 296941
Seq. ID LIB3136-010-Q1-K1-E5
Method BLASTX
NCBI GI g3757521
BLAST score 245
E value 7.0e-21
Match length 120
% identity 45
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 296942
Seq. ID LIB3136-010-Q1-K1-F3
Method BLASTN

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NCBI GI	g3885883
BLAST score	43
E value	3.0e-15
Match length	83
% identity	90
NCBI Description	Oryza sativa 60S ribosomal protein L21 (RPL21) mRNA, complete cds
Seq. No.	296943
Seq. ID	LIB3136-011-Q1-K1-A5
Method	BLASTX
NCBI GI	g1171429
BLAST score	217
E value	9.0e-18
Match length	95
% identity	48
NCBI Description	(U44028) CKC [Arabidopsis thaliana]
Seq. No.	296944
Seq. ID	LIB3136-011-Q1-K1-C9
Method	BLASTX
NCBI GI	g3831455
BLAST score	209
E value	1.0e-16
Match length	64
% identity	64
NCBI Description	(AC005700) putative ubiquitin activating enzyme [Arabidopsis thaliana]
Seq. No.	296945
Seq. ID	LIB3136-011-Q1-K1-D2
Method	BLASTX
NCBI GI	g2984709
BLAST score	402
E value	2.0e-39
Match length	105
% identity	76
NCBI Description	(AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.	296946
Seq. ID	LIB3136-011-Q1-K1-D6
Method	BLASTX
NCBI GI	g3212869
BLAST score	416
E value	5.0e-41
Match length	113
% identity	70
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.	296947
Seq. ID	LIB3136-011-Q1-K1-E3
Method	BLASTX
NCBI GI	g4454010
BLAST score	310
E value	1.0e-28
Match length	97
% identity	64

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NCBI Description (AL035396) putative protein [Arabidopsis thaliana]
Seq. No. 296948
Seq. ID LIB3136-011-Q1-K1-E7
Method BLASTX
NCBI GI g82696
BLAST score 376
E value 3.0e-36
Match length 79
% identity 92
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]

Seq. No. 296949
Seq. ID LIB3136-011-Q1-K1-F3
Method BLASTX
NCBI GI g4646221
BLAST score 192
E value 9.0e-15
Match length 45
% identity 80
NCBI Description (AC007290) putative membrane-associated protein, 3' partial [Arabidopsis thaliana]

Seq. No. 296950
Seq. ID LIB3136-011-Q1-K1-G4
Method BLASTX
NCBI GI g1497987
BLAST score 296
E value 5.0e-27
Match length 90
% identity 63
NCBI Description (U62798) SCARECROW [Arabidopsis thaliana]

Seq. No. 296951
Seq. ID LIB3136-011-Q1-K1-H6
Method BLASTX
NCBI GI g2393724
BLAST score 154
E value 3.0e-10
Match length 77
% identity 36
NCBI Description (U80819) glutathione-S-transferase homolog [Mus musculus]

Seq. No. 296952
Seq. ID LIB3136-012-Q1-K1-A5
Method BLASTX
NCBI GI g3746431
BLAST score 251
E value 2.0e-24
Match length 86
% identity 70
NCBI Description (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1 [Zea mays]

Seq. No. 296953
Seq. ID LIB3136-012-Q1-K1-B1

Method BLASTX
NCBI GI g3822403
BLAST score 185
E value 7.0e-14
Match length 51
% identity 63
NCBI Description (AF087932) hydroperoxide lyase [Arabidopsis thaliana]

Seq. No. 296954
Seq. ID LIB3136-012-Q1-K1-C11
Method BLASTX
NCBI GI g119350
BLAST score 137
E value 1.0e-08
Match length 30
% identity 90
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir_JQ1187
phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
[Arabidopsis thaliana]
>gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase
(2-phospho-D-glycerate hydroylase); identical to P25696
[Arabidopsis thaliana]

Seq. No. 296955
Seq. ID LIB3136-012-Q1-K1-E5
Method BLASTX
NCBI GI g3415134
BLAST score 343
E value 2.0e-32
Match length 122
% identity 59
NCBI Description (AF082024) Phyb1 [Pimpinella brachycarpa]

Seq. No. 296956
Seq. ID LIB3136-012-Q1-K1-G12
Method BLASTX
NCBI GI g3043415
BLAST score 327
E value 9.0e-31
Match length 72
% identity 89
NCBI Description (Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No. 296957
Seq. ID LIB3136-012-Q1-K1-H9
Method BLASTX
NCBI GI g4490316
BLAST score 146
E value 3.0e-09
Match length 54
% identity 46
NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No. 296958
Seq. ID LIB3136-013-Q1-K1-C10

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Method	BLASTN
NCBI GI	g2431766
BLAST score	151
E value	9.0e-80
Match length	171
% identity	98
NCBI Description	Zea mays acidic ribosomal protein P3a (rpp3a) mRNA, complete cds
Seq. No.	296959
Seq. ID	LIB3136-013-Q1-K1-C12
Method	BLASTX
NCBI GI	g1778093
BLAST score	344
E value	5.0e-33
Match length	122
% identity	63
NCBI Description	(U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]
Seq. No.	296960
Seq. ID	LIB3136-013-Q1-K1-C6
Method	BLASTX
NCBI GI	g4646217
BLAST score	305
E value	5.0e-28
Match length	103
% identity	56
NCBI Description	(AC007290) putative phosphoprotein phosphatase [Arabidopsis thaliana]
Seq. No.	296961
Seq. ID	LIB3136-013-Q1-K1-C9
Method	BLASTX
NCBI GI	g3249105
BLAST score	146
E value	8.0e-10
Match length	60
% identity	50
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
Seq. No.	296962
Seq. ID	LIB3136-013-Q1-K1-D4
Method	BLASTX
NCBI GI	g2894534
BLAST score	403
E value	2.0e-39
Match length	91
% identity	86
NCBI Description	(AJ224327) aquaporin [Oryza sativa]
Seq. No.	296963
Seq. ID	LIB3136-013-Q1-K1-F3
Method	BLASTX
NCBI GI	g3355468

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BLAST score	218
E value	6.0e-18
Match length	72
% identity	68
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]
Seq. No.	296964
Seq. ID	LIB3136-013-Q1-K1-F9
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	8.0e-11
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	296965
Seq. ID	LIB3136-013-Q1-K1-G9
Method	BLASTX
NCBI GI	g542157
BLAST score	219
E value	3.0e-18
Match length	61
% identity	70
NCBI Description	ribosomal 5S RNA-binding protein - Rice
Seq. No.	296966
Seq. ID	LIB3136-013-Q1-K1-H2
Method	BLASTX
NCBI GI	g4107009
BLAST score	340
E value	6.0e-32
Match length	70
% identity	94
NCBI Description	(D82039) OSK1 [Oryza sativa]
Seq. No.	296967
Seq. ID	LIB3136-013-Q1-K1-H5
Method	BLASTX
NCBI GI	g3107931
BLAST score	158
E value	4.0e-11
Match length	79
% identity	47
NCBI Description	(AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]
Seq. No.	296968
Seq. ID	LIB3136-013-Q1-K1-H8
Method	BLASTX
NCBI GI	g2781433
BLAST score	286
E value	1.0e-25
Match length	94
% identity	56
NCBI Description	(AF030052) RSW1-like cellulose synthase catalytic subunit [Oryza sativa subsp. japonica]

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Seq. No.	296969
Seq. ID	LIB3136-014-Q1-K1-A8
Method	BLASTX
NCBI GI	g3122013
BLAST score	185
E value	9.0e-14
Match length	80
% identity	47
NCBI Description	DNAJ PROTEIN >gi_1750265 (U72720) DnaJ [Streptococcus pneumoniae]
Seq. No.	296970
Seq. ID	LIB3136-014-Q1-K1-C7
Method	BLASTX
NCBI GI	g4432983
BLAST score	233
E value	1.0e-19
Match length	53
% identity	83
NCBI Description	(D87044) protein kinase catalytic domain (fragment) [Zea mays]
Seq. No.	296971
Seq. ID	LIB3136-014-Q1-K2-C11
Method	BLASTX
NCBI GI	g3163946
BLAST score	273
E value	5.0e-32
Match length	96
% identity	75
NCBI Description	(AJ005599) alpha-tubulin 1 [Eleusine indica]
Seq. No.	296972
Seq. ID	LIB3136-014-Q1-K2-D1
Method	BLASTX
NCBI GI	g3913239
BLAST score	448
E value	1.0e-44
Match length	93
% identity	92
NCBI Description	PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like protein [Oryza sativa]
Seq. No.	296973
Seq. ID	LIB3136-015-Q1-K1-A2
Method	BLASTX
NCBI GI	g3236249
BLAST score	445
E value	3.0e-44
Match length	138
% identity	59
NCBI Description	(AC004684) hypothetical protein [Arabidopsis thaliana]
Seq. No.	296974
Seq. ID	LIB3136-015-Q1-K1-A6

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Method	BLASTX
NCBI GI	g4165550
BLAST score	217
E value	1.0e-17
Match length	49
% identity	86
NCBI Description	(AJ004915) apgm [Malus domestica]
Seq. No.	296975
Seq. ID	LIB3136-015-Q1-K1-B2
Method	BLASTX
NCBI GI	g3928084
BLAST score	184
E value	7.0e-14
Match length	101
% identity	43
NCBI Description	(AC005770) retrotransposon-like protein [Arabidopsis thaliana]
Seq. No.	296976
Seq. ID	LIB3136-015-Q1-K1-C10
Method	BLASTX
NCBI GI	g1418331
BLAST score	218
E value	1.0e-17
Match length	98
% identity	51
NCBI Description	(X95909) receptor like protein kinase [Arabidopsis thaliana]
Seq. No.	296977
Seq. ID	LIB3136-015-Q1-K1-C4
Method	BLASTX
NCBI GI	g4512674
BLAST score	160
E value	7.0e-11
Match length	111
% identity	37
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana]
Seq. No.	296978
Seq. ID	LIB3136-015-Q1-K1-D10
Method	BLASTX
NCBI GI	g3913427
BLAST score	287
E value	6.0e-26
Match length	88
% identity	67
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1532073_emb_CAA69075 (Y07767) S-adenosylmethionine decarboxylase [Zea mays]
Seq. No.	296979
Seq. ID	LIB3136-015-Q1-K1-D6
Method	BLASTX
NCBI GI	g3913464
BLAST score	205

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E value 5.0e-25
Match length 101
% identity 55
NCBI Description BETAINE-ALDEHYDE DEHYDROGENASE (BADH)
>gi_2244604_dbj_BAA21098 (AB001348) betaine aldehyde dehydrogenase [Oryza sativa]

Seq. No. 296980
Seq. ID LIB3136-015-Q1-K1-G1
Method BLASTX
NCBI GI g3309086
BLAST score 228
E value 7.0e-19
Match length 56
% identity 79
NCBI Description (AF076253) calcineurin B-like protein 3 [Arabidopsis thaliana]

Seq. No. 296981
Seq. ID LIB3136-015-Q1-K1-H7
Method BLASTX
NCBI GI g1550738
BLAST score 141
E value 9.0e-09
Match length 68
% identity 46
NCBI Description (Y08061) endomembrane-associated protein [Arabidopsis thaliana] >gi_2982443_emb_CAA18251_ (AL022224)
endomembrane-associated protein [Arabidopsis thaliana]

Seq. No. 296982
Seq. ID LIB3136-016-Q1-K1-C3
Method BLASTX
NCBI GI g4587512
BLAST score 360
E value 2.0e-34
Match length 132
% identity 54
NCBI Description (AC007060) Strong similarity to gi_2245113
glycerol-3-phosphate permease homolog from Arabidopsis
thaliana BAC gb_Z97343 and a member of the PF_00083 Sugar
transporter family

Seq. No. 296983
Seq. ID LIB3136-016-Q1-K1-D1
Method BLASTX
NCBI GI g3075394
BLAST score 173
E value 5.0e-13
Match length 71
% identity 52
NCBI Description (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No. 296984
Seq. ID LIB3136-016-Q1-K1-D5

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Method BLASTX
NCBI GI g3337350
BLAST score 370
E value 2.0e-43
Match length 127
% identity 72
NCBI Description (AC004481) putative permease [Arabidopsis thaliana]

Seq. No. 296985
Seq. ID LIB3136-016-Q1-K1-E1
Method BLASTX
NCBI GI g4314378
BLAST score 148
E value 8.0e-10
Match length 89
% identity 40
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 296986
Seq. ID LIB3136-016-Q1-K1-E8
Method BLASTX
NCBI GI g82696
BLAST score 208
E value 9.0e-17
Match length 69
% identity 59
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]

Seq. No. 296987
Seq. ID LIB3136-016-Q1-K1-F10
Method BLASTX
NCBI GI g3152608
BLAST score 517
E value 1.0e-52
Match length 126
% identity 78
NCBI Description (AC004482) putative BELL-like homeotic protein [Arabidopsis thaliana]

Seq. No. 296988
Seq. ID LIB3136-016-Q1-K1-F4
Method BLASTX
NCBI GI g2384758
BLAST score 204
E value 4.0e-16
Match length 67
% identity 60
NCBI Description (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza sativa]

Seq. No. 296989
Seq. ID LIB3136-016-Q1-K1-G2
Method BLASTX
NCBI GI g1899175
BLAST score 150
E value 1.0e-09

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Match length 71
% identity 45
NCBI Description (U90262) calcium-dependent calmodulin-independent protein kinase CDPK [Cucurbita pepo]

Seq. No. 296990
Seq. ID LIB3136-016-Q1-K1-H7
Method BLASTX
NCBI GI g2894592
BLAST score 153
E value 1.0e-10
Match length 64
% identity 48
NCBI Description (AL021889) predicted protein [Arabidopsis thaliana]

Seq. No. 296991
Seq. ID LIB3136-017-Q1-K1-C12
Method BLASTX
NCBI GI g3135543
BLAST score 326
E value 2.0e-30
Match length 104
% identity 64
NCBI Description (AF062393) aquaporin [Oryza sativa]

Seq. No. 296992
Seq. ID LIB3136-017-Q1-K1-E8
Method BLASTX
NCBI GI g3075397
BLAST score 242
E value 2.0e-20
Match length 63
% identity 67
NCBI Description (AC004484) hypothetical protein [Arabidopsis thaliana]

Seq. No. 296993
Seq. ID LIB3136-017-Q1-K1-F11
Method BLASTN
NCBI GI g296593
BLAST score 60
E value 5.0e-25
Match length 76
% identity 95
NCBI Description H. vulgare pZE40 gene

Seq. No. 296994
Seq. ID LIB3136-017-Q1-K1-H7
Method BLASTX
NCBI GI g1705651
BLAST score 341
E value 4.0e-32
Match length 92
% identity 71
NCBI Description 20 KD NUCLEAR CAP BINDING PROTEIN (NCBP 20 KD SUBUNIT)
(CBP20) >gi_984139_emb_CAA58962 (X84157) subunit of the
dimeric cap binding complex CBC [Homo sapiens]
>gi_1582342_prf_2118330A cap-binding protein [Homo

sapiens]

Seq. No. 296995
Seq. ID LIB3136-018-Q1-K1-C11
Method BLASTN
NCBI GI g2463510
BLAST score 87
E value 2.0e-41
Match length 101
% identity 25
NCBI Description Z.mays small nuclear RNA genes snoR1.1, snoR2.2, snoR3.2, U14.1a, U14.1b, U14.1c and U14.1d

Seq. No. 296996
Seq. ID LIB3136-018-Q1-K1-F7
Method BLASTX
NCBI GI g2351374
BLAST score 147
E value 3.0e-09
Match length 29
% identity 100
NCBI Description (U54560) putative 26S proteasome subunit athMOV34 [Arabidopsis thaliana]

Seq. No. 296997
Seq. ID LIB3136-018-Q1-K1-F8
Method BLASTX
NCBI GI g349379
BLAST score 271
E value 8.0e-24
Match length 115
% identity 56
NCBI Description (L22847) HAHB-1 [Helianthus annuus]

Seq. No. 296998
Seq. ID LIB3136-018-Q1-K1-G6
Method BLASTX
NCBI GI g2213594
BLAST score 445
E value 3.0e-44
Match length 133
% identity 59
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No. 296999
Seq. ID LIB3136-019-Q1-K1-C12
Method BLASTX
NCBI GI g4388534
BLAST score 165
E value 5.0e-12
Match length 33
% identity 100
NCBI Description (Y15179) F1-ATP synthase, beta subunit [Sorghum bicolor]

Seq. No. 297000
Seq. ID LIB3136-019-Q1-K1-C9
Method BLASTX

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NCBI GI	g2961375
BLAST score	242
E value	4.0e-21
Match length	68
% identity	72
NCBI Description	(AL022141) NAM like protein [Arabidopsis thaliana]
Seq. No.	297001
Seq. ID	LIB3136-019-Q1-K1-E12
Method	BLASTX
NCBI GI	g1346396
BLAST score	154
E value	1.0e-10
Match length	33
% identity	73
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE ZMPK1 PRECURSOR >gi_100913_pir_S10930 probable receptor protein kinase (EC 2.7.1.-) precursor - maize >gi_22432_emb_CAA36611_ (X52384) precursor protein (AA -26 to 791) [Zea mays] >gi_22436_emb_CAA47962_ (X67733) receptor-like protein kinase [Zea mays] >gi_226927_prf_1611404A receptor protein kinase [Zea mays]
Seq. No.	297002
Seq. ID	LIB3136-019-Q1-K1-G9
Method	BLASTX
NCBI GI	g3478637
BLAST score	349
E value	4.0e-33
Match length	117
% identity	55
NCBI Description	(AC005546) R29425_1 [Homo sapiens]
Seq. No.	297003
Seq. ID	LIB3136-019-Q1-K1-H1
Method	BLASTX
NCBI GI	g2497824
BLAST score	203
E value	5.0e-16
Match length	110
% identity	42
NCBI Description	DNA REPLICATION LICENSING FACTOR MCM6 (P105MCM) >gi_1688042_dbj_BAA12699_ (D84557) HsMcm6 [Homo sapiens]
Seq. No.	297004
Seq. ID	LIB3136-020-Q1-K1-A10
Method	BLASTX
NCBI GI	g445613
BLAST score	319
E value	1.0e-29
Match length	87
% identity	69
NCBI Description	ribosomal protein L7 [Solanum tuberosum]
Seq. No.	297005
Seq. ID	LIB3136-020-Q1-K1-B5
Method	BLASTX

NCBI GI g1352679
BLAST score 216
E value 1.0e-17
Match length 119
% identity 42
NCBI Description PROTEIN PHOSPHATASE 2C ABI1 (PP2C) >gi_2129699_pir_A54588
protein phosphatase ABI1 - Arabidopsis thaliana
>gi_509419_emb_CAA55484_ (X78886) ABI1 [Arabidopsis
thaliana]

Seq. No. 297006
Seq. ID LIB3136-020-Q1-K1-C1
Method BLASTX
NCBI GI g2832677
BLAST score 233
E value 2.0e-19
Match length 62
% identity 69
NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297007
Seq. ID LIB3136-020-Q1-K1-E12
Method BLASTX
NCBI GI g445612
BLAST score 242
E value 2.0e-20
Match length 62
% identity 73
NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No. 297008
Seq. ID LIB3136-020-Q1-K1-F12
Method BLASTX
NCBI GI g3618320
BLAST score 466
E value 1.0e-46
Match length 135
% identity 67
NCBI Description (AB001888) zinc finger protein [Oryza sativa]

Seq. No. 297009
Seq. ID LIB3136-020-Q1-K1-F4
Method BLASTN
NCBI GI g1245938
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100
NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
heart atrium, mRNA, 2998 nt]

Seq. No. 297010
Seq. ID LIB3136-021-Q1-K1-E11
Method BLASTX
NCBI GI g4417276
BLAST score 174
E value 2.0e-12

Match length 50
% identity 68
NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]

Seq. No. 297011
Seq. ID LIB3136-021-Q1-K1-E7
Method BLASTX
NCBI GI g2462748
BLAST score 465
E value 1.0e-46
Match length 97
% identity 94
NCBI Description (AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]

Seq. No. 297012
Seq. ID LIB3136-021-Q1-K1-F11
Method BLASTX
NCBI GI g2625154
BLAST score 162
E value 3.0e-13
Match length 77
% identity 61
NCBI Description (AF032877) alpha-tubulin [Chloromonas sp. ANT3]

Seq. No. 297013
Seq. ID LIB3136-021-Q1-K1-F6
Method BLASTX
NCBI GI g1170937
BLAST score 440
E value 1.0e-43
Match length 88
% identity 97
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No. 297014
Seq. ID LIB3136-022-Q1-K1-A10
Method BLASTX
NCBI GI g2498778
BLAST score 333
E value 4.0e-31
Match length 136
% identity 52
NCBI Description PIR7A PROTEIN >gi_629799_pir_S47086 pir7a protein - rice
>gi_498744_emb_CAA84025_ (Z34271) Pir7a [Oryza sativa]

Seq. No. 297015
Seq. ID LIB3136-022-Q1-K1-C8
Method BLASTX
NCBI GI g135398
BLAST score 497
E value 2.0e-50
Match length 91
% identity 100

NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir_S15773 tubulin alpha-1 chain - maize >gi_22147_emb_CAA33734_ (X15704)
alpha1-tubulin [Zea mays]

Seq. No. 297016
Seq. ID LIB3136-022-Q1-K1-D6
Method BLASTX
NCBI GI g4191810
BLAST score 248
E value 3.0e-21
Match length 124
% identity 41
NCBI Description (AB006532) DNA helicase [Homo sapiens]

Seq. No. 297017
Seq. ID LIB3136-022-Q1-K1-G8
Method BLASTX
NCBI GI g82696
BLAST score 308
E value 2.0e-28
Match length 82
% identity 76
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_ (X61121) glycine-rich protein [Zea mays]

Seq. No. 297018
Seq. ID LIB3136-023-Q1-K1-A2
Method BLASTX
NCBI GI g3341509
BLAST score 164
E value 2.0e-11
Match length 74
% identity 45
NCBI Description (AJ231133) caffeic acid 3-O-Methyltransferase [Saccharum officinarum]

Seq. No. 297019
Seq. ID LIB3136-023-Q1-K1-C10
Method BLASTX
NCBI GI g4530585
BLAST score 175
E value 1.0e-12
Match length 50
% identity 64
NCBI Description (AF130978) B12D protein [Ipomoea batatas]

Seq. No. 297020
Seq. ID LIB3136-023-Q1-K1-D3
Method BLASTN
NCBI GI g440170
BLAST score 63
E value 6.0e-27
Match length 107
% identity 96
NCBI Description Z.mays (C6000237) trpA gene

Seq. No. 297021

Seq. ID LIB3136-023-Q1-K1-G6
Method BLASTX
NCBI GI g4056421
BLAST score 256
E value 5.0e-22
Match length 77
% identity 61
NCBI Description (AC005322) Similar to gb_Z30094 basic transcription factor 2, 44 kD subunit from Homo sapiens. EST gb_W43325 comes from this gene. [Arabidopsis thaliana]

Seq. No. 297022
Seq. ID LIB3136-024-Q1-K1-B7
Method BLASTX
NCBI GI g2496731
BLAST score 295
E value 1.0e-26
Match length 91
% identity 66
NCBI Description HYPOTHETICAL 30.2 KD PROTEIN Y4oV >gi_2182566 (AE000089)
Y4oV [Rhizobium sp. NGR234]

Seq. No. 297023
Seq. ID LIB3136-024-Q1-K1-E9
Method BLASTX
NCBI GI g2191175
BLAST score 158
E value 1.0e-10
Match length 117
% identity 32
NCBI Description (AF007270) A_IG002P16.24 gene product [Arabidopsis thaliana]

Seq. No. 297024
Seq. ID LIB3136-025-Q1-K1-B10
Method BLASTX
NCBI GI g3850569
BLAST score 254
E value 5.0e-22
Match length 97
% identity 49
NCBI Description (AC005278) ESTs gb_T21276, gb_T45403, and gb_AA586113 come from this gene. [Arabidopsis thaliana]

Seq. No. 297025
Seq. ID LIB3136-025-Q1-K1-C6
Method BLASTX
NCBI GI g2668742
BLAST score 364
E value 8.0e-35
Match length 84
% identity 83
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 297026
Seq. ID LIB3136-025-Q1-K1-G3
Method BLASTX

NCBI GI g498643
BLAST score 350
E value 3.0e-34
Match length 92
% identity 93
NCBI Description (U10270) G-box binding factor 1 [Zea mays]

Seq. No. 297027
Seq. ID LIB3136-026-Q1-K1-A11
Method BLASTX
NCBI GI g2909846
BLAST score 321
E value 7.0e-30
Match length 75
% identity 81
NCBI Description (AF045570) (S)-adenosyl-L-methionine:delta 24-sterol methyltransferase [Zea mays]

Seq. No. 297028
Seq. ID LIB3136-026-Q1-K1-D10
Method BLASTX
NCBI GI g544250
BLAST score 243
E value 1.0e-20
Match length 81
% identity 64
NCBI Description ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR)
>gi_541860_pir_A49677 endoplasmic reticulum retention
receptor Erd2 - Arabidopsis thaliana

Seq. No. 297029
Seq. ID LIB3136-027-P1-K1-A10
Method BLASTX
NCBI GI g2497538
BLAST score 260
E value 4.0e-23
Match length 70
% identity 77
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632)
pyruvate kinase [Glycine max]

Seq. No. 297030
Seq. ID LIB3136-027-P1-K1-D1
Method BLASTX
NCBI GI g4249390
BLAST score 152
E value 3.0e-10
Match length 67
% identity 51
NCBI Description (AC005966) Similar to gb_AF039182 probable aldo-keto
reductase from Fragaria x ananassa. This gene may be cut
off. EST gb_U74151 comes from this gene. [Arabidopsis
thaliana]

Seq. No. 297031
Seq. ID LIB3136-027-P1-K1-D11
Method BLASTX

NCBI GI g1008904
 BLAST score 197
 E value 2.0e-15
 Match length 71
 % identity 55
 NCBI Description (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]

Seq. No. 297032
 Seq. ID LIB3136-027-P1-K1-F10
 Method BLASTN
 NCBI GI g559535
 BLAST score 222
 E value 1.0e-122
 Match length 314
 % identity 93
 NCBI Description Z.mays mRNA for metallothionein

Seq. No. 297033
 Seq. ID LIB3136-027-P1-K1-G12
 Method BLASTX
 NCBI GI g2952328
 BLAST score 246
 E value 3.0e-21
 Match length 69
 % identity 65
 NCBI Description (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza sativa]

Seq. No. 297034
 Seq. ID LIB3136-028-Q1-K1-A11
 Method BLASTN
 NCBI GI g602605
 BLAST score 67
 E value 2.0e-29
 Match length 95
 % identity 48
 NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin

Seq. No. 297035
 Seq. ID LIB3136-028-Q1-K1-B8
 Method BLASTX
 NCBI GI g119958
 BLAST score 212
 E value 3.0e-17
 Match length 39
 % identity 97
 NCBI Description FERREDOXIN III PRECURSOR (FD III) >gi_168473 (M73831)
 ferredoxin [Zea mays] >gi_1864001_dbj_BAA19251_ (AB001387)
 Fd III [Zea mays] >gi_444686_prf_1907324C
 ferredoxin:ISOTYPE=III [Zea mays]

Seq. No. 297036
 Seq. ID LIB3136-028-Q1-K1-D7
 Method BLASTX
 NCBI GI g2252634
 BLAST score 216
 E value 1.0e-17

Match length 80
% identity 51
NCBI Description (U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297037
Seq. ID LIB3136-028-Q1-K1-E10
Method BLASTX
NCBI GI g1172818
BLAST score 315
E value 3.0e-29
Match length 83
% identity 77
NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal protein S16 [Oryza sativa] >gi_1096552_prf_2111468A ribosomal protein S16 [Oryza sativa]

Seq. No. 297038
Seq. ID LIB3136-028-Q1-K1-H10
Method BLASTX
NCBI GI g2267595
BLAST score 173
E value 1.0e-12
Match length 69
% identity 52
NCBI Description (AF009412) plastocyanin precursor [Oryza sativa]

Seq. No. 297039
Seq. ID LIB3136-029-Q1-K1-A9
Method BLASTX
NCBI GI g1350720
BLAST score 162
E value 2.0e-11
Match length 62
% identity 56
NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 297040
Seq. ID LIB3136-029-Q1-K1-G6
Method BLASTX
NCBI GI g168489
BLAST score 276
E value 1.0e-24
Match length 81
% identity 68
NCBI Description (M16902) glutathione S-transferase I [Zea mays] >gi_168491 (M16901) glutathione S-transferase I [Zea mays] >gi_225458_prf_1303351A transferase,glutathione S [Zea mays]

Seq. No. 297041
Seq. ID LIB3136-029-Q1-K1-G8
Method BLASTX
NCBI GI g3786009
BLAST score 235
E value 8.0e-29
Match length 112
% identity 62

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NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 297042
 Seq. ID LIB3136-030-Q1-K1-D8
 Method BLASTX
 NCBI GI g2668742
 BLAST score 277
 E value 5.0e-25
 Match length 63
 % identity 87

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 297043
 Seq. ID LIB3136-030-Q1-K1-G2
 Method BLASTX
 NCBI GI g70642
 BLAST score 510
 E value 4.0e-52
 Match length 105
 % identity 19

NCBI Description ubiquitin precursor - Arabidopsis thaliana
 >gi_17678_emb_CAA31331_(X12853) polyubiquitin (AA 1 - 382)
 [Arabidopsis thaliana] >gi_987519_(U33014) polyubiquitin
 [Arabidopsis thaliana] >gi_226499_prf_1515347A
 poly-ubiquitin [Arabidopsis thaliana]

Seq. No. 297044
 Seq. ID LIB3136-030-Q1-K1-G7
 Method BLASTX
 NCBI GI g2589164
 BLAST score 256
 E value 2.0e-22
 Match length 79
 % identity 66

NCBI Description (D88452) aldehyde oxidase-2 [Zea mays]

Seq. No. 297045
 Seq. ID LIB3136-030-Q1-K1-G8
 Method BLASTX
 NCBI GI g1350969
 BLAST score 146
 E value 8.0e-10
 Match length 61
 % identity 51

NCBI Description 40S RIBOSOMAL PROTEIN S26 (S31) >gi_971284_dbj_BAA07208_(D38011) ribosomal protein S31 [Oryza sativa]

Seq. No. 297046
 Seq. ID LIB3136-030-Q1-K1-H8
 Method BLASTX
 NCBI GI g1877393
 BLAST score 258
 E value 2.0e-22
 Match length 103
 % identity 57

NCBI Description (Y11527) serine/threonine protein kinase [Oryza sativa]

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Seq. No. 297047
Seq. ID LIB3136-032-Q1-K1-B2
Method BLASTX
NCBI GI g2384760
BLAST score 265
E value 2.0e-31
Match length 99
% identity 72
NCBI Description (AF016897) GDP dissociation inhibitor protein OsGDI2 [Oryza sativa]

Seq. No. 297048
Seq. ID LIB3136-032-Q1-K1-B7
Method BLASTX
NCBI GI g3033400
BLAST score 153
E value 4.0e-10
Match length 76
% identity 42
NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 297049
Seq. ID LIB3136-032-Q1-K1-B9
Method BLASTX
NCBI GI g3183405
BLAST score 175
E value 1.0e-12
Match length 84
% identity 43
NCBI Description HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I
>gi_3451305_emb_CAA20442_(AL031324) very hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 297050
Seq. ID LIB3136-032-Q1-K1-D8
Method BLASTN
NCBI GI g1778148
BLAST score 59
E value 1.0e-24
Match length 207
% identity 83
NCBI Description Zea mays plastid phosphate/phosphoenolpyruvate translocator precursor (M2PPT4) mRNA, complete cds

Seq. No. 297051
Seq. ID LIB3136-032-Q1-K1-D9
Method BLASTN
NCBI GI g2341060
BLAST score 53
E value 5.0e-21
Match length 210
% identity 87
NCBI Description Zea mays translational initiation factor eIF-4A (tif-4A3) mRNA, complete cds

Seq. No. 297052

Seq. ID LIB3136-032-Q1-K1-E6
Method BLASTN
NCBI GI g435312
BLAST score 45
E value 4.0e-16
Match length 192
% identity 86
NCBI Description Z.mays mRNA for beta-D-glucosidase

Seq. No. 297053
Seq. ID LIB3136-032-Q1-K1-H8
Method BLASTX
NCBI GI g1001263
BLAST score 167
E value 7.0e-12
Match length 86
% identity 41
NCBI Description (D64003) hypothetical protein [Synechocystis sp.]

Seq. No. 297054
Seq. ID LIB3136-033-Q1-K1-A4
Method BLASTX
NCBI GI g4432844
BLAST score 139
E value 1.0e-08
Match length 53
% identity 47
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 297055
Seq. ID LIB3136-033-Q1-K1-A8
Method BLASTX
NCBI GI g1552860
BLAST score 146
E value 3.0e-09
Match length 85
% identity 38
NCBI Description (Z80343) hypothetical protein Rv3777 [Mycobacterium tuberculosis]

Seq. No. 297056
Seq. ID LIB3136-033-Q1-K1-B6
Method BLASTX
NCBI GI g606811
BLAST score 173
E value 6.0e-13
Match length 60
% identity 33
NCBI Description (U08401) carbonic anhydrase [Zea mays]

Seq. No. 297057
Seq. ID LIB3136-033-Q1-K1-G7
Method BLASTN
NCBI GI g2921303
BLAST score 85
E value 5.0e-40
Match length 317

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% identity 86
NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA, complete cds

Seq. No. 297058
Seq. ID LIB3136-034-Q1-K1-A8
Method BLASTN
NCBI GI g170784
BLAST score 37
E value 2.0e-11
Match length 93
% identity 85
NCBI Description Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds

Seq. No. 297059
Seq. ID LIB3136-034-Q1-K1-B6
Method BLASTX
NCBI GI g4027891
BLAST score 312
E value 5.0e-29
Match length 77
% identity 66
NCBI Description (AF049350) alpha-expansin precursor [Nicotiana tabacum]

Seq. No. 297060
Seq. ID LIB3136-034-Q1-K1-D2
Method BLASTX
NCBI GI g2668742
BLAST score 186
E value 2.0e-14
Match length 63
% identity 63
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 297061
Seq. ID LIB3136-034-Q1-K1-E10
Method BLASTX
NCBI GI g1084479
BLAST score 148
E value 2.0e-09
Match length 30
% identity 97
NCBI Description H+-transporting ATP synthase (EC 3.6.1.34) delta chain - maize (fragment) >gi_311237_emb_CAA46804_ (X66005)
H(+) -transporting ATP synthase [Zea mays]

Seq. No. 297062
Seq. ID LIB3136-035-Q1-K1-A11
Method BLASTX
NCBI GI g2281086
BLAST score 353
E value 2.0e-33
Match length 127
% identity 51
NCBI Description (AC002333) indole-3-acetate beta-glucosyltransferase isolog [Arabidopsis thaliana]

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Seq. No.	297063
Seq. ID	LIB3136-036-Q1-K1-A4
Method	BLASTX
NCBI GI	g312179
BLAST score	477
E value	2.0e-48
Match length	92
% identity	99
NCBI Description	(X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.	297064
Seq. ID	LIB3136-036-Q1-K1-B12
Method	BLASTX
NCBI GI	g1431629
BLAST score	292
E value	2.0e-26
Match length	138
% identity	46
NCBI Description	(X99348) pectinacetyl esterase precursor [Vigna radiata]
Seq. No.	297065
Seq. ID	LIB3136-036-Q1-K1-C7
Method	BLASTX
NCBI GI	g3080420
BLAST score	158
E value	1.0e-10
Match length	62
% identity	50
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]
Seq. No.	297066
Seq. ID	LIB3136-036-Q1-K1-G1
Method	BLASTX
NCBI GI	g4056425
BLAST score	239
E value	9.0e-21
Match length	73
% identity	67
NCBI Description	(AC005322) ESTs gb_H36249, gb_AA59732 and gb_AA651219 come from this gene. [Arabidopsis thaliana]
Seq. No.	297067
Seq. ID	LIB3136-036-Q1-K1-H10
Method	BLASTN
NCBI GI	g258165
BLAST score	41
E value	7.0e-14
Match length	49
% identity	96
NCBI Description	Wx (wx-B5)=waxy gene {long terminal repeat} [maize, Genomic Mutant, 299 nt]

Seq. No. 297068
Seq. ID LIB3136-037-P1-K1-C7
Method BLASTX
NCBI GI g12426
BLAST score 245
E value 6.0e-21
Match length 62
% identity 81
NCBI Description (X17438) NDH-C protein (AA 1 - 120) [Zea mays]

Seq. No. 297069
Seq. ID LIB3136-038-P1-K1-C11
Method BLASTX
NCBI GI g3892709
BLAST score 426
E value 3.0e-42
Match length 93
% identity 78
NCBI Description (AL033545) putative protein [Arabidopsis thaliana]

Seq. No. 297070
Seq. ID LIB3136-038-P1-K1-H7
Method BLASTX
NCBI GI g2191187
BLAST score 273
E value 4.0e-24
Match length 89
% identity 61
NCBI Description (AF007271) contains similarity to a DNAJ-like domain [Arabidopsis thaliana]

Seq. No. 297071
Seq. ID LIB3136-039-P1-K1-G5
Method BLASTX
NCBI GI g2130051
BLAST score 262
E value 1.0e-25
Match length 79
% identity 76
NCBI Description xylose isomerase (EC 5.3.1.5) - barley
>gi_1296807_emb_CAA64544 (X95256) xylose isomerase
[Hordeum vulgare] >gi_1588664_prf_2209268A xylose
isomerase [Hordeum vulgare]

Seq. No. 297072
Seq. ID LIB3136-039-P1-K1-H1
Method BLASTX
NCBI GI g2827143
BLAST score 417
E value 4.0e-41
Match length 105
% identity 78
NCBI Description (AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No. 297073
Seq. ID LIB3136-040-P1-K1-A10

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Method	BLASTX
NCBI GI	g3643608
BLAST score	206
E value	3.0e-16
Match length	104
% identity	45
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]
Seq. No.	297074
Seq. ID	LIB3136-040-P1-K1-A5
Method	BLASTN
NCBI GI	g22163
BLAST score	100
E value	4.0e-49
Match length	212
% identity	87
NCBI Description	Z.mays MANT2 mRNA for adenine nucleotide translocator (ADP/ATP translocase)
Seq. No.	297075
Seq. ID	LIB3136-040-P1-K1-B8
Method	BLASTX
NCBI GI	g606815
BLAST score	351
E value	3.0e-33
Match length	93
% identity	28
NCBI Description	(U08403) carbonic anhydrase [Zea mays]
Seq. No.	297076
Seq. ID	LIB3136-040-P1-K1-C2
Method	BLASTN
NCBI GI	g413915
BLAST score	54
E value	2.0e-21
Match length	90
% identity	92
NCBI Description	Rice mRNA for isocitrate dehydrogenase, partial cds >gi_3106666_dbj_D42386_D42386 Rice callus cDNA, AK088
Seq. No.	297077
Seq. ID	LIB3136-040-P1-K1-D12
Method	BLASTN
NCBI GI	g3264597
BLAST score	98
E value	7.0e-48
Match length	255
% identity	84
NCBI Description	Zea mays trypsin inhibitor mRNA, complete cds
Seq. No.	297078
Seq. ID	LIB3136-040-P1-K1-D9
Method	BLASTX
NCBI GI	g541112
BLAST score	186
E value	7.0e-14
Match length	139

% identity 27
NCBI Description hypothetical protein f678 - Escherichia coli >gi_304982
(L19201) ORF_f678 [Escherichia coli]

Seq. No. 297079
Seq. ID LIB3136-042-P1-K1-E9
Method BLASTX
NCBI GI g1296955
BLAST score 284
E value 1.0e-25
Match length 62
% identity 45
NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]

Seq. No. 297080
Seq. ID LIB3136-043-P1-K1-D10
Method BLASTX
NCBI GI g2191140
BLAST score 147
E value 2.0e-09
Match length 91
% identity 47
NCBI Description (AF007269) contains weak similarity to MYB-related proteins
[Arabidopsis thaliana]

Seq. No. 297081
Seq. ID LIB3136-044-P1-K1-E3
Method BLASTN
NCBI GI g248336
BLAST score 69
E value 2.0e-30
Match length 137
% identity 46
NCBI Description polyubiquitin [maize, Genomic, 3841 nt]

Seq. No. 297082
Seq. ID LIB3136-044-P1-K1-H10
Method BLASTX
NCBI GI g2191172
BLAST score 175
E value 4.0e-13
Match length 44
% identity 73
NCBI Description (AF007270) contains similarity to GATA-type zinc fingers
(PS:PS00344) [Arabidopsis thaliana]

Seq. No. 297083
Seq. ID LIB3136-045-Q1-K1-A2
Method BLASTX
NCBI GI g4490317
BLAST score 157
E value 2.0e-10
Match length 89
% identity 39
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 297084

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Seq. ID	LIB3136-045-Q1-K1-B6
Method	BLASTX
NCBI GI	g4263722
BLAST score	509
E value	8.0e-52
Match length	126
% identity	79
NCBI Description	(AC006223) putative glucan synthase [Arabidopsis thaliana]
Seq. No.	297085
Seq. ID	LIB3136-045-Q1-K1-C1
Method	BLASTN
NCBI GI	g1546918
BLAST score	33
E value	4.0e-09
Match length	49
% identity	92
NCBI Description	Z.mays mRNA for translation initiation factor 5A
Seq. No.	297086
Seq. ID	LIB3136-045-Q1-K1-C2
Method	BLASTX
NCBI GI	g4336205
BLAST score	259
E value	7.0e-23
Match length	81
% identity	68
NCBI Description	(AF077372) cytochrome b5 reductase [Zea mays]
Seq. No.	297087
Seq. ID	LIB3136-045-Q1-K1-C8
Method	BLASTX
NCBI GI	g4218120
BLAST score	172
E value	3.0e-20
Match length	99
% identity	58
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]
Seq. No.	297088
Seq. ID	LIB3136-045-Q1-K1-E4
Method	BLASTX
NCBI GI	g1172809
BLAST score	370
E value	2.0e-35
Match length	113
% identity	70
NCBI Description	60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) >gi_468056 (U06108) QM protein [Zea mays]
Seq. No.	297089
Seq. ID	LIB3136-045-Q1-K1-F2
Method	BLASTX
NCBI GI	g1321661
BLAST score	164
E value	1.0e-11

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Match length	61
% identity	61
NCBI Description	(D45423) ascorbate peroxidase [Oryza sativa]
Seq. No.	297090
Seq. ID	LIB3136-045-Q1-K1-F7
Method	BLASTX
NCBI GI	g1532135
BLAST score	207
E value	2.0e-16
Match length	47
% identity	85
NCBI Description	(U49442) chloroplast mRNA-binding protein CSP41 precursor [Spinacia oleracea]
Seq. No.	297091
Seq. ID	LIB3136-045-Q1-K1-G11
Method	BLASTX
NCBI GI	g2826882
BLAST score	175
E value	3.0e-13
Match length	62
% identity	56
NCBI Description	(AJ223634) transcription factor IIA small subunit [Arabidopsis thaliana]
Seq. No.	297092
Seq. ID	LIB3136-045-Q1-K1-H10
Method	BLASTX
NCBI GI	g3513727
BLAST score	209
E value	1.0e-16
Match length	110
% identity	37
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]
Seq. No.	297093
Seq. ID	LIB3136-045-Q1-K1-H7
Method	BLASTX
NCBI GI	g2497539
BLAST score	194
E value	6.0e-27
Match length	104
% identity	65
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703 (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]
Seq. No.	297094
Seq. ID	LIB3136-045-Q1-K1-H9
Method	BLASTX
NCBI GI	g3513727
BLAST score	235
E value	1.0e-19

Match length	101
% identity	50
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]
Seq. No.	297095
Seq. ID	LIB3136-047-Q1-K1-B3
Method	BLASTX
NCBI GI	g4567249
BLAST score	261
E value	3.0e-23
Match length	61
% identity	75
NCBI Description	(AC007070) hypothetical protein [Arabidopsis thaliana]
Seq. No.	297096
Seq. ID	LIB3136-047-Q1-K1-E11
Method	BLASTX
NCBI GI	g2668742
BLAST score	201
E value	3.0e-16
Match length	45
% identity	87
NCBI Description	(AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.	297097
Seq. ID	LIB3136-047-Q1-K1-E12
Method	BLASTX
NCBI GI	g421787
BLAST score	207
E value	2.0e-16
Match length	109
% identity	45
NCBI Description	jacalin prepropeptide - jackfruit >gi_289162 (L03796) jacalin [Artocarpus integrifolia]
Seq. No.	297098
Seq. ID	LIB3136-047-Q1-K1-F5
Method	BLASTX
NCBI GI	g576192
BLAST score	357
E value	1.0e-34
Match length	82
% identity	91
NCBI Description	Dioscoreophyllum cumminsii >gi_576193_pdb_1MOL_B Dioscoreophyllum cumminsii
Seq. No.	297099
Seq. ID	LIB3136-048-Q1-K1-A5
Method	BLASTN
NCBI GI	g550541
BLAST score	121
E value	2.0e-61
Match length	350

% identity 88
NCBI Description Z.mays CYP71C4 mRNA for cytochrome P-450

Seq. No. 297100
Seq. ID LIB3136-048-Q1-K1-C8
Method BLASTN
NCBI GI g236729
BLAST score 53
E value 4.0e-21
Match length 117
% identity 86
NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]

Seq. No. 297101
Seq. ID LIB3136-048-Q1-K1-D1
Method BLASTX
NCBI GI g3759184
BLAST score 169
E value 4.0e-12
Match length 54
% identity 61
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 297102
Seq. ID LIB3136-048-Q1-K1-F4
Method BLASTX
NCBI GI g729103
BLAST score 184
E value 4.0e-14
Match length 50
% identity 72
NCBI Description CHALCONE--FLAVONONE ISOMERASE >gi_542181_pir_S41570
chalcone isomerase (EC 5.5.1.6) - maize
>gi_396149_emb_CAA80441_ (Z22760) chalcone flavonone
isomerase [Zea mays]

Seq. No. 297103
Seq. ID LIB3136-048-Q1-K1-G2
Method BLASTX
NCBI GI g4204372
BLAST score 299
E value 3.0e-27
Match length 79
% identity 77
NCBI Description (U62748) acidic ribosomal protein P2a-2 [Zea mays]

Seq. No. 297104
Seq. ID LIB3136-049-Q1-K1-A12
Method BLASTX
NCBI GI g3982632
BLAST score 513
E value 3.0e-52
Match length 104
% identity 93
NCBI Description (AF056160) disease resistance gene analog PIC20 [Zea mays]

Seq. No. 297105

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Seq. ID LIB3136-049-Q1-K1-B2
Method BLASTX
NCBI GI g347855
BLAST score 288
E value 8.0e-26
Match length 138
% identity 43
NCBI Description (L21753) glucose transporter [Saccharum hybrid cultivar H65-7052]

Seq. No. 297106
Seq. ID LIB3136-049-Q1-K1-B5
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 6.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 297107
Seq. ID LIB3136-049-Q1-K1-D12
Method BLASTX
NCBI GI g1711036
BLAST score 178
E value 2.0e-13
Match length 44
% identity 77
NCBI Description (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]

Seq. No. 297108
Seq. ID LIB3136-049-Q1-K1-D5
Method BLASTX
NCBI GI g4586039
BLAST score 363
E value 1.0e-34
Match length 108
% identity 66
NCBI Description (AC007109) unknown protein [Arabidopsis thaliana]

Seq. No. 297109
Seq. ID LIB3136-049-Q1-K1-D7
Method BLASTX
NCBI GI g4586027
BLAST score 159
E value 3.0e-11
Match length 46
% identity 67
NCBI Description (AC007109) putative ribosomal protein L14 [Arabidopsis thaliana]

Seq. No. 297110
Seq. ID LIB3136-049-Q1-K1-F9
Method BLASTN
NCBI GI g550437
BLAST score 146

E value 2.0e-76
Match length 274
% identity 89
NCBI Description Z.mays CYP71C2 mRNA for cytochrome P-450

Seq. No. 297111
Seq. ID LIB3136-050-Q1-K1-E10
Method BLASTX
NCBI GI g4572673
BLAST score 209
E value 6.0e-17
Match length 89
% identity 54
NCBI Description (AC006954) putative sarcosine oxidase [Arabidopsis thaliana]

Seq. No. 297112
Seq. ID LIB3136-050-Q1-K1-F9
Method BLASTX
NCBI GI g4455338
BLAST score 265
E value 4.0e-23
Match length 91
% identity 55
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 297113
Seq. ID LIB3136-051-Q1-K1-B1
Method BLASTX
NCBI GI g1619300
BLAST score 166
E value 7.0e-12
Match length 71
% identity 51
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

Seq. No. 297114
Seq. ID LIB3136-051-Q1-K1-C11
Method BLASTX
NCBI GI g2668744
BLAST score 340
E value 4.0e-32
Match length 70
% identity 90
NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No. 297115
Seq. ID LIB3136-051-Q1-K1-D11
Method BLASTX
NCBI GI g2668742
BLAST score 382
E value 4.0e-37
Match length 80
% identity 94
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 297116

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Seq. ID	LIB3136-051-Q1-K1-D6
Method	BLASTX
NCBI GI	g2244965
BLAST score	144
E value	6.0e-09
Match length	74
% identity	39
NCBI Description	(Z97340) unnamed protein product [Arabidopsis thaliana]
Seq. No.	297117
Seq. ID	LIB3136-051-Q1-K1-D9
Method	BLASTX
NCBI GI	g2288969
BLAST score	227
E value	5.0e-19
Match length	61
% identity	77
NCBI Description	(Y12862) glutathione transferase [Zea mays]
Seq. No.	297118
Seq. ID	LIB3136-051-Q1-K1-F7
Method	BLASTX
NCBI GI	g2119187
BLAST score	237
E value	8.0e-20
Match length	47
% identity	96
NCBI Description	transmembrane protein, glucose starvation-induced - maize >gi_575731_emb_CAA57955_ (X82633) transmembrane protein [Zea mays]
Seq. No.	297119
Seq. ID	LIB3136-051-Q1-K1-H1
Method	BLASTX
NCBI GI	g1272505
BLAST score	140
E value	1.0e-08
Match length	45
% identity	73
NCBI Description	(D49551) peroxidase [Oryza sativa]
Seq. No.	297120
Seq. ID	LIB3136-052-Q1-K1-C2
Method	BLASTX
NCBI GI	g1173055
BLAST score	244
E value	3.0e-34
Match length	82
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir_S42497 ribosomal protein L11.e - alfalfa >gi_1076504_pir_S51819 RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_ (X78284) RL5 ribosomal protein [Medicago sativa]
Seq. No.	297121
Seq. ID	LIB3136-052-Q1-K1-C9
Method	BLASTX

NCBI GI g1711240
 BLAST score 145
 E value 3.0e-09
 Match length 48
 % identity 52
 NCBI Description (D86728) TIS [Mus musculus]

Seq. No. 297122
 Seq. ID LIB3136-052-Q1-K1-D6
 Method BLASTX
 NCBI GI g120670
 BLAST score 346
 E value 1.0e-32
 Match length 67
 % identity 99
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 >gi_100879_pir_S06879 glyceraldehyde-3-phosphate
 dehydrogenase (EC 1.2.1.12) C - maize
 >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]

Seq. No. 297123
 Seq. ID LIB3136-052-Q1-K1-D9
 Method BLASTN
 NCBI GI g1532072
 BLAST score 56
 E value 9.0e-23
 Match length 104
 % identity 88
 NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No. 297124
 Seq. ID LIB3136-052-Q1-K1-F3
 Method BLASTN
 NCBI GI g644492
 BLAST score 43
 E value 5.0e-15
 Match length 156
 % identity 89
 NCBI Description Corn elongation factor 1alpha gene, complete cds

Seq. No. 297125
 Seq. ID LIB3136-054-Q1-K1-A10
 Method BLASTX
 NCBI GI g1168536
 BLAST score 183
 E value 4.0e-14
 Match length 66
 % identity 58
 NCBI Description PHYTEPSIN PRECURSOR (ASPARTIC PROTEINASE)
 >gi_100567_pir_S19697 aspartic proteinase (EC 3.4.23.-)
 precursor - barley >gi_18904_emb_CAA39602_ (X56136)
 aspartic proteinase [Hordeum vulgare]

Seq. No. 297126
 Seq. ID LIB3136-054-Q1-K1-A5
 Method BLASTX
 NCBI GI g1362103

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BLAST score	204
E value	3.0e-16
Match length	89
% identity	51
NCBI Description	ubiquitin conjugating enzyme - tomato >gi_886679_emb_CAA58111_ (X82938) ubiquitin conjugating enzyme [Lycopersicon esculentum]
Seq. No.	297127
Seq. ID	LIB3136-054-Q1-K1-A7
Method	BLASTX
NCBI GI	g4586255
BLAST score	181
E value	4.0e-25
Match length	79
% identity	73
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]
Seq. No.	297128
Seq. ID	LIB3136-054-Q1-K1-C11
Method	BLASTX
NCBI GI	g3421413
BLAST score	171
E value	4.0e-12
Match length	63
% identity	60
NCBI Description	(AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] >gi_3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]
Seq. No.	297129
Seq. ID	LIB3136-054-Q1-K1-D2
Method	BLASTN
NCBI GI	g1854377
BLAST score	59
E value	1.0e-24
Match length	271
% identity	81
NCBI Description	Saccharum officinarum RNA for Sucrose-Phosphate Synthase, complete cds
Seq. No.	297130
Seq. ID	LIB3136-054-Q1-K1-D8
Method	BLASTX
NCBI GI	g4106389
BLAST score	182
E value	2.0e-13
Match length	79
% identity	54
NCBI Description	(AF074849) MEI1 [Arabidopsis thaliana]
Seq. No.	297131
Seq. ID	LIB3136-055-Q1-K1-B12
Method	BLASTN
NCBI GI	g2894376
BLAST score	39
E value	2.0e-12

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Match length	63
% identity	90
NCBI Description	Hordeum vulgare DNA for chromosome 4H
Seq. No.	297132
Seq. ID	LIB3136-055-Q1-K1-H10
Method	BLASTX
NCBI GI	g2791896
BLAST score	147
E value	1.0e-09
Match length	92
% identity	37
NCBI Description	(Y08997) 146kDa nuclear protein [Xenopus laevis]
Seq. No.	297133
Seq. ID	LIB3136-056-Q1-K1-B12
Method	BLASTX
NCBI GI	g2506277
BLAST score	154
E value	1.0e-10
Match length	56
% identity	52
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_806808 (U21139) chaperonin precursor [Pisum sativum]
Seq. No.	297134
Seq. ID	LIB3136-056-Q1-K1-B2
Method	BLASTX
NCBI GI	g115786
BLAST score	301
E value	1.0e-27
Match length	77
% identity	79
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays]
Seq. No.	297135
Seq. ID	LIB3136-056-Q1-K1-B3
Method	BLASTX
NCBI GI	g4586112
BLAST score	194
E value	8.0e-15
Match length	84
% identity	45
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]
Seq. No.	297136
Seq. ID	LIB3136-056-Q1-K1-B4
Method	BLASTX
NCBI GI	g3789952
BLAST score	166
E value	1.0e-11
Match length	52
% identity	62

NCBI Description (AF094775) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 297137
Seq. ID LIB3136-056-Q1-K1-C11
Method BLASTX
NCBI GI g3668091
BLAST score 368
E value 3.0e-35
Match length 103
% identity 61
NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297138
Seq. ID LIB3136-056-Q1-K1-D12
Method BLASTX
NCBI GI g4538903
BLAST score 214
E value 3.0e-17
Match length 134
% identity 40
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]

Seq. No. 297139
Seq. ID LIB3136-056-Q1-K1-E1
Method BLASTX
NCBI GI g4589962
BLAST score 163
E value 1.0e-11
Match length 77
% identity 47
NCBI Description (AC007169) putative fructokinase [Arabidopsis thaliana]

Seq. No. 297140
Seq. ID LIB3136-056-Q1-K1-G5
Method BLASTX
NCBI GI g1514643
BLAST score 158
E value 1.0e-10
Match length 56
% identity 55
NCBI Description (Z70524) PDR5-like ABC transporter [Spirodes polyrrhiza]

Seq. No. 297141
Seq. ID LIB3136-056-Q1-K1-G8
Method BLASTX
NCBI GI g1709970
BLAST score 428
E value 3.0e-42
Match length 125
% identity 66
NCBI Description 60S RIBOSOMAL PROTEIN L10A

Seq. No. 297142
Seq. ID LIB3136-057-Q1-K1-C2
Method BLASTX
NCBI GI g1272685

BLAST score 559
E value 1.0e-57
Match length 116
% identity 89
NCBI Description (Z24449) acetyl CoA carboxylase [Zea mays]

Seq. No. 297143
Seq. ID LIB3136-057-Q1-K1-D10
Method BLASTX
NCBI GI g1769901
BLAST score 161
E value 1.0e-11
Match length 54
% identity 57
NCBI Description (X95737) proline transporter 1 [Arabidopsis thaliana]
>gi_2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana]

Seq. No. 297144
Seq. ID LIB3136-057-Q1-K1-E10
Method BLASTN
NCBI GI g22646
BLAST score 54
E value 2.0e-21
Match length 131
% identity 92
NCBI Description Z.mays MFS18 mRNA

Seq. No. 297145
Seq. ID LIB3136-057-Q1-K1-F7
Method BLASTX
NCBI GI g3292827
BLAST score 328
E value 6.0e-31
Match length 78
% identity 81
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 297146
Seq. ID LIB3136-058-Q1-K1-B5
Method BLASTX
NCBI GI g2765837
BLAST score 157
E value 2.0e-10
Match length 76
% identity 47
NCBI Description (Z96936) NAP16kDa protein [Arabidopsis thaliana]

Seq. No. 297147
Seq. ID LIB3136-058-Q1-K1-B6
Method BLASTX
NCBI GI g4539009
BLAST score 267
E value 1.0e-23
Match length 99
% identity 51
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 297148
Seq. ID LIB3136-058-Q1-K1-C5
Method BLASTX
NCBI GI g746540
BLAST score 210
E value 1.0e-16
Match length 97
% identity 44
NCBI Description (U23521) No definition line found [Caenorhabditis elegans]

Seq. No. 297149
Seq. ID LIB3136-058-Q1-K1-C6
Method BLASTX
NCBI GI g520544
BLAST score 217
E value 1.0e-17
Match length 107
% identity 53
NCBI Description (U12195) betaine aldehyde dehydrogenase [Sorghum bicolor]

Seq. No. 297150
Seq. ID LIB3136-058-Q1-K1-C7
Method BLASTX
NCBI GI g2674203
BLAST score 345
E value 1.0e-32
Match length 124
% identity 58
NCBI Description (AF036328) CLP protease regulatory subunit CLPX [Arabidopsis thaliana]

Seq. No. 297151
Seq. ID LIB3136-058-Q1-K1-D6
Method BLASTX
NCBI GI g4038471
BLAST score 196
E value 2.0e-15
Match length 62
% identity 66
NCBI Description (AF111029) 40S ribosomal protein S27 homolog [Zea mays]

Seq. No. 297152
Seq. ID LIB3136-058-Q1-K1-F2
Method BLASTX
NCBI GI g4262236
BLAST score 245
E value 7.0e-21
Match length 74
% identity 65
NCBI Description (AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No. 297153
Seq. ID LIB3136-058-Q1-K1-F7
Method BLASTX
NCBI GI g2832625

BLAST score 153
E value 4.0e-10
Match length 60
% identity 53
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 297154
Seq. ID LIB3136-058-Q1-K1-H11
Method BLASTX
NCBI GI g3618312
BLAST score 258
E value 2.0e-22
Match length 80
% identity 65
NCBI Description (AB001884) zinc finger protein [Oryza sativa]

Seq. No. 297155
Seq. ID LIB3136-059-Q1-K1-C11
Method BLASTX
NCBI GI g464705
BLAST score 154
E value 2.0e-10
Match length 66
% identity 58
NCBI Description 40S RIBOSOMAL PROTEIN S13 >gi_419802_pir_S30146 ribosomal protein S13.e - maize >gi_288059_emb_CAA44311 (X62455) cytoplasmatic ribosomal protein S13 [Zea mays]

Seq. No. 297156
Seq. ID LIB3136-059-Q1-K1-D9
Method BLASTX
NCBI GI g3047117
BLAST score 342
E value 1.0e-32
Match length 84
% identity 80
NCBI Description (AF058919) similar to ATP-dependent RNA helicases [Arabidopsis thaliana]

Seq. No. 297157
Seq. ID LIB3136-059-Q1-K1-E7
Method BLASTX
NCBI GI g1076719
BLAST score 154
E value 4.0e-10
Match length 39
% identity 67
NCBI Description glycine rich protein - barley (fragment) >gi_728596_emb_CAA88559 (Z48625) glycine rich protein [Hordeum vulgare]

Seq. No. 297158
Seq. ID LIB3136-059-Q1-K1-F10
Method BLASTX
NCBI GI g2132925
BLAST score 160
E value 8.0e-11

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Match length 122
% identity 33
NCBI Description probable membrane protein YOR245c - yeast (Saccharomyces cerevisiae) >gi_1420558_emb_CAA99466_ (Z75153) ORF YOR245c [Saccharomyces cerevisiae]

Seq. No. 297159
Seq. ID LIB3136-059-Q1-K1-F12
Method BLASTX
NCBI GI g4512653
BLAST score 410
E value 3.0e-45
Match length 150
% identity 61
NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No. 297160
Seq. ID LIB3136-059-Q1-K1-G12
Method BLASTX
NCBI GI g3687249
BLAST score 201
E value 8.0e-16
Match length 54
% identity 74
NCBI Description (AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No. 297161
Seq. ID LIB3136-060-Q1-K1-A4
Method BLASTX
NCBI GI g1871180
BLAST score 196
E value 3.0e-15
Match length 48
% identity 73
NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

Seq. No. 297162
Seq. ID LIB3136-060-Q1-K1-B8
Method BLASTN
NCBI GI g2062705
BLAST score 34
E value 9.0e-10
Match length 34
% identity 100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 297163
Seq. ID LIB3136-060-Q1-K1-C11
Method BLASTX
NCBI GI g2388580
BLAST score 253
E value 1.0e-21
Match length 86
% identity 50
NCBI Description (AC000098) Similar to Sequence 10 from patent 5477002 (gb_1253956). [Arabidopsis thaliana]

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Seq. No.	297164
Seq. ID	LIB3136-060-Q1-K1-D1
Method	BLASTN
NCBI GI	g167082
BLAST score	35
E value	3.0e-10
Match length	35
% identity	100
NCBI Description	H.vulgare peroxidase BP 2A (Prx6) gene, complete cds
Seq. No.	297165
Seq. ID	LIB3136-060-Q1-K1-D11
Method	BLASTX
NCBI GI	g2293566
BLAST score	211
E value	6.0e-27
Match length	128
% identity	57
NCBI Description	(AF012896) ADP-ribosylation factor 1 [Oryza sativa]
Seq. No.	297166
Seq. ID	LIB3136-060-Q1-K1-F8
Method	BLASTN
NCBI GI	g3057119
BLAST score	34
E value	7.0e-10
Match length	66
% identity	88
NCBI Description	Zea mays starch synthase DULL1 (dull1) mRNA, complete cds
Seq. No.	297167
Seq. ID	LIB3136-060-Q1-K1-F9
Method	BLASTX
NCBI GI	g266578
BLAST score	259
E value	2.0e-22
Match length	56
% identity	82
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir_S17560 metallothionein-like protein - maize >gi_236730_bbs_57629 (S57628) metallothionein homologue [Zea mays, Peptide, 76 aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186) metallothionein- like protein [Zea mays] >gi_228095_prf_1717215A metallothionein-like protein [Zea mays]
Seq. No.	297168
Seq. ID	LIB3137-001-Q1-K1-A8
Method	BLASTX
NCBI GI	g2642648
BLAST score	314
E value	5.0e-29
Match length	87
% identity	72
NCBI Description	(AF033852) cytosolic heat shock 70 protein; HSC70-3 [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat

shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617)
cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No. 297169
Seq. ID LIB3137-001-Q1-K1-F4
Method BLASTX
NCBI GI g417745
BLAST score 240
E value 2.0e-20
Match length 91
% identity 58
NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_170773 (L11872)
S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

Seq. No. 297170
Seq. ID LIB3137-001-Q1-K1-F5
Method BLASTX
NCBI GI g3242075
BLAST score 146
E value 1.0e-09
Match length 49
% identity 59
NCBI Description (Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No. 297171
Seq. ID LIB3137-001-Q1-K1-G12
Method BLASTN
NCBI GI g22229
BLAST score 132
E value 2.0e-68
Match length 203
% identity 91
NCBI Description Z.mays cab-m7 gene for light harvesting chlorophyll a/b binding protein

Seq. No. 297172
Seq. ID LIB3137-001-Q1-K1-H4
Method BLASTX
NCBI GI g1430887
BLAST score 185
E value 7.0e-14
Match length 36
% identity 100
NCBI Description (X99197) 70 kD heatshockprotein [Medicago sativa]

Seq. No. 297173
Seq. ID LIB3137-002-Q1-K1-A2
Method BLASTX
NCBI GI g2668742
BLAST score 344
E value 2.0e-32
Match length 79
% identity 82
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

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Seq. No. 297174
Seq. ID LIB3137-002-Q1-K1-E8
Method BLASTX
NCBI GI g2995953
BLAST score 145
E value 5.0e-09
Match length 63
% identity 49
NCBI Description (AF053565) glutaredoxin I [Mesembryanthemum crystallinum]

Seq. No. 297175
Seq. ID LIB3137-002-Q1-K1-E9
Method BLASTX
NCBI GI g3024657
BLAST score 378
E value 1.0e-36
Match length 103
% identity 72
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
>gi_2668740 (AF034944) translation initiation factor; GOS2
[Zea mays]

Seq. No. 297176
Seq. ID LIB3137-002-Q1-K1-F3
Method BLASTX
NCBI GI g2984709
BLAST score 336
E value 1.0e-31
Match length 72
% identity 92
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 297177
Seq. ID LIB3137-002-Q1-K1-F8
Method BLASTX
NCBI GI g578549
BLAST score 152
E value 3.0e-10
Match length 43
% identity 72
NCBI Description (Z22614) ubiquitin [Tetrahymena pyriformis]

Seq. No. 297178
Seq. ID LIB3137-002-Q1-K1-G2
Method BLASTN
NCBI GI g551482
BLAST score 106
E value 1.0e-52
Match length 231
% identity 95
NCBI Description Zea mays ABA- and ripening-inducible-like protein mRNA,
complete cds

Seq. No. 297179
Seq. ID LIB3137-002-Q1-K1-G6
Method BLASTX
NCBI GI g1703374

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BLAST score	209
E value	7.0e-17
Match length	92
% identity	53
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_2129457_pir_S66337 ADP-ribosylation factor 1 - <i>Chlamydomonas reinhardtii</i> >gi_861205 (U27120) ADP-ribosylation factor [<i>Chlamydomonas reinhardtii</i>]
Seq. No.	297180
Seq. ID	LIB3137-002-Q1-K1-G8
Method	BLASTX
NCBI GI	g1362010
BLAST score	202
E value	4.0e-16
Match length	55
% identity	20
NCBI Description	ubiquitin-like protein 9 - <i>Arabidopsis thaliana</i>
Seq. No.	297181
Seq. ID	LIB3137-002-Q1-K1-H4
Method	BLASTX
NCBI GI	g4588012
BLAST score	180
E value	3.0e-18
Match length	104
% identity	49
NCBI Description	(AF085717) putative callose synthase catalytic subunit [<i>Gossypium hirsutum</i>]
Seq. No.	297182
Seq. ID	LIB3137-003-Q1-K1-B10
Method	BLASTX
NCBI GI	g1769887
BLAST score	171
E value	3.0e-12
Match length	42
% identity	81
NCBI Description	(X95736) amino acid permease 6 [<i>Arabidopsis thaliana</i>]
Seq. No.	297183
Seq. ID	LIB3137-003-Q1-K1-B3
Method	BLASTX
NCBI GI	g1321661
BLAST score	293
E value	1.0e-26
Match length	65
% identity	86
NCBI Description	(D45423) ascorbate peroxidase [<i>Oryza sativa</i>]
Seq. No.	297184
Seq. ID	LIB3137-003-Q1-K1-C10
Method	BLASTX
NCBI GI	g3293031
BLAST score	288
E value	6.0e-26
Match length	109

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% identity 56
NCBI Description (AJ007574) amino acid carrier [Ricinus communis]

Seq. No. 297185
Seq. ID LIB3137-003-Q1-K1-D3
Method BLASTX
NCBI GI g3776578
BLAST score 195
E value 6.0e-15
Match length 112
% identity 36
NCBI Description (AC005388) ESTs gb_F13915 and gb_F13916 come from this gene. [Arabidopsis thaliana]

Seq. No. 297186
Seq. ID LIB3137-003-Q1-K1-D8
Method BLASTX
NCBI GI g115815
BLAST score 246
E value 5.0e-21
Match length 94
% identity 55
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-M9). (LHCP) >gi_100866_pir_S13098 chlorophyll a/b-binding protein precursor - maize >gi_22355_emb_CAA39376_ (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays]

Seq. No. 297187
Seq. ID LIB3137-003-Q1-K1-G12
Method BLASTX
NCBI GI g1174592
BLAST score 280
E value 5.0e-36
Match length 106
% identity 73
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir_S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No. 297188
Seq. ID LIB3137-003-Q1-K1-G6
Method BLASTX
NCBI GI g2499611
BLAST score 281
E value 5.0e-25
Match length 63
% identity 81
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7) (ATMPK7) >gi_629548_pir_S40473 mitogen-activated protein kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457406_dbj_BAA04870_ (D21843) MAP kinase [Arabidopsis thaliana]

Seq. No. 297189
Seq. ID LIB3137-004-Q1-K1-D1
Method BLASTX

NCBI GI g113595
 BLAST score 268
 E value 1.0e-30
 Match length 81
 % identity 85
 NCBI Description ALDOSE REDUCTASE (AR) (ALDEHYDE REDUCTASE)
 >gi_100562_pir_S15024 aldose reductase-related protein -
 barley >gi_18891_emb_CAA40747_ (X57526) aldose
 reductase-related protein [Hordeum vulgare]

Seq. No. 297190
 Seq. ID LIB3137-004-Q1-K1-E2
 Method BLASTX
 NCBI GI g4038037
 BLAST score 192
 E value 1.0e-14
 Match length 134
 % identity 15
 NCBI Description (AC005936) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297191
 Seq. ID LIB3137-004-Q1-K1-E5
 Method BLASTX
 NCBI GI g2505870
 BLAST score 142
 E value 5.0e-09
 Match length 88
 % identity 42
 NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297192
 Seq. ID LIB3137-004-Q1-K1-F8
 Method BLASTX
 NCBI GI g1171579
 BLAST score 241
 E value 2.0e-20
 Match length 61
 % identity 72
 NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No. 297193
 Seq. ID LIB3137-004-Q1-K1-H4
 Method BLASTX
 NCBI GI g3913793
 BLAST score 290
 E value 5.0e-26
 Match length 82
 % identity 68
 NCBI Description GLUTATHIONE PEROXIDASE 2 >gi_2569989_emb_CAA75009_ (Y14707)
 glutathione peroxidase [Helianthus annuus]

Seq. No. 297194
 Seq. ID LIB3137-005-Q1-K1-A12
 Method BLASTX
 NCBI GI g488573
 BLAST score 427
 E value 4.0e-42

Match length 87
% identity 99
NCBI Description (U09463) histone H3.2 [Medicago sativa]

Seq. No. 297195
Seq. ID LIB3137-005-Q1-K1-B10
Method BLASTX
NCBI GI g4325344
BLAST score 240
E value 4.0e-20
Match length 61
% identity 70
NCBI Description (AF128393) similar to beta-transducins (Pfam: PF00400, Score=71.7, E=1.5e-17, N=6) [Arabidopsis thaliana]

Seq. No. 297196
Seq. ID LIB3137-005-Q1-K1-B5
Method BLASTN
NCBI GI g902200
BLAST score 90
E value 6.0e-43
Match length 207
% identity 43
NCBI Description Z.mays complete chloroplast genome

Seq. No. 297197
Seq. ID LIB3137-005-Q1-K1-B6
Method BLASTX
NCBI GI g2340108
BLAST score 321
E value 6.0e-30
Match length 57
% identity 100
NCBI Description (U65948) starch branching enzyme IIa [Zea mays]

Seq. No. 297198
Seq. ID LIB3137-005-Q1-K1-B9
Method BLASTX
NCBI GI g122084
BLAST score 363
E value 1.0e-34
Match length 80
% identity 93
NCBI Description HISTONE H3 >gi_70754_pir_HSBH3 histone H3 - barley (fragment) >gi_167061 (M34928) histone H3 protein [Hordeum vulgare] >gi_225348_prf_1301219A histone H3 [Hordeum vulgare var. distichum]

Seq. No. 297199
Seq. ID LIB3137-005-Q1-K1-C10
Method BLASTX
NCBI GI g2760606
BLAST score 654
E value 1.0e-68
Match length 143
% identity 86
NCBI Description (AB001568) phospholipid hydroperoxide glutathione

peroxidase-like protein [Arabidopsis thaliana] >gi_3004869
(AF030132) glutathione peroxidase; ATGP1 [Arabidopsis
thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500)
phospholipid hydroperoxide glutathione peroxidase
[Arabidopsis thaliana]

Seq. No. 297200
Seq. ID LIB3137-005-Q1-K1-C11
Method BLASTX
NCBI GI g136640
BLAST score 611
E value 1.0e-63
Match length 115
% identity 98
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_170785 (M62720)
ubiquitin carrier protein [Triticum aestivum]

Seq. No. 297201
Seq. ID LIB3137-005-Q1-K1-C12
Method BLASTX
NCBI GI g136640
BLAST score 173
E value 2.0e-12
Match length 100
% identity 45
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_170785 (M62720)
ubiquitin carrier protein [Triticum aestivum]

Seq. No. 297202
Seq. ID LIB3137-005-Q1-K1-C8
Method BLASTX
NCBI GI g168523
BLAST score 518
E value 8.0e-53
Match length 101
% identity 99
NCBI Description (M31483) glyceraldehyde-3-phosphate dehydrogenase precursor
[Zea mays]

Seq. No. 297203
Seq. ID LIB3137-005-Q1-K1-D10
Method BLASTX
NCBI GI g3372230
BLAST score 487
E value 4.0e-49
Match length 133
% identity 68
NCBI Description (AF017074) RNA polymerase I, II and III 16.5 kDa subunit
[Arabidopsis thaliana] >gi_4585968_gb_AAD25604.1_AC005287_6
(AC005287) RNA polymerase I, II and III 16.5 kDa subunit
[Arabidopsis thaliana]

Seq. No. 297204
Seq. ID LIB3137-005-Q1-K1-D5
Method BLASTX

NCBI GI g3915826
BLAST score 387
E value 1.0e-37
Match length 101
% identity 74
NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 297205
Seq. ID LIB3137-005-Q1-K1-D9
Method BLASTX
NCBI GI g2213583
BLAST score 377
E value 3.0e-36
Match length 141
% identity 55
NCBI Description (AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No. 297206
Seq. ID LIB3137-005-Q1-K1-E12
Method BLASTX
NCBI GI g1370174
BLAST score 559
E value 2.0e-57
Match length 122
% identity 86
NCBI Description (Z73936) RAB1Y [Lotus japonicus]

Seq. No. 297207
Seq. ID LIB3137-005-Q1-K1-E3
Method BLASTX
NCBI GI g2921304
BLAST score 558
E value 1.0e-57
Match length 121
% identity 93
NCBI Description (AF033496) herbicide safener binding protein [Zea mays]

Seq. No. 297208
Seq. ID LIB3137-005-Q1-K1-F11
Method BLASTX
NCBI GI g2253219
BLAST score 540
E value 2.0e-55
Match length 128
% identity 83
NCBI Description (AF002689) actin 2 [Podocarpus macrophyllus]

Seq. No. 297209
Seq. ID LIB3137-005-Q1-K1-G10
Method BLASTX
NCBI GI g122085
BLAST score 439
E value 2.0e-43
Match length 133
% identity 73
NCBI Description HISTONE H3 >gi_81641_pir_S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir_S04099 histone H3 (variant H3R-21)

- rice >gi_1362194_pir_S57626 histone H3 - maize
 >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136)
 [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3
 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3
 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays]
 >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506
 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone
 H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3
 [Petroselinum crispum] >gi_169659 (M77495) histone H3
 [Petroselinum crispum] >gi_387565 (M17130) histone H3
 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3
 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377)
 histone 3 [Zea mays] >gi_1040764 (M35387) histone H3
 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3
 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414)
 Histone H3 [Asparagus officinalis] >gi_1667592 (U77296)
 histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to
 histone H3 gene gb_M17131 and gb_M35387 from A. thaliana.
 ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and
 gb_T42306 come from this gene. [Arabidopsis thaliana]
 >gi_225459_prf_1303352A histone H3 [Helicoverpa zea]
 >gi_225839_prf_1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 297210
 Seq. ID LIB3137-005-Q1-K1-G11
 Method BLASTX
 NCBI GI g4490293
 BLAST score 607
 E value 4.0e-63
 Match length 153
 % identity 70
 NCBI Description (AL035678) WD-repeat protein-like protein [Arabidopsis thaliana]

Seq. No. 297211
 Seq. ID LIB3137-005-Q1-K1-G9
 Method BLASTX
 NCBI GI g70774
 BLAST score 409
 E value 6.0e-40
 Match length 82
 % identity 99
 NCBI Description histone H4 (TH091) - wheat >gi_170747 (M12277) histone H4 [Triticum aestivum]

Seq. No. 297212
 Seq. ID LIB3137-005-Q1-K1-H11
 Method BLASTX
 NCBI GI g4193388
 BLAST score 508
 E value 1.0e-51
 Match length 130
 % identity 77
 NCBI Description (AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No. 297213

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Seq. ID	LIB3137-005-Q1-K1-H9
Method	BLASTX
NCBI GI	g2245069
BLAST score	364
E value	6.0e-35
Match length	98
% identity	62
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.	297214
Seq. ID	LIB3137-006-Q1-K1-D9
Method	BLASTX
NCBI GI	g4507793
BLAST score	167
E value	1.0e-11
Match length	42
% identity	69
NCBI Description	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) >gi_2501432_sp_Q16781_UBCC_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_2146981_pir_JC4894 ubiquitin-conjugating enzyme (EC 6.3.2.-) E2 - human >gi_1181558_dbj_BAA11675_ (D83004) ubiquitin-conjugating enzyme E2 UbcH-ben [Homo sapiens]
Seq. No.	297215
Seq. ID	LIB3137-007-Q1-K1-B3
Method	BLASTX
NCBI GI	g4091008
BLAST score	200
E value	7.0e-16
Match length	85
% identity	49
NCBI Description	(AF040700) methionyl-tRNA synthetase [Oryza sativa]
Seq. No.	297216
Seq. ID	LIB3137-007-Q1-K1-E12
Method	BLASTX
NCBI GI	g2335101
BLAST score	271
E value	7.0e-24
Match length	87
% identity	57
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]
Seq. No.	297217
Seq. ID	LIB3137-007-Q1-K1-E8
Method	BLASTX
NCBI GI	g1076800
BLAST score	362
E value	2.0e-34
Match length	74
% identity	92
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme - maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi_1096503_prf_2111423A ascorbate peroxidase [Zea mays]

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Seq. No. 297218
Seq. ID LIB3137-007-Q1-K1-G8
Method BLASTX
NCBI GI g112994
BLAST score 346
E value 7.0e-33
Match length 78
% identity 88
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
>gi_82685_pir_S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea
mays]

Seq. No. 297219
Seq. ID LIB3137-007-Q1-K1-H1
Method BLASTX
NCBI GI g4586117
BLAST score 399
E value 4.0e-39
Match length 100
% identity 73
NCBI Description (AL049638) putative protein [Arabidopsis thaliana]

Seq. No. 297220
Seq. ID LIB3137-008-Q1-K1-B3
Method BLASTX
NCBI GI g1129145
BLAST score 188
E value 2.0e-14
Match length 88
% identity 45
NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No. 297221
Seq. ID LIB3137-008-Q1-K1-C6
Method BLASTX
NCBI GI g4335756
BLAST score 185
E value 7.0e-14
Match length 80
% identity 50
NCBI Description (AC006284) putative ankyrin [Arabidopsis thaliana]

Seq. No. 297222
Seq. ID LIB3137-008-Q1-K1-E6
Method BLASTX
NCBI GI g4455129
BLAST score 191
E value 2.0e-14
Match length 116
% identity 37
NCBI Description (AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]

Seq. No. 297223

Seq. ID LIB3137-008-Q1-K1-F5
Method BLASTX
NCBI GI g120670
BLAST score 341
E value 2.0e-32
Match length 78
% identity 85
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi_100879_pir_S06879 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) C - maize
>gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]

Seq. No. 297224
Seq. ID LIB3137-008-Q1-K1-F6
Method BLASTN
NCBI GI g168490
BLAST score 44
E value 8.0e-16
Match length 92
% identity 87
NCBI Description Maize glutathione S-transferase (GST-I) mRNA, complete cds

Seq. No. 297225
Seq. ID LIB3137-009-Q1-K1-D12
Method BLASTX
NCBI GI g2119187
BLAST score 157
E value 9.0e-11
Match length 31
% identity 94
NCBI Description transmembrane protein, glucose starvation-induced - maize
>gi_575731_emb_CAA57955_ (X82633) transmembrane protein
[Zea mays]

Seq. No. 297226
Seq. ID LIB3137-009-Q1-K1-D3
Method BLASTX
NCBI GI g3256035
BLAST score 365
E value 8.0e-35
Match length 140
% identity 51
NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum
bicolor]

Seq. No. 297227
Seq. ID LIB3137-009-Q1-K1-D9
Method BLASTX
NCBI GI g2384673
BLAST score 164
E value 2.0e-11
Match length 67
% identity 49
NCBI Description (AF012658) putative potassium transporter AtKT3p
[Arabidopsis thaliana]

Seq. No. 297228

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Seq. ID LIB3137-009-Q1-K1-F1
Method BLASTX
NCBI GI g2623298
BLAST score 261
E value 7.0e-23
Match length 108
% identity 50
NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana]

Seq. No. 297229
Seq. ID LIB3137-009-Q1-K1-F2
Method BLASTX
NCBI GI g4510339
BLAST score 144
E value 2.0e-09
Match length 36
% identity 81
NCBI Description (AC006921) putative ABC transporter protein [Arabidopsis thaliana]

Seq. No. 297230
Seq. ID LIB3137-009-Q1-K1-G4
Method BLASTN
NCBI GI g3414828
BLAST score 113
E value 6.0e-57
Match length 121
% identity 98
NCBI Description Zea mays subsp. mays race Tuxpeno globulin-1 gene, partial cds

Seq. No. 297231
Seq. ID LIB3137-009-Q1-K1-G8
Method BLASTX
NCBI GI g4567273
BLAST score 305
E value 8.0e-28
Match length 102
% identity 58
NCBI Description (AC006841) putative vacuolar proton ATPase subunit [Arabidopsis thaliana]

Seq. No. 297232
Seq. ID LIB3137-009-Q1-K1-H10
Method BLASTX
NCBI GI g1170937
BLAST score 159
E value 2.0e-11
Match length 35
% identity 86
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
>gi_450549_emb_CAA81481_(Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No. 297233

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Seq. ID	LIB3137-010-Q1-K1-A12
Method	BLASTX
NCBI GI	g1495251
BLAST score	259
E value	2.0e-22
Match length	126
% identity	48
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]
Seq. No.	297234
Seq. ID	LIB3137-010-Q1-K1-B7
Method	BLASTX
NCBI GI	g4512667
BLAST score	312
E value	8.0e-29
Match length	112
% identity	56
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]
Seq. No.	297235
Seq. ID	LIB3137-010-Q1-K1-C11
Method	BLASTX
NCBI GI	g1911166
BLAST score	163
E value	5.0e-23
Match length	107
% identity	59
NCBI Description	(X94400) soluble-starch-synthase [Solanum tuberosum]
Seq. No.	297236
Seq. ID	LIB3137-010-Q1-K1-F11
Method	BLASTX
NCBI GI	g3785977
BLAST score	252
E value	9.0e-22
Match length	111
% identity	50
NCBI Description	(AC005560) putative growth regulator protein [Arabidopsis thaliana]
Seq. No.	297237
Seq. ID	LIB3137-010-Q1-K1-F5
Method	BLASTX
NCBI GI	g115786
BLAST score	279
E value	5.0e-25
Match length	80
% identity	68
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays]
Seq. No.	297238
Seq. ID	LIB3137-010-Q1-K1-G2
Method	BLASTX
NCBI GI	g4455225

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BLAST score 169
E value 6.0e-12
Match length 57
% identity 56
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 297239
Seq. ID LIB3137-010-Q1-K1-G6
Method BLASTX
NCBI GI g3511285
BLAST score 315
E value 3.0e-29
Match length 99
% identity 61
NCBI Description (AF081534) cellulose synthase [Populus alba x Populus tremula]

Seq. No. 297240
Seq. ID LIB3137-010-Q1-K1-G8
Method BLASTX
NCBI GI g548605
BLAST score 200
E value 1.0e-15
Match length 83
% identity 63
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
>gi_539055_pir_A48527 photosystem I protein psaK precursor
- barley >gi_304220 (L12707) photosystem I PSI-K subunit
[Hordeum vulgare]

Seq. No. 297241
Seq. ID LIB3137-010-Q1-K1-H6
Method BLASTX
NCBI GI g129232
BLAST score 157
E value 6.0e-14
Match length 90
% identity 58
NCBI Description ORYZAIN BETA CHAIN PRECURSOR >gi_67645_pir_KHRZOB oryzain
(EC 3.4.22.-) beta precursor - rice
>gi_218183_dbj_BAA14403_ (D90407) oryzain beta precursor
[Oryza sativa]

Seq. No. 297242
Seq. ID LIB3137-011-Q1-K1-C12
Method BLASTN
NCBI GI g1213278
BLAST score 54
E value 2.0e-21
Match length 54
% identity 100
NCBI Description Z.mays ZEMb gene

Seq. No. 297243
Seq. ID LIB3137-011-Q1-K1-C4
Method BLASTN

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NCBI GI	g18963
BLAST score	42
E value	1.0e-14
Match length	90
% identity	87
NCBI Description	Z.mays mRNA for dehydrin (dhn3)
Seq. No.	297244
Seq. ID	LIB3137-011-Q1-K1-C7
Method	BLASTX
NCBI GI	g82684
BLAST score	164
E value	1.0e-11
Match length	64
% identity	55
NCBI Description	dehydrin 3 - maize >gi_18964_emb_CAA33364_ (X15290) dehydrin (AA 1-167) [Zea mays]
Seq. No.	297245
Seq. ID	LIB3137-012-Q1-K1-A8
Method	BLASTX
NCBI GI	g425194
BLAST score	291
E value	7.0e-28
Match length	99
% identity	70
NCBI Description	(L26243) heat shock protein [Spinacia oleracea] >gi_2660772 (AF034618) cytosolic heat shock 70 protein [Spinacia oleracea]
Seq. No.	297246
Seq. ID	LIB3137-012-Q1-K1-B12
Method	BLASTN
NCBI GI	g1698669
BLAST score	40
E value	2.0e-13
Match length	129
% identity	84
NCBI Description	Zea mays S-like RNase (kin1) mRNA, complete cds
Seq. No.	297247
Seq. ID	LIB3137-012-Q1-K1-B3
Method	BLASTX
NCBI GI	g2832616
BLAST score	221
E value	6.0e-18
Match length	131
% identity	41
NCBI Description	(AL021711) heat shock transcription factor - like protein [Arabidopsis thaliana]
Seq. No.	297248
Seq. ID	LIB3137-012-Q1-K1-C12
Method	BLASTX
NCBI GI	g2098575
BLAST score	156
E value	2.0e-10

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Match length 86
% identity 42
NCBI Description (AC002115) F25451_2 [Homo sapiens]

Seq. No. 297249
Seq. ID LIB3137-012-Q1-K1-D4
Method BLASTX
NCBI GI g2098575
BLAST score 300
E value 2.0e-27
Match length 74
% identity 73
NCBI Description (AC002115) F25451_2 [Homo sapiens]

Seq. No. 297250
Seq. ID LIB3137-012-Q1-K1-D6
Method BLASTN
NCBI GI g3821780
BLAST score 37
E value 2.0e-11
Match length 37
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 297251
Seq. ID LIB3137-012-Q1-K1-E9
Method BLASTX
NCBI GI g129591
BLAST score 333
E value 4.0e-31
Match length 96
% identity 71
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_(X16099) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No. 297252
Seq. ID LIB3137-012-Q1-K1-F12
Method BLASTX
NCBI GI g2708806
BLAST score 206
E value 2.0e-16
Match length 71
% identity 61
NCBI Description (AF037359) superoxide dismutase [Paulownia kawakamii]

Seq. No. 297253
Seq. ID LIB3137-012-Q1-K1-G5
Method BLASTX
NCBI GI g3335378
BLAST score 267
E value 2.0e-23
Match length 78
% identity 72
NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No. 297254

Seq. ID LIB3137-012-Q1-K1-H5
Method BLASTN
NCBI GI g2687357
BLAST score 66
E value 6.0e-29
Match length 122
% identity 89
NCBI Description Zea mays nonphototropic hypocotyl 1 (nph1) mRNA, complete cds

Seq. No. 297255
Seq. ID LIB3137-013-Q1-K1-A5
Method BLASTX
NCBI GI g2580440
BLAST score 245
E value 6.0e-21
Match length 61
% identity 72
NCBI Description (D87261) PCF2 [Oryza sativa]

Seq. No. 297256
Seq. ID LIB3137-013-Q1-K1-B2
Method BLASTX
NCBI GI g730919
BLAST score 195
E value 4.0e-15
Match length 75
% identity 55
NCBI Description T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON)
(CCT-EPSILON) (TCP-K19) >gi_542112_pir_S40461 t-complex
polypeptide 1 - oat >gi_435173_emb_CAA53396_ (X75777) T
complex polypeptide 1 [Avena sativa]

Seq. No. 297257
Seq. ID LIB3137-013-Q1-K1-B7
Method BLASTX
NCBI GI g295355
BLAST score 300
E value 5.0e-30
Match length 118
% identity 56
NCBI Description (L13653) peroxidase [Lycopersicon esculentum]

Seq. No. 297258
Seq. ID LIB3137-013-Q1-K1-D2
Method BLASTX
NCBI GI g4469023
BLAST score 223
E value 2.0e-36
Match length 93
% identity 87
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 297259
Seq. ID LIB3137-013-Q1-K1-D8
Method BLASTX
NCBI GI g3004950

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BLAST score 346
E value 1.0e-32
Match length 86
% identity 79
NCBI Description (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]

Seq. No. 297260
Seq. ID LIB3137-013-Q1-K1-E7
Method BLASTX
NCBI GI g1170242
BLAST score 200
E value 4.0e-16
Match length 55
% identity 76
NCBI Description FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) >gi_474966_dbj_BAA05101_ (D26105) ferrochelatase [Hordeum vulgare]

Seq. No. 297261
Seq. ID LIB3137-013-Q1-K1-G3
Method BLASTN
NCBI GI g313759
BLAST score 48
E value 5.0e-18
Match length 60
% identity 95
NCBI Description Z.mays hsp 70-1 gene for heat shock protein

Seq. No. 297262
Seq. ID LIB3137-013-Q1-K1-G7
Method BLASTX
NCBI GI g3915029
BLAST score 202
E value 7.0e-16
Match length 70
% identity 57
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_976257_dbj_BAA07631_ (D38753) stearyl-ACP desaturase [Oryza sativa]

Seq. No. 297263
Seq. ID LIB3137-013-Q1-K1-H5
Method BLASTX
NCBI GI g465835
BLAST score 155
E value 1.0e-10
Match length 85
% identity 44
NCBI Description HYPOTHETICAL 272.0 KD PROTEIN C50C3.6 IN CHROMOSOME III >gi_630577_pir_S44625 C50C3.6 protein - Caenorhabditis elegans >gi_289658 (L14433) putative [Caenorhabditis elegans]

Seq. No. 297264
Seq. ID LIB3137-014-Q1-K1-A10
Method BLASTX
NCBI GI g1345683

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BLAST score	234
E value	2.0e-19
Match length	48
% identity	94
NCBI Description	CATALASE ISOZYME 3 >gi_487045_pir_S37379 catalase (EC 1.11.1.6) 3 - maize >gi_168437 (L05934) catalase [Zea mays]
Seq. No.	297265
Seq. ID	LIB3137-014-Q1-K1-B6
Method	BLASTX
NCBI GI	g82696
BLAST score	352
E value	2.0e-33
Match length	81
% identity	88
NCBI Description	glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]
Seq. No.	297266
Seq. ID	LIB3137-014-Q1-K1-D2
Method	BLASTX
NCBI GI	g4263509
BLAST score	164
E value	6.0e-17
Match length	112
% identity	51
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]
Seq. No.	297267
Seq. ID	LIB3137-014-Q1-K1-D7
Method	BLASTX
NCBI GI	g3063706
BLAST score	173
E value	1.0e-12
Match length	75
% identity	44
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]
Seq. No.	297268
Seq. ID	LIB3137-014-Q1-K1-F1
Method	BLASTX
NCBI GI	g1076809
BLAST score	353
E value	2.0e-33
Match length	90
% identity	76
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - maize >gi_758355_emb_CAA59800_(X85805) H(+) -transporting ATPase [Zea mays]
Seq. No.	297269
Seq. ID	LIB3137-014-Q1-K1-F6
Method	BLASTX
NCBI GI	g3789954
BLAST score	461
E value	3.0e-46
Match length	122

% identity	75
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]
Seq. No.	297270
Seq. ID	LIB3137-014-Q1-K1-G12
Method	BLASTX
NCBI GI	g3913182
BLAST score	227
E value	8.0e-19
Match length	67
% identity	67
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi_2239258_emb_CAA74070_ (Y13733) cinnamyl alcohol dehydrogenase [Zea mays]
Seq. No.	297271
Seq. ID	LIB3137-015-Q1-K1-A9
Method	BLASTX
NCBI GI	g82696
BLAST score	244
E value	3.0e-21
Match length	58
% identity	83
NCBI Description	glycine-rich protein - maize >gi_22293_emb_CAA43431_ (X61121) glycine-rich protein [Zea mays]
Seq. No.	297272
Seq. ID	LIB3137-015-Q1-K1-F10
Method	BLASTN
NCBI GI	g296593
BLAST score	60
E value	4.0e-25
Match length	76
% identity	95
NCBI Description	H. vulgare pZE40 gene
Seq. No.	297273
Seq. ID	LIB3137-015-Q1-K1-H12
Method	BLASTX
NCBI GI	g1654140
BLAST score	329
E value	6.0e-31
Match length	82
% identity	74
NCBI Description	(U37840) lipoxygenase [Lycopersicon esculentum]
Seq. No.	297274
Seq. ID	LIB3137-016-Q1-K1-A2
Method	BLASTX
NCBI GI	g2829894
BLAST score	234
E value	9.0e-20
Match length	84
% identity	51
NCBI Description	(AC002311) Unknown protein [Arabidopsis thaliana]

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Seq. No.	297275
Seq. ID	LIB3137-016-Q1-K1-A5
Method	BLASTX
NCBI GI	g283038
BLAST score	467
E value	7.0e-47
Match length	104
% identity	88
NCBI Description	chlorophyll a/b-binding protein (cab-m7) precursor - maize >gi_22230_emb_CAA37474_ (X53398) light harvesting chlorophyll a /b binding protein [Zea mays]
Seq. No.	297276
Seq. ID	LIB3137-016-Q1-K1-B2
Method	BLASTN
NCBI GI	g2921303
BLAST score	105
E value	5.0e-52
Match length	219
% identity	94
NCBI Description	Zea mays herbicide safener binding protein (SBP1) mRNA, complete cds
Seq. No.	297277
Seq. ID	LIB3137-016-Q1-K1-D10
Method	BLASTX
NCBI GI	g4567232
BLAST score	217
E value	1.0e-17
Match length	71
% identity	62
NCBI Description	(AC007119) putative 40S ribosomal protein S25 [Arabidopsis thaliana]
Seq. No.	297278
Seq. ID	LIB3137-016-Q1-K1-E6
Method	BLASTX
NCBI GI	g4539343
BLAST score	208
E value	2.0e-16
Match length	49
% identity	76
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]
Seq. No.	297279
Seq. ID	LIB3137-016-Q1-K1-F2
Method	BLASTX
NCBI GI	g4006893
BLAST score	333
E value	2.0e-33
Match length	97
% identity	75
NCBI Description	(Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
Seq. No.	297280
Seq. ID	LIB3137-016-Q1-K1-H6
Method	BLASTX

NCBI GI g266578
 BLAST score 224
 E value 9.0e-21
 Match length 57
 % identity 89
 NCBI Description METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir_S17560
 metallothionein-like protein - maize >gi_236730_bbs_57629
 (S57628) metallothionein homologue [Zea mays, Peptide, 76
 aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186)
 metallothionein- like protein [Zea mays]
 >gi_228095_prf_1717215A metallothionein-like protein [Zea
 mays]

Seq. No. 297281
 Seq. ID LIB3137-017-Q1-K1-E11
 Method BLASTX
 NCBI GI g2829275
 BLAST score 161
 E value 5.0e-11
 Match length 99
 % identity 44
 NCBI Description (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis
 thaliana] >gi_3513740 (AF080118) contains similarity to
 nucleoside diphosphate kinases (Pfam: NDK.hmm, score:
 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_
 (AL049525) nucleoside diphosphate kinase 3 (ndpk3)
 [Arabidopsis thaliana]

Seq. No. 297282
 Seq. ID LIB3137-017-Q1-K1-G12
 Method BLASTX
 NCBI GI g2464852
 BLAST score 178
 E value 7.0e-13
 Match length 120
 % identity 36
 NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 297283
 Seq. ID LIB3137-017-Q1-K1-G4
 Method BLASTX
 NCBI GI g2984709
 BLAST score 513
 E value 3.0e-52
 Match length 98
 % identity 99
 NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 297284
 Seq. ID LIB3137-018-Q1-K1-A8
 Method BLASTX
 NCBI GI g1418125
 BLAST score 263
 E value 5.0e-23
 Match length 69
 % identity 68
 NCBI Description (D58404) CTP:phosphocholine cytidylyltransferase [Brassica

Q D S E T C I G A D C O C

napus]

Seq. No. 297285
Seq. ID LIB3137-018-Q1-K1-B10
Method BLASTX
NCBI GI g3785973
BLAST score 187
E value 5.0e-14
Match length 62
% identity 65
NCBI Description (AC005560) putative homeobox protein [Arabidopsis thaliana]

Seq. No. 297286
Seq. ID LIB3137-018-Q1-K1-C5
Method BLASTX
NCBI GI g3136311
BLAST score 169
E value 1.0e-16
Match length 71
% identity 56
NCBI Description (AF062734) soluble acid invertase [Saccharum robustum]

Seq. No. 297287
Seq. ID LIB3137-018-Q1-K1-D1
Method BLASTX
NCBI GI g1155261
BLAST score 288
E value 7.0e-26
Match length 64
% identity 88
NCBI Description (U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]

Seq. No. 297288
Seq. ID LIB3137-018-Q1-K1-D3
Method BLASTX
NCBI GI g112994
BLAST score 401
E value 3.0e-39
Match length 89
% identity 92
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
>gi_82685_pir_S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 297289
Seq. ID LIB3137-018-Q1-K1-E6
Method BLASTX
NCBI GI g2792238
BLAST score 155
E value 3.0e-10
Match length 88
% identity 40
NCBI Description (AF032697) NBS-LRR type resistance protein [Oryza sativa]

D E S C R I P T I O N

Seq. No. 297290
Seq. ID LIB3137-018-Q1-K1-G5
Method BLASTX
NCBI GI g4468048
BLAST score 173
E value 2.0e-12
Match length 110
% identity 40
NCBI Description (X78703) catechol O-methyltransferase [Vanilla planifolia]

Seq. No. 297291
Seq. ID LIB3137-018-Q1-K1-G7
Method BLASTX
NCBI GI g2984709
BLAST score 329
E value 1.0e-30
Match length 66
% identity 97
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 297292
Seq. ID LIB3137-019-Q1-K1-A7
Method BLASTX
NCBI GI g4220528
BLAST score 333
E value 4.0e-31
Match length 111
% identity 59
NCBI Description (AL035356) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No. 297293
Seq. ID LIB3137-019-Q1-K1-A8
Method BLASTX
NCBI GI g2984709
BLAST score 532
E value 2.0e-54
Match length 101
% identity 99
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 297294
Seq. ID LIB3137-019-Q1-K1-E7
Method BLASTX
NCBI GI g3861366
BLAST score 237
E value 8.0e-20
Match length 145
% identity 40
NCBI Description (AJ235273) 5-AMINOLEVULINIC ACID SYNTHASE (hemA) [Rickettsia prowazekii]

Seq. No. 297295
Seq. ID LIB3137-019-Q1-K1-G9
Method BLASTX
NCBI GI g4204912

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BLAST score	160
E value	4.0e-11
Match length	53
% identity	58
NCBI Description	(U58918) MEK kinase [Arabidopsis thaliana]
Seq. No.	297296
Seq. ID	LIB3137-019-Q1-K1-H4
Method	BLASTX
NCBI GI	g4584545
BLAST score	492
E value	9.0e-50
Match length	142
% identity	65
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]
Seq. No.	297297
Seq. ID	LIB3137-020-Q1-K1-C1
Method	BLASTN
NCBI GI	g550433
BLAST score	85
E value	3.0e-40
Match length	204
% identity	83
NCBI Description	Z.mays CYP71C1 gene for cytochrome P-450
Seq. No.	297298
Seq. ID	LIB3137-020-Q1-K1-C2
Method	BLASTX
NCBI GI	g3687235
BLAST score	340
E value	7.0e-32
Match length	119
% identity	61
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
Seq. No.	297299
Seq. ID	LIB3137-020-Q1-K1-F1
Method	BLASTX
NCBI GI	g4586103
BLAST score	292
E value	3.0e-26
Match length	73
% identity	71
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]
Seq. No.	297300
Seq. ID	LIB3137-020-Q1-K1-F11
Method	BLASTX
NCBI GI	g118104
BLAST score	662
E value	1.0e-69
Match length	140
% identity	89
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)

D E S C R I P T I O N

>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 297301
Seq. ID LIB3137-020-Q1-K1-F3
Method BLASTX
NCBI GI g2160170
BLAST score 193
E value 1.0e-14
Match length 81
% identity 58
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 297302
Seq. ID LIB3137-020-Q1-K1-F6
Method BLASTX
NCBI GI g2996096
BLAST score 273
E value 5.0e-24
Match length 140
% identity 42
NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No. 297303
Seq. ID LIB3137-020-Q1-K1-H12
Method BLASTX
NCBI GI g4097565
BLAST score 172
E value 6.0e-18
Match length 65
% identity 64
NCBI Description (U64920) ATGP3 [Arabidopsis thaliana]

Seq. No. 297304
Seq. ID LIB3137-021-Q1-K1-B10
Method BLASTX
NCBI GI g1619602
BLAST score 323
E value 5.0e-30
Match length 90
% identity 62
NCBI Description (Y08726) MtN3 [Medicago truncatula]

Seq. No. 297305
Seq. ID LIB3137-021-Q1-K1-D9
Method BLASTX
NCBI GI g4210330
BLAST score 322
E value 8.0e-30
Match length 97
% identity 65
NCBI Description (AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No. 297306

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Seq. ID	LIB3137-021-Q1-K1-F11
Method	BLASTX
NCBI GI	g112994
BLAST score	274
E value	2.0e-24
Match length	82
% identity	71
NCBI Description	GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN >gi_82685_pir_S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564) ABA-inducible gene protein [Zea mays] >gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]
Seq. No.	297307
Seq. ID	LIB3137-021-Q1-K1-F5
Method	BLASTX
NCBI GI	g120670
BLAST score	235
E value	7.0e-20
Match length	81
% identity	59
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_100879_pir_S06879 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C - maize >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]
Seq. No.	297308
Seq. ID	LIB3137-021-Q1-K1-H1
Method	BLASTX
NCBI GI	g2190550
BLAST score	218
E value	1.0e-17
Match length	94
% identity	53
NCBI Description	(AC001229) ESTs gb_T45673,gb_N37512 come from this gene. [Arabidopsis thaliana]
Seq. No.	297309
Seq. ID	LIB3137-021-Q1-K1-H8
Method	BLASTX
NCBI GI	g1346109
BLAST score	302
E value	1.0e-27
Match length	88
% identity	70
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231) RWD [Oryza sativa]
Seq. No.	297310
Seq. ID	LIB3137-022-Q1-K1-B7
Method	BLASTX
NCBI GI	g2984709
BLAST score	522
E value	3.0e-53
Match length	99

% identity 99
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 297311
Seq. ID LIB3137-022-Q1-K1-C3
Method BLASTX
NCBI GI g4512615
BLAST score 208
E value 2.0e-16
Match length 52
% identity 81
NCBI Description (AC004793) Strong similarity to gb_X59970 3-isopropylmalate dehydrogenase (IMDH) from Brassica napus. EST gb_F14478 comes from this gene. [Arabidopsis thaliana]

Seq. No. 297312
Seq. ID LIB3137-022-Q1-K1-C4
Method BLASTX
NCBI GI g3450842
BLAST score 296
E value 8.0e-27
Match length 91
% identity 57
NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No. 297313
Seq. ID LIB3137-022-Q1-K1-C6
Method BLASTN
NCBI GI g18963
BLAST score 146
E value 2.0e-76
Match length 222
% identity 91
NCBI Description Z.mays mRNA fordehydin (dhn3)

Seq. No. 297314
Seq. ID LIB3137-022-Q1-K1-D12
Method BLASTX
NCBI GI g2500959
BLAST score 449
E value 1.0e-44
Match length 111
% identity 76
NCBI Description ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS) >gi_1653611_dbj_BAA18523_ (D90915) alanyl-tRNA synthetase [Synechocystis sp.]

Seq. No. 297315
Seq. ID LIB3137-022-Q1-K1-H9
Method BLASTX
NCBI GI g1373209
BLAST score 174
E value 2.0e-12
Match length 94
% identity 49
NCBI Description (U53855) prostacyclin synthase [Rattus norvegicus]

Seq. No. 297316
Seq. ID LIB3137-023-Q1-K1-A12
Method BLASTX
NCBI GI g4337174
BLAST score 271
E value 4.0e-24
Match length 104
% identity 52
NCBI Description (AC006416) Similar to gi_1573829 HI0816 aminopeptidase P homolog (pepP) from Haemophilus influenzae genome gb_U32764. [Arabidopsis thaliana]

Seq. No. 297317
Seq. ID LIB3137-023-Q1-K1-C2
Method BLASTX
NCBI GI g3334756
BLAST score 292
E value 2.0e-26
Match length 117
% identity 53
NCBI Description (Y16672) putative arginine-serine-rich splicing factor [Medicago sativa].

Seq. No. 297318
Seq. ID LIB3137-023-Q1-K1-C5
Method BLASTX
NCBI GI g400578
BLAST score 214
E value 4.0e-17
Match length 86
% identity 47
NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR (COMPLEX I-18 KD) (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ) >gi_346531_pir_S28240 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-18(IP) - bovine >gi_226_emb_CAA44900_(X63215) NADH dehydrogenase [Bos taurus]

Seq. No. 297319
Seq. ID LIB3137-023-Q1-K1-C8
Method BLASTN
NCBI GI g342631
BLAST score 46
E value 4.0e-17
Match length 110
% identity 85
NCBI Description Maize mitochondrial F-1-ATPase subunit-2 mRNA, complete cds

Seq. No. 297320
Seq. ID LIB3137-023-Q1-K1-D3
Method BLASTX
NCBI GI g2425066
BLAST score 237
E value 7.0e-20
Match length 126
% identity 51
NCBI Description (AF019147) cysteine proteinase Mir3 [Zea mays]

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Seq. No. 297321
Seq. ID LIB3137-023-Q1-K1-D5
Method BLASTX
NCBI GI g633110
BLAST score 256
E value 5.0e-31
Match length 126
% identity 63
NCBI Description (D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No. 297322
Seq. ID LIB3137-023-Q1-K1-E1
Method BLASTX
NCBI GI g4115379
BLAST score 158
E value 3.0e-11
Match length 62
% identity 53
NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No. 297323
Seq. ID LIB3137-023-Q1-K1-E9
Method BLASTX
NCBI GI g131772
BLAST score 197
E value 9.0e-20
Match length 90
% identity 68
NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
>gi_82723_pir_A30097 ribosomal protein S14 (clone MCH1) - maize

Seq. No. 297324
Seq. ID LIB3137-023-Q1-K1-F12
Method BLASTX
NCBI GI g3688398
BLAST score 310
E value 2.0e-28
Match length 118
% identity 58
NCBI Description (AJ006358) ascorbate peroxidase [Hordeum vulgare]

Seq. No. 297325
Seq. ID LIB3137-023-Q1-K1-G3
Method BLASTX
NCBI GI g4580461
BLAST score 310
E value 5.0e-29
Match length 73
% identity 79
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 297326
Seq. ID LIB3137-023-Q1-K1-H2
Method BLASTX

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NCBI GI	g1174391
BLAST score	257
E value	3.0e-22
Match length	119
% identity	39
NCBI Description	SUPEROXIDE DISMUTASE 3.4 PRECURSOR (MN) >gi_539066_pir_B48684 superoxide dismutase (EC 1.15.1.1) (Mn) 3.2 precursor - maize
Seq. No.	297327
Seq. ID	LIB3137-023-Q1-K1-H3
Method	BLASTX
NCBI GI	g4186184
BLAST score	148
E value	2.0e-09
Match length	34
% identity	74
NCBI Description	(AF111168) unknown [Homo sapiens]
Seq. No.	297328
Seq. ID	LIB3137-024-Q1-K1-A12
Method	BLASTX
NCBI GI	g3264596
BLAST score	209
E value	6.0e-17
Match length	62
% identity	74
NCBI Description	(AF057183) putative tonoplast aquaporin [Zea mays]
Seq. No.	297329
Seq. ID	LIB3137-024-Q1-K1-A7
Method	BLASTX
NCBI GI	g3885882
BLAST score	191
E value	1.0e-14
Match length	81
% identity	53
NCBI Description	(AF093629) inorganic pyrophosphatase [Oryza sativa]
Seq. No.	297330
Seq. ID	LIB3137-024-Q1-K1-C12
Method	BLASTX
NCBI GI	g3163946
BLAST score	525
E value	1.0e-53
Match length	109
% identity	90
NCBI Description	(AJ005599) alpha-tubulin 1 [Eleusine indica]
Seq. No.	297331
Seq. ID	LIB3137-024-Q1-K1-C7
Method	BLASTN
NCBI GI	g2921303
BLAST score	166
E value	2.0e-88
Match length	286
% identity	90

NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA,
incomplete cds

Seq. No. 297332
Seq. ID LIB3137-024-Q1-K1-D9
Method BLASTN
NCBI GI g397395
BLAST score 76
E value 8.0e-35
Match length 132
% identity 89
NCBI Description Z.mays MNB1b mRNA for DNA-binding protein

Seq. No. 297333
Seq. ID LIB3137-024-Q1-K1-F1
Method BLASTX
NCBI GI g2832696
BLAST score 155
E value 2.0e-10
Match length 113
% identity 29
NCBI Description (AL021713) putative protein [Arabidopsis thaliana]

Seq. No. 297334
Seq. ID LIB3137-024-Q1-K1-F4
Method BLASTX
NCBI GI g729773
BLAST score 218
E value 1.0e-17
Match length 66
% identity 64
NCBI Description HEAT SHOCK FACTOR PROTEIN 1 (HSF 1) (HEAT SHOCK
TRANSCRIPTION FACTOR 1) (HSTF 1) >gi_429155_emb_CAA53761_
(X76167) heat shock factor [Arabidopsis thaliana]

Seq. No. 297335
Seq. ID LIB3137-024-Q1-K1-F6
Method BLASTX
NCBI GI g2911073
BLAST score 454
E value 3.0e-45
Match length 141
% identity 68
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 297336
Seq. ID LIB3137-024-Q1-K1-F8
Method BLASTX
NCBI GI g3355780
BLAST score 220
E value 6.0e-18
Match length 83
% identity 57
NCBI Description (AJ004997) expansin18 [Lycopersicon esculentum]

Seq. No. 297337
Seq. ID LIB3137-024-Q1-K1-G9

Method BLASTX
NCBI GI g1706260
BLAST score 317
E value 2.0e-29
Match length 60
% identity 97
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir_S59597
cysteine proteinase 1 precursor - maize
>gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays]

Seq. No. 297338
Seq. ID LIB3137-024-Q1-K1-H1
Method BLASTX
NCBI GI g2244915
BLAST score 213
E value 5.0e-17
Match length 122
% identity 35
NCBI Description (Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]

Seq. No. 297339
Seq. ID LIB3137-024-Q1-K1-H3
Method BLASTX
NCBI GI g132724
BLAST score 198
E value 2.0e-15
Match length 50
% identity 74
NCBI Description 50S RIBOSOMAL PROTEIN L18 >gi_71259_pir_R5BS8F ribosomal protein L18 - Bacillus stearothermophilus

Seq. No. 297340
Seq. ID LIB3137-027-Q1-K1-B11
Method BLASTN
NCBI GI g3004949
BLAST score 58
E value 5.0e-24
Match length 94
% identity 90
NCBI Description Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA, complete cds

Seq. No. 297341
Seq. ID LIB3137-027-Q1-K1-C10
Method BLASTX
NCBI GI g1665867
BLAST score 178
E value 1.0e-22
Match length 105
% identity 53
NCBI Description (Y09123) aspartic proteinase [Centaurea calcitrapa]

Seq. No. 297342
Seq. ID LIB3137-027-Q1-K1-D3
Method BLASTX

NCBI GI g4432856
BLAST score 183
E value 1.0e-13
Match length 95
% identity 46
NCBI Description (AC006300) putative 2A6 protein [Arabidopsis thaliana]

Seq. No. 297343
Seq. ID LIB3137-027-Q1-K1-E10
Method BLASTX
NCBI GI g113621
BLAST score 250
E value 4.0e-35
Match length 100
% identity 82
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
>gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A
cytoplasmic aldolase [Zea mays]

Seq. No. 297344
Seq. ID LIB3137-027-Q1-K1-E3
Method BLASTX
NCBI GI g4587577
BLAST score 142
E value 9.0e-09
Match length 54
% identity 46
NCBI Description (AC006550) F1003.17 [Arabidopsis thaliana]

Seq. No. 297345
Seq. ID LIB3137-027-Q1-K1-E4
Method BLASTX
NCBI GI g2598575
BLAST score 181
E value 2.0e-13
Match length 110
% identity 37
NCBI Description (Y15293) MtN21 [Medicago truncatula]

Seq. No. 297346
Seq. ID LIB3137-027-Q1-K1-G6
Method BLASTX
NCBI GI g710626
BLAST score 154
E value 2.0e-10
Match length 41
% identity 59
NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
(AC004625) dehydration-induced protein ERD15 [Arabidopsis
thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis
thaliana]

Seq. No. 297347
Seq. ID LIB3137-027-Q1-K1-H2

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Method	BLASTX
NCBI GI	g2182267
BLAST score	407
E value	6.0e-40
Match length	115
% identity	71
NCBI Description	(L37359) lipoxygenase [Hordeum vulgare]
Seq. No.	297348
Seq. ID	LIB3137-027-Q1-K1-H7
Method	BLASTN
NCBI GI	g22312
BLAST score	37
E value	2.0e-11
Match length	49
% identity	94
NCBI Description	Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)
Seq. No.	297349
Seq. ID	LIB3137-028-Q1-K1-A5
Method	BLASTX
NCBI GI	g4056432
BLAST score	553
E value	6.0e-57
Match length	142
% identity	70
NCBI Description	(AC005990) Similar to gi_2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this gene. [Arabidopsis thaliana]
Seq. No.	297350
Seq. ID	LIB3137-028-Q1-K1-A7
Method	BLASTN
NCBI GI	g11957
BLAST score	221
E value	1.0e-121
Match length	261
% identity	48
NCBI Description	Rice complete chloroplast genome
Seq. No.	297351
Seq. ID	LIB3137-028-Q1-K1-C10
Method	BLASTX
NCBI GI	g2702281
BLAST score	227
E value	6.0e-19
Match length	72
% identity	60
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]
Seq. No.	297352
Seq. ID	LIB3137-028-Q1-K1-E8
Method	BLASTX
NCBI GI	g2160690

BLAST score 251
E value 1.0e-21
Match length 71
% identity 59
NCBI Description (U73526) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No. 297353
Seq. ID LIB3137-028-Q1-K1-G7
Method BLASTX
NCBI GI g2952328
BLAST score 305
E value 7.0e-28
Match length 83
% identity 72
NCBI Description (AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza sativa]

Seq. No. 297354
Seq. ID LIB3137-029-Q1-K1-A7
Method BLASTX
NCBI GI g2462832
BLAST score 290
E value 4.0e-26
Match length 113
% identity 53
NCBI Description (AF000657) similar to Bacillus CotA [Arabidopsis thaliana]

Seq. No. 297355
Seq. ID LIB3137-029-Q1-K1-B4
Method BLASTX
NCBI GI g3236253
BLAST score 387
E value 2.0e-37
Match length 134
% identity 54
NCBI Description (AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 297356
Seq. ID LIB3137-029-Q1-K1-B8
Method BLASTX
NCBI GI g3337367
BLAST score 204
E value 3.0e-16
Match length 87
% identity 54
NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297357
Seq. ID LIB3137-029-Q1-K1-C10
Method BLASTX
NCBI GI g136640
BLAST score 195
E value 6.0e-15
Match length 86
% identity 55

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NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN-CARRIER PROTEIN) >gi_170785 (M62720)
ubiquitin carrier protein [Triticum aestivum]

Seq. No. 297358
Seq. ID LIB3137-029-Q1-K1-F11
Method BLASTN
NCBI GI g1504051
BLAST score 51
E value 8.0e-20
Match length 249
% identity 81
NCBI Description Zea mays mRNA for Calcium-dependent protein kinase,
complete cds

Seq. No. 297359
Seq. ID LIB3137-029-Q1-K1-F4
Method BLASTX
NCBI GI g2804280
BLAST score 242
E value 2.0e-20
Match length 122
% identity 43
NCBI Description (AB003687) 6-4 photolyase [Arabidopsis thaliana]
>gi_3929918_dbj_BAA34711_ (AB017331) 6-4 photolyase
[Arabidopsis thaliana]

Seq. No. 297360
Seq. ID LIB3137-029-Q1-K1-F6
Method BLASTX
NCBI GI g1504052
BLAST score 278
E value 1.0e-24
Match length 113
% identity 57
NCBI Description (D87042) Calcium-dependent protein kinase [Zea mays]

Seq. No. 297361
Seq. ID LIB3137-029-Q1-K1-G7
Method BLASTX
NCBI GI g2827619
BLAST score 257
E value 2.0e-22
Match length 87
% identity 62
NCBI Description (AL021636) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297362
Seq. ID LIB3137-030-Q1-K1-E6
Method BLASTX
NCBI GI g4126809
BLAST score 394
E value 3.0e-38
Match length 89
% identity 46
NCBI Description (AB017042) glyoxalase I [Oryza sativa]

Q1-K1-A9

Seq. No.	297363
Seq. ID	LIB3137-030-Q1-K1-F7
Method	BLASTX
NCBI GI	g1706965
BLAST score	145
E value	1.0e-09
Match length	61
% identity	49
NCBI Description	(U60754) delta-24-sterol methyltransferase [Triticum aestivum]
Seq. No.	297364
Seq. ID	LIB3137-030-Q1-K1-H6
Method	BLASTX
NCBI GI	g115815
BLAST score	468
E value	4.0e-47
Match length	112
% identity	79
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-M9) -(LHCP) >gi_100866_pir_S13098 chlorophyll a/b-binding protein precursor - maize >gi_22355_emb_CAA39376_ (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays]
Seq. No.	297365
Seq. ID	LIB3137-032-Q1-K1-A9
Method	BLASTX
NCBI GI	g2673947
BLAST score	259
E value	2.0e-22
Match length	119
% identity	27
NCBI Description	(U62931) multidrug resistance protein 1 [Aspergillus flavus] >gi_2673949 (U62932) multidrug resistance protein 1 [Aspergillus flavus]
Seq. No.	297366
Seq. ID	LIB3137-032-Q1-K1-C9
Method	BLASTX
NCBI GI	g3522937
BLAST score	354
E value	1.0e-33
Match length	116
% identity	54
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]
Seq. No.	297367
Seq. ID	LIB3137-033-Q1-K1-A10
Method	BLASTX
NCBI GI	g1574938
BLAST score	209
E value	6.0e-17
Match length	68
% identity	63
NCBI Description	(U34726) superoxide dismutase 4 [Zea mays]

Seq. No. 297368
Seq. ID LIB3137-033-Q1-K1-A7
Method BLASTX
NCBI GI g115786
BLAST score 390
E value 6.0e-38
Match length 92
% identity 83
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII-TYPE I PRECURSOR (CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays]

Seq. No. 297369
Seq. ID LIB3137-033-Q1-K1-B2
Method BLASTN
NCBI GI g3955072
BLAST score 105
E value 5.0e-52
Match length 235
% identity 85
NCBI Description Zea mays PHYT II gene for acidic phytase

Seq. No. 297370
Seq. ID LIB3137-033-Q1-K1-C1
Method BLASTX
NCBI GI g542157
BLAST score 141
E value 9.0e-09
Match length 31
% identity 84
NCBI Description ribosomal 5S RNA-binding protein - Rice

Seq. No. 297371
Seq. ID LIB3137-033-Q1-K1-C6
Method BLASTX
NCBI GI g1519249
BLAST score 157
E value 4.0e-11
Match length 58
% identity 62
NCBI Description (U65956) GF14-b protein [Oryza sativa]

Seq. No. 297372
Seq. ID LIB3137-033-Q1-K1-E4
Method BLASTX
NCBI GI g1346735
BLAST score 169
E value 5.0e-12
Match length 73
% identity 48
NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_1076562_pir_S49647 phosphoglycerate mutase (EC 5.4.2.1) - castor bean >gi_474170_emb_CAA49995_ (X70652) phosphoglycerate mutase [Ricinus communis]

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Seq. No.	297373
Seq. ID	LIB3137-033-Q1-K1-F11
Method	BLASTX
NCBI GI	g2668742
BLAST score	378
E value	2.0e-36
Match length	85
% identity	88
NCBI Description	(AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.	297374
Seq. ID	LIB3137-033-Q1-K1-G10
Method	BLASTX
NCBI GI	g66009
BLAST score	235
E value	8.0e-22
Match length	68
% identity	82
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C, cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH (AA 1-337) [Zea mays]
Seq. No.	297375
Seq. ID	LIB3137-033-Q1-K1-G9
Method	BLASTX
NCBI GI	g170033
BLAST score	383
E value	5.0e-37
Match length	108
% identity	64
NCBI Description	(L00353) uricase II subunit [Glycine max]
Seq. No.	297376
Seq. ID	LIB3137-035-Q1-K1-A12
Method	BLASTN
NCBI GI	g22354
BLAST score	42
E value	1.0e-14
Match length	70
% identity	91
NCBI Description	Zea mays L. mRNA for light-harvesting chlorophyll a/b binding protein
Seq. No.	297377
Seq. ID	LIB3137-035-Q1-K1-B9
Method	BLASTN
NCBI GI	g3135542
BLAST score	71
E value	1.0e-31
Match length	87
% identity	95
NCBI Description	Oryza sativa aquaporin (PIP2a) mRNA, complete cds
Seq. No.	297378
Seq. ID	LIB3137-035-Q1-K1-C1
Method	BLASTX
NCBI GI	g4539422

BLAST score	141
E value	7.0e-09
Match length	67
% identity	46
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]
Seq. No.	297379
Seq. ID	LIB3137-035-Q1-K1-C7
Method	BLASTX
NCBI GI	g121631
BLAST score	225
E value	1.0e-18
Match length	69
% identity	61
NCBI Description	GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR >gi_72323_pir_KNNT2S glycine-rich protein 2 - wood tobacco >gi_19743_emb_CAA42622_ (X60007) nsGRP-2 [Nicotiana sylvestris]
Seq. No.	297380
Seq. ID	LIB3137-035-Q1-K1-D11
Method	BLASTX
NCBI GI	g2921304
BLAST score	328
E value	8.0e-31
Match length	91
% identity	77
NCBI Description	(AF033496) herbicide safener binding protein [Zea mays]
Seq. No.	297381
Seq. ID	LIB3137-035-Q1-K1-D8
Method	BLASTX
NCBI GI	g3080439
BLAST score	161
E value	5.0e-11
Match length	54
% identity	57
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]
Seq. No.	297382
Seq. ID	LIB3137-035-Q1-K1-E4
Method	BLASTN
NCBI GI	g2655030
BLAST score	241
E value	1.0e-133
Match length	269
% identity	97
NCBI Description	Zea mays starch synthase isoform zSTSII-2 (zSSIIb) mRNA, complete cds
Seq. No.	297383
Seq. ID	LIB3137-035-Q1-K1-F6
Method	BLASTX
NCBI GI	g134598
BLAST score	446
E value	2.0e-44
Match length	84

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% identity 98
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)

Seq. No. 297384
Seq. ID LIB3137-035-Q1-K1-H2
Method BLASTX
NCBI GI g3128206
BLAST score 423
E value 8.0e-42
Match length 108
% identity 70
NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]

Seq. No. 297385
Seq. ID LIB3137-035-Q1-K1-H3
Method BLASTX
NCBI GI g2431769
BLAST score 178
E value 3.0e-13
Match length 68
% identity 59
NCBI Description (U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No. 297386
Seq. ID LIB3137-035-Q1-K1-H5
Method BLASTX
NCBI GI g2425066
BLAST score 155
E value 4.0e-15
Match length 73
% identity 66
NCBI Description (AF019147) cysteine proteinase Mir3 [Zea mays]

Seq. No. 297387
Seq. ID LIB3137-035-Q1-K1-H8
Method BLASTX
NCBI GI g1498597
BLAST score 228
E value 4.0e-19
Match length 75
% identity 64
NCBI Description (U66105) phospholipid transfer protein [Zea mays]

Seq. No. 297388
Seq. ID LIB3137-036-Q1-K1-A11
Method BLASTX
NCBI GI g2244749
BLAST score 395
E value 2.0e-38
Match length 107
% identity 70
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 297389
Seq. ID LIB3137-036-Q1-K1-B11
Method BLASTN
NCBI GI g3452297

BLAST score 57
E value 3.0e-23
Match length 138
% identity 88
NCBI Description Zea mays retrotransposon Ji-4 5' LTR, partial sequence

Seq. No. 297390
Seq. ID LIB3137-036-Q1-K1-D12
Method BLASTX
NCBI GI g1653626
BLAST score 153
E value 4.0e-10
Match length 90
% identity 36
NCBI Description (D90915) hypothetical protein [Synechocystis sp.]

Seq. No. 297391
Seq. ID LIB3137-036-Q1-K1-G10
Method BLASTX
NCBI GI g134598
BLAST score 207
E value 1.0e-16
Match length 64
% identity 70
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)

Seq. No. 297392
Seq. ID LIB3137-038-Q1-K1-B11
Method BLASTX
NCBI GI g4335745
BLAST score 214
E value 3.0e-17
Match length 115
% identity 42
NCBI Description (AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 297393
Seq. ID LIB3137-038-Q1-K1-B2
Method BLASTX
NCBI GI g479386
BLAST score 150
E value 3.0e-12
Match length 65
% identity 63
NCBI Description isocitrate dehydrogenase - soybean

Seq. No. 297394
Seq. ID LIB3137-038-Q1-K1-C1
Method BLASTX
NCBI GI g2499608
BLAST score 260
E value 2.0e-27
Match length 105
% identity 64
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4)

(ATMPK4) >gi_2129645_pir_S40470 mitogen-activated protein kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana
>gi_457400_dbj_BAA04867_ (D21840) MAP kinase [Arabidopsis thaliana]

Seq. No. 297395
Seq. ID LIB3137-038-Q1-K1-D3
Method BLASTX
NCBI GI g1655637
BLAST score 166
E value 1.0e-11
Match length 82
% identity 48
NCBI Description (Z54179) orf [Mus musculus]

Seq. No. 297396
Seq. ID LIB3137-038-Q1-K1-E1
Method BLASTN
NCBI GI g2668739
BLAST score 96
E value 2.0e-46
Match length 180
% identity 88
NCBI Description Zea mays translation initiation factor GOS2 (TIF) mRNA, complete cds

Seq. No. 297397
Seq. ID LIB3137-038-Q1-K1-E2
Method BLASTX
NCBI GI g1086833
BLAST score 144
E value 5.0e-09
Match length 96
% identity 31
NCBI Description (U41264) coded for by C. elegans cDNA CEESN26F; coded for by C. elegans cDNA CEESI89F; similar to 60S acidic ribosomal protein Po (L10) [Caenorhabditis elegans]

Seq. No. 297398
Seq. ID LIB3137-038-Q1-K1-G10
Method BLASTX
NCBI GI g1203832
BLAST score 176
E value 6.0e-13
Match length 98
% identity 41
NCBI Description (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf_2208395A beta-D-glucan exohydrolase [Hordeum vulgare]

Seq. No. 297399
Seq. ID LIB3137-038-Q1-K1-G6
Method BLASTN
NCBI GI g18963
BLAST score 219
E value 1.0e-120
Match length 246

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% identity	98
NCBI Description	Z.mays mRNA for dehydrin (dhn3)
Seq. No.	297400
Seq. ID	LIB3137-038-Q1-K1-H11
Method	BLASTX
NCBI GI	g2293566
BLAST score	386
E value	2.0e-37
Match length	109
% identity	72
NCBI Description	(AF012896) ADP-ribosylation factor 1 [Oryza sativa]
Seq. No.	297401
Seq. ID	LIB3137-039-Q1-K1-C8
Method	BLASTX
NCBI GI	g2984709
BLAST score	278
E value	9.0e-25
Match length	78
% identity	74
NCBI Description	(AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.	297402
Seq. ID	LIB3137-039-Q1-K1-D4
Method	BLASTX
NCBI GI	g4337179
BLAST score	188
E value	3.0e-14
Match length	54
% identity	63
NCBI Description	(AC006416) This gene is continued on the 5' end of BAC T12M14. [Arabidopsis thaliana]
Seq. No.	297403
Seq. ID	LIB3137-040-Q1-K1-A11
Method	BLASTN
NCBI GI	g2921303
BLAST score	207
E value	1.0e-113
Match length	309
% identity	100
NCBI Description	Zea mays herbicide safener binding protein (SBP1) mRNA, complete cds
Seq. No.	297404
Seq. ID	LIB3137-040-Q1-K1-A8
Method	BLASTX
NCBI GI	g2623307
BLAST score	403
E value	3.0e-39
Match length	97
% identity	73
NCBI Description	(AC002409) putative ubiquitin protease [Arabidopsis thaliana]
Seq. No.	297405

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Seq. ID LIB3137-040-Q1-K1-B10
Method BLASTX
NCBI GI g1403675
BLAST score 493
E value 7.0e-50
Match length 136
% identity 74
NCBI Description (U41323) beta-1,3-glucanase [Glycine max]

Seq. No. 297406
Seq. ID LIB3137-040-Q1-K1-B12
Method BLASTX
NCBI GI g585963
BLAST score 260
E value 1.0e-22
Match length 69
% identity 77
NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No. 297407
Seq. ID LIB3137-040-Q1-K1-B8
Method BLASTX
NCBI GI g3337356
BLAST score 206
E value 2.0e-16
Match length 71
% identity 56
NCBI Description (AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No. 297408
Seq. ID LIB3137-040-Q1-K1-B9
Method BLASTX
NCBI GI g4097880
BLAST score 154
E value 4.0e-21
Match length 115
% identity 57
NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 297409
Seq. ID LIB3137-040-Q1-K1-C11
Method BLASTX
NCBI GI g4097880
BLAST score 265
E value 2.0e-23
Match length 92
% identity 61
NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 297410
Seq. ID LIB3137-040-Q1-K1-C8
Method BLASTN
NCBI GI g2773153
BLAST score 99
E value 3.0e-48
Match length 219

COMPARISON

% identity 86
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asrl) mRNA, complete cds

Seq. No. 297411
Seq. ID LIB3137-040-Q1-K1-F11
Method BLASTX
NCBI GI g2239083
BLAST score 166
E value 2.0e-11
Match length 108
% identity 40
NCBI Description (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_2239087_emb CAB06429_ (Z84385) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No. 297412
Seq. ID LIB3137-040-Q1-K1-G12
Method BLASTX
NCBI GI g541943
BLAST score 202
E value 9.0e-16
Match length 39
% identity 90
NCBI Description metallothionein - soybean >gi_228682_prf_ 1808316A metallothionein-like protein [Glycine max]

Seq. No. 297413
Seq. ID LIB3137-040-Q1-K1-H10
Method BLASTX
NCBI GI g4262183
BLAST score 158
E value 9.0e-11
Match length 61
% identity 51
NCBI Description (AC005508) 51434 [Arabidopsis thaliana]

Seq. No. 297414
Seq. ID LIB3137-041-Q1-K1-C2
Method BLASTX
NCBI GI g2829912
BLAST score 222
E value 3.0e-18
Match length 57
% identity 74
NCBI Description (AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]

Seq. No. 297415
Seq. ID LIB3137-041-Q1-K1-C5
Method BLASTX
NCBI GI g4008159
BLAST score 274
E value 3.0e-24
Match length 70
% identity 76

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NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
Seq. No. 297416
Seq. ID LIB3137-041-Q1-K1-C9
Method BLASTX
NCBI GI g4325282
BLAST score 186
E value 3.0e-14
Match length 69
% identity 52
NCBI Description (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
>gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
[Arabidopsis thaliana]

Seq. No. 297417
Seq. ID LIB3137-041-Q1-K1-D12
Method BLASTX
NCBI GI g1524115
BLAST score 285
E value 1.0e-25
Match length 111
% identity 49
NCBI Description (X95270) subtilisin-like endoprotease [Lycopersicon
esculentum] >gi_4200334_emb_CAA76724_ (Y17275) P69A protein
[Lycopersicon esculentum]

Seq. No. 297418
Seq. ID LIB3137-041-Q1-K1-E7
Method BLASTX
NCBI GI g2655888
BLAST score 268
E value 9.0e-24
Match length 94
% identity 50
NCBI Description (AL009171) 62D9.a [Drosophila melanogaster]

Seq. No. 297419
Seq. ID LIB3137-041-Q1-K1-H9
Method BLASTX
NCBI GI g1708236
BLAST score 259
E value 1.0e-22
Match length 65
% identity 75
NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
(3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
>gi_2129617_pir_JC4567 hydroxymethylglutaryl-CoA synthase
(EC 4.1.3.5) - Arabidopsis thaliana
>gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
>gi_1586548_prf_2204245A hydroxy methylglutaryl CoA
synthase [Arabidopsis thaliana]

Seq. No. 297420
Seq. ID LIB3137-042-Q1-K1-H10
Method BLASTX
NCBI GI g626042

DRAFT

BLAST score 394
E value 2.0e-38
Match length 97
% identity 80
NCBI Description beta-glucosidase, root meristem (EC 3.2.1.-) precursor - maize >gi_435313_emb_CAA52293_ (X74217) beta-glucosidase [Zea mays]

Seq. No. 297421
Seq. ID LIB3137-043-Q1-K1-C10
Method BLASTX
NCBI GI g115771
BLAST score 530
E value 3.0e-54
Match length 117
% identity 86
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll a/b-binding protein precursor - maize >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

Seq. No. 297422
Seq. ID LIB3137-043-Q1-K1-D8
Method BLASTX
NCBI GI g517500
BLAST score 144
E value 1.0e-10
Match length 69
% identity 71
NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf_1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No. 297423
Seq. ID LIB3137-043-Q1-K1-E11
Method BLASTX
NCBI GI g1619300
BLAST score 170
E value 3.0e-12
Match length 74
% identity 51
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

Seq. No. 297424
Seq. ID LIB3137-043-Q1-K1-E2
Method BLASTX
NCBI GI g3403236
BLAST score 382
E value 6.0e-37
Match length 128
% identity 58
NCBI Description (AF071544) ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I [Spinacia oleracea]

Seq. No. 297425
Seq. ID LIB3137-043-Q1-K1-F4

SEQUENCE DATA

Method BLASTX
NCBI GI g4336747
BLAST score 322
E value 8.0e-30
Match length 130
% identity 55
NCBI Description (AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No. 297426
Seq. ID LIB3137-043-Q1-K1-F5
Method BLASTX
NCBI GI g4584548
BLAST score 430
E value 4.0e-43
Match length 104
% identity 83
NCBI Description (AL049608) putative protein [Arabidopsis thaliana]

Seq. No. 297427
Seq. ID LIB3137-044-Q1-K1-B7
Method BLASTN
NCBI GI g1518674
BLAST score 193
E value 1.0e-104
Match length 264
% identity 93
NCBI Description Zea mays beta-D-glucosidase (glu1) gene, intron 10 transposon 2, complete sequence

Seq. No. 297428
Seq. ID LIB3137-044-Q1-K1-B9
Method BLASTX
NCBI GI g2668742
BLAST score 349
E value 3.0e-33
Match length 81
% identity 85
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 297429
Seq. ID LIB3137-044-Q1-K1-C3
Method BLASTX
NCBI GI g100918
BLAST score 219
E value 6.0e-18
Match length 80
% identity 57
NCBI Description RAB-17 protein - maize >gi_239236_bbs_66621 RAB-17 protein=substrate for casein kinase 2 [Zea mays L.=maize, line W64 A, Peptide, 168 aa]

Seq. No. 297430
Seq. ID LIB3137-044-Q1-K1-D7
Method BLASTX
NCBI GI g2109457
BLAST score 152
E value 4.0e-10

SEARCHED

Match length	94
% identity	47
NCBI Description	(AF001501) chitinase [Oryza sativa]
Seq. No.	297431
Seq. ID	LIB3137-044-Q1-K1-D9
Method	BLASTX
NCBI GI	g481031
BLAST score	148
E value	7.0e-10
Match length	45
% identity	60
NCBI Description	transcription factor SF3 - common sunflower
Seq. No.	297432
Seq. ID	LIB3137-044-Q1-K1-E9
Method	BLASTX
NCBI GI	g464707
BLAST score	186
E value	4.0e-14
Match length	76
% identity	51
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir_S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]
Seq. No.	297433
Seq. ID	LIB3137-044-Q1-K1-F1
Method	BLASTX
NCBI GI	g3647355
BLAST score	314
E value	6.0e-29
Match length	115
% identity	54
NCBI Description	(Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w), Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249_HUMA
Seq. No.	297434
Seq. ID	LIB3137-044-Q1-K1-H5
Method	BLASTX
NCBI GI	g2827709
BLAST score	235
E value	5.0e-20

SEARCHED

Match length 85
% identity 58
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 297435
Seq. ID LIB3137-045-Q1-K1-C1
Method BLASTX
NCBI GI g3549681
BLAST score 334
E value 3.0e-31
Match length 140
% identity 46
NCBI Description (AL031394) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No. 297436
Seq. ID LIB3137-045-Q1-K1-E11
Method BLASTX
NCBI GI g3080427
BLAST score 206
E value 3.0e-16
Match length 102
% identity 45
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 297437
Seq. ID LIB3137-045-Q1-K1-F10
Method BLASTX
NCBI GI g2109457
BLAST score 385
E value 4.0e-37
Match length 115
% identity 66
NCBI Description (AF001501) chitinase [Oryza sativa]

Seq. No. 297438
Seq. ID LIB3137-045-Q1-K1-H9
Method BLASTX
NCBI GI g464987
BLAST score 204
E value 3.0e-16
Match length 57
% identity 70
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
>gi_421858_pir_S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana
>gi_297878_emb_CAA78715 (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No. 297439
Seq. ID LIB3137-047-Q1-K1-C7
Method BLASTX
NCBI GI g2668742
BLAST score 431
E value 1.0e-42

bio

Match length	86
% identity	99
NCBI Description	(AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.	297440
Seq. ID	LIB3137-047-Q1-K1-F4
Method	BLASTX
NCBI GI	g477226
BLAST score	448
E value	6.0e-45
Match length	87
% identity	97
NCBI Description	heat shock protein HSP82 - maize >gi_300083_bbs_130886 (S59780) HSP82=82 kda heat shock protein [Zea mays, seedling, leaves, Peptide, 715 aa] [Zea mays]
Seq. No.	297441
Seq. ID	LIB3137-047-Q1-K1-H3
Method	BLASTX
NCBI GI	g4539423
BLAST score	432
E value	7.0e-43
Match length	112
% identity	73
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]
Seq. No.	297442
Seq. ID	LIB3137-047-Q1-K1-H6
Method	BLASTN
NCBI GI	g2921303
BLAST score	195
E value	1.0e-106
Match length	283
% identity	93
NCBI Description	Zea mays herbicide safener binding protein (SBP1) mRNA, complete cds
Seq. No.	297443
Seq. ID	LIB3137-049-Q1-K1-A11
Method	BLASTX
NCBI GI	g3551954
BLAST score	172
E value	2.0e-12
Match length	93
% identity	40
NCBI Description	(AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]
Seq. No.	297444
Seq. ID	LIB3137-049-Q1-K1-D2
Method	BLASTX
NCBI GI	g3024122
BLAST score	487
E value	3.0e-49
Match length	121
% identity	79

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821
(U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No. 297445
Seq. ID LIB3137-049-Q1-K1-G1
Method BLASTX
NCBI GI g3258635
BLAST score 158
E value 1.0e-10
Match length 112
% identity 30
NCBI Description (AF041049) 4-coumarate:CoA ligase [Populus tremuloides]

Seq. No. 297446
Seq. ID LIB3137-049-Q1-K1-G3
Method BLASTX
NCBI GI g67529
BLAST score 164
E value 2.0e-11
Match length 95
% identity 41
NCBI Description membrane alanyl aminopeptidase (EC 3.4.11.2) - Escherichia coli

Seq. No. 297447
Seq. ID LIB3137-050-Q1-K1-B10
Method BLASTX
NCBI GI g729671
BLAST score 221
E value 3.0e-25
Match length 78
% identity 83
NCBI Description HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]

Seq. No. 297448
Seq. ID LIB3137-050-Q1-K1-C2
Method BLASTN
NCBI GI g1177368
BLAST score 55
E value 2.0e-22
Match length 95
% identity 89
NCBI Description Z.mays mRNA for ribosomal protein L39

Seq. No. 297449
Seq. ID LIB3137-050-Q1-K1-F9
Method BLASTX
NCBI GI g2673918
BLAST score 198
E value 1.0e-15
Match length 57
% identity 72
NCBI Description (AC002561) unkwnon protein [Arabidopsis thaliana]

Seq. No. 297450
Seq. ID LIB3137-050-Q1-K1-H12

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Method BLASTX
NCBI GI g2668742
BLAST score 421
E value 2.0e-41
Match length 85
% identity 95
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 297451
Seq. ID LIB3137-050-Q1-K1-H7
Method BLASTX
NCBI GI g3414817
BLAST score 206
E value 8.0e-21
Match length 95
% identity 57
NCBI Description (AF064212) globulin-1 [Zea mays subsp. mays]

Seq. No. 297452
Seq. ID LIB3137-056-Q1-K1-B9
Method BLASTN
NCBI GI g20266
BLAST score 54
E value 1.0e-21
Match length 82
% identity 91
NCBI Description O.sativa mRNA for lipoxygenase L-2
>gi_2171696_dbj_E03480_E03480 cDNA encoding rice
lipoxygenase L-3

Seq. No. 297453
Seq. ID LIB3137-056-Q1-K1-D10
Method BLASTX
NCBI GI g3702351
BLAST score 242
E value 2.0e-20
Match length 95
% identity 49
NCBI Description (AC005397) putative desiccation protectant protein
[Arabidopsis thaliana]

Seq. No. 297454
Seq. ID LIB3137-057-Q1-K1-A12
Method BLASTX
NCBI GI g4406759
BLAST score 171
E value 1.0e-12
Match length 75
% identity 51
NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297455
Seq. ID LIB3137-057-Q1-K1-B11
Method BLASTX
NCBI GI g3025299
BLAST score 152
E value 7.0e-10

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Match length	122
% identity	30
NCBI Description	HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi_2088660 (AF002109) ABC1 isolog [Arabidopsis thaliana]
Seq. No.	297456
Seq. ID	LIB3137-057-Q1-K1-F5
Method	BLASTX
NCBI GI	g2984709
BLAST score	179
E value	3.0e-13
Match length	40
% identity	88
NCBI Description	(AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.	297457
Seq. ID	LIB3137-057-Q1-K1-H3
Method	BLASTX
NCBI GI	g2498077
BLAST score	184
E value	7.0e-14
Match length	96
% identity	47
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase [Saccharum officinarum]
Seq. No.	297458
Seq. ID	LIB3137-058-Q1-K1-B12
Method	BLASTX
NCBI GI	g123617
BLAST score	137
E value	1.0e-08
Match length	45
% identity	64
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_99707_pir_JA0170 heat shock protein 70-2 - Arabidopsis thaliana (fragment) >gi_166766 (M23106) heat shock protein HSP70-2 [Arabidopsis thaliana]
Seq. No.	297459
Seq. ID	LIB3137-058-Q1-K1-B7
Method	BLASTX
NCBI GI	g2127458
BLAST score	210
E value	1.0e-16
Match length	118
% identity	37
NCBI Description	abc1 protein - Mycobacterium leprae >gi_466965 (U00016) abc1; B1937_C3_233 [Mycobacterium leprae]
Seq. No.	297460
Seq. ID	LIB3137-058-Q1-K1-D5
Method	BLASTX
NCBI GI	g3367593
BLAST score	165
E value	2.0e-11

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D O U T O F T E C C C

Match length 54
& identity 52
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
>gi_3805841_emb_CAA21461_ (AL031986) putative protein
[Arabidopsis thaliana]

Seq. No. 297461
Seq. ID LIB3137-058-Q1-K1-E12
Method BLASTX
NCBI GI g741983
BLAST score 221
E value 3.0e-18
Match length 73
& identity 67
NCBI Description sucrose synthase:ISOTYPE=2 [Zea mays]

Seq. No. 297462
Seq. ID LIB3137-058-Q1-K1-E5
Method BLASTX
NCBI GI g4335745
BLAST score 366
E value 5.0e-35
Match length 131
& identity 50
NCBI Description (AC006284) putative hydrolase (contains an
esterase/lipase/thioesterase active site serine domain
(prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 297463
Seq. ID LIB3137-058-Q1-K1-F10
Method BLASTX
NCBI GI g1351136
BLAST score 150
E value 5.0e-11
Match length 62
& identity 66
NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
>gi_514946 (L22296) UDP-glucose:D-fructose
2-glucosyl-transferase [Zea mays] >gi_533252 (L33244)
sucrose synthase 2 [Zea mays]

Seq. No. 297464
Seq. ID LIB3137-058-Q1-K1-F4
Method BLASTX
NCBI GI g3047111
BLAST score 276
E value 1.0e-24
Match length 69
& identity 57
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 297465
Seq. ID LIB3137-058-Q1-K1-G4
Method BLASTX
NCBI GI g4158230
BLAST score 218
E value 4.0e-18

DRAFT

Match length 48
% identity 88
NCBI Description (Y18625) amylogenin [Triticum aestivum]

Seq. No. 297466
Seq. ID LIB3137-059-Q1-K1-A1
Method BLASTX
NCBI GI g1169383
BLAST score 232
E value 2.0e-23
Match length 63
% identity 85
NCBI Description DNAJ PROTEIN HOMOLOG ATJ >gi_535588 (L36113) putative [Arabidopsis thaliana] >gi_1582356_prf_2118338A AtJ2 protein [Arabidopsis thaliana]

Seq. No. 297467
Seq. ID LIB3137-059-Q1-K1-C12
Method BLASTX
NCBI GI g283038
BLAST score 337
E value 5.0e-36
Match length 101
% identity 79
NCBI Description chlorophyll a/b-binding protein (cab-m7) precursor - maize >gi_22230_emb_CAA37474_ (X53398) light harvesting chlorophyll a /b binding protein [Zea mays]

Seq. No. 297468
Seq. ID LIB3137-059-Q1-K1-D11
Method BLASTX
NCBI GI g710626
BLAST score 154
E value 4.0e-10
Match length 68
% identity 49
NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No. 297469
Seq. ID LIB3137-059-Q1-K1-D3
Method BLASTN
NCBI GI g236729
BLAST score 105
E value 8.0e-52
Match length 133
% identity 97
NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]

Seq. No. 297470
Seq. ID LIB3137-059-Q1-K1-F7
Method BLASTN
NCBI GI g4140643
BLAST score 45
E value 4.0e-16

Match length 97
% identity 87
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
complete sequence

Seq. No. 297471
Seq. ID LIB3137-059-Q1-K1-G2
Method BLASTX
NCBI GI g135411
BLAST score 401
E value 4.0e-52
Match length 111
% identity 92
NCBI Description TUBULIN ALPHA-2 CHAIN >gi_82732_pir_S15772 tubulin alpha-2
chain - maize >gi_22148_emb_CAA33733_ (X15704)
alpha2-tubulin [Zea mays]

Seq. No. 297472
Seq. ID LIB3137-059-Q1-K1-H11
Method BLASTX
NCBI GI g2494280
BLAST score 145
E value 3.0e-09
Match length 59
% identity 47
NCBI Description ELONGATION FACTOR TS (EF-TS) >gi_1653231_dbj_BAA18146_
(D90912) elongation factor TS [Synechocystis sp.]

Seq. No. 297473
Seq. ID LIB3137-059-Q1-K1-H3
Method BLASTX
NCBI GI g2832700
BLAST score 191
E value 3.0e-18
Match length 93
% identity 61
NCBI Description (AL021713) unknown protein [Arabidopsis thaliana]

Seq. No. 297474
Seq. ID LIB3137-060-Q1-K1-E11
Method BLASTX
NCBI GI g3452497
BLAST score 139
E value 1.0e-08
Match length 87
% identity 37
NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum]

Seq. No. 297475
Seq. ID LIB3137-060-Q1-K1-F5
Method BLASTX
NCBI GI g1039332
BLAST score 158
E value 1.0e-10
Match length 98
% identity 41
NCBI Description (X86101) glutamyl tRNA reductase [Hordeum vulgare]

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Seq. No.	297476
Seq. ID	LIB3137-060-Q1-K1-F7
Method	BLASTX
NCBI GI	g116380
BLAST score	208
E value	2.0e-16
Match length	43
% identity	91
NCBI Description	CHALCONE SYNTHASE C2 (NARINGENIN-CHALCONE SYNTHASE C2) >gi_66554_pir__SYZMCC naringenin-chalcone synthase (EC 2.3.1.74) c2 - maize >gi_22218_emb_CAA42764_ (X60205) chalcone synthase [Zea mays]
Seq. No.	297477
Seq. ID	LIB3137-061-Q1-K1-D9
Method	BLASTX
NCBI GI	g2499614
BLAST score	195
E value	1.0e-15
Match length	49
% identity	82
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF3 (P43) >gi_481830_pir__S39559 mitogen-activated protein kinase 3 homolog ntf3 - common tobacco >gi_406751_emb_CAA49592_ (X69971) NTF3 [Nicotiana tabacum]
Seq. No.	297478
Seq. ID	LIB3137-061-Q1-K1-E6
Method	BLASTX
NCBI GI	g548770
BLAST score	194
E value	3.0e-25
Match length	108
% identity	61
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]
Seq. No.	297479
Seq. ID	LIB3137-061-Q1-K1-E7
Method	BLASTN
NCBI GI	g3004949
BLAST score	116
E value	1.0e-58
Match length	255
% identity	84
NCBI Description	Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA, complete cds
Seq. No.	297480
Seq. ID	LIB3137-061-Q1-K1-F8
Method	BLASTX
NCBI GI	g2326947
BLAST score	165
E value	7.0e-12
Match length	78

% identity 49
NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor [Zea mays]

Seq. No. 297481
Seq. ID LIB3137-061-Q1-K1-G12
Method BLASTX
NCBI GI g2979555
BLAST score 205
E value 3.0e-16
Match length 85
% identity 44
NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

Seq. No. 297482
Seq. ID LIB3137-061-Q1-K1-H12
Method BLASTX
NCBI GI g4585873
BLAST score 198
E value 1.0e-15
Match length 54
% identity 69
NCBI Description (AC005850) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 297483
Seq. ID LIB3137-062-Q1-K1-A11
Method BLASTX
NCBI GI g1321661
BLAST score 317
E value 1.0e-29
Match length 83
% identity 75
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 297484
Seq. ID LIB3137-062-Q1-K1-B3
Method BLASTX
NCBI GI g3914468
BLAST score 244
E value 6.0e-21
Match length 89
% identity 55
NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
>gi_478411_pir_JQ2257 nuclear antigen 21D7 - carrot
>gi_217911_dbj_BAA02696_ (D13434) 21D7 antigen [Daucus carota]

Seq. No. 297485
Seq. ID LIB3137-062-Q1-K1-B6
Method BLASTX
NCBI GI g2829688
BLAST score 164
E value 2.0e-11
Match length 61
% identity 66
NCBI Description CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE)
(O-ACETYL SERINE (THIOL)-LYASE) (CSASE)

>gi_1076798_pir_S52738 cysteine synthase (EC 4.2.99.8)
precursor - maize >gi_758353_emb_CAA59798_ (X85803)
cysteine synthase [Zea mays]

Seq. No. 297486
Seq. ID LIB3137-062-Q1-K1-D2
Method BLASTX
NCBI GI g3550985
BLAST score 157
E value 2.0e-13
Match length 65
% identity 66
NCBI Description (AB010740) Oss5a [Oryza sativa]

Seq. No. 297487
Seq. ID LIB3137-062-Q1-K1-D6
Method BLASTN
NCBI GI g20248
BLAST score 38
E value 5.0e-12
Match length 106
% identity 84
NCBI Description O.sativa gt-2 gene

Seq. No. 297488
Seq. ID LIB3137-062-Q1-K1-E4
Method BLASTX
NCBI GI g82696
BLAST score 253
E value 5.0e-22
Match length 60
% identity 82
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_ (X61121) glycine-rich protein [Zea mays]

Seq. No. 297489
Seq. ID LIB3137-062-Q1-K1-E8
Method BLASTX
NCBI GI g123620
BLAST score 476
E value 5.0e-48
Match length 101
% identity 94
NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir_S14950
heat shock cognate protein 70 - tomato
>gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate
70 [Lycopersicon esculentum]

Seq. No. 297490
Seq. ID LIB3137-062-Q1-K1-E9
Method BLASTX
NCBI GI g4587611
BLAST score 337
E value 7.0e-32
Match length 91
% identity 75
NCBI Description (AC006951) putative 40S ribosomal protein S17 [Arabidopsis

00000000000000000000000000000000

thaliana]

Seq. No. 297491
Seq. ID LIB3137-062-Q1-K1-F11
Method BLASTX
NCBI GI g112994
BLAST score 270
E value 3.0e-24
Match length 63
% identity 86
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
>gi_82685_pir_S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea
mays]

Seq. No. 297492
Seq. ID LIB3137-062-Q1-K1-F2
Method BLASTX
NCBI GI g3915826
BLAST score 239
E value 2.0e-20
Match length 65
% identity 74
NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 297493
Seq. ID LIB3137-062-Q1-K1-G6
Method BLASTX
NCBI GI g3719211
BLAST score 195
E value 2.0e-15
Match length 51
% identity 75
NCBI Description (U97021) UIP2 [Arabidopsis thaliana]

Seq. No. 297494
Seq. ID LIB3150-001-Q1-N1-B2
Method BLASTX
NCBI GI g4454032
BLAST score 222
E value 4.0e-18
Match length 137
% identity 34
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 297495
Seq. ID LIB3150-001-Q1-N1-C2
Method BLASTX
NCBI GI g4584548
BLAST score 199
E value 2.0e-15
Match length 62
% identity 61
NCBI Description (AL049608) putative protein [Arabidopsis thaliana]

Seq. No. 297496
Seq. ID LIB3150-001-Q1-N1-D7
Method BLASTX
NCBI GI g1184776
BLAST score 633
E value 2.0e-66
Match length 135
% identity 90
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]

Seq. No. 297497
Seq. ID LIB3150-001-Q1-N1-E3
Method BLASTX
NCBI GI g4079800
BLAST score 251
E value 7.0e-24
Match length 87
% identity 75
NCBI Description (AF052503) S-phase-specific ribosomal protein [Oryza sativa]

Seq. No. 297498
Seq. ID LIB3150-001-Q1-N1-E5
Method BLASTX
NCBI GI g1321661
BLAST score 164
E value 2.0e-11
Match length 82
% identity 48
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 297499
Seq. ID LIB3150-001-Q1-N1-F10
Method BLASTX
NCBI GI g1184776
BLAST score 370
E value 1.0e-35
Match length 85
% identity 86
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]

Seq. No. 297500
Seq. ID LIB3150-001-Q1-N1-G3
Method BLASTX
NCBI GI g4522007
BLAST score 256
E value 4.0e-22
Match length 66
% identity 76
NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]

Seq. No. 297501
Seq. ID LIB3150-001-Q1-N1-H1
Method BLASTX
NCBI GI g123549

BLAST score 227
 E value 3.0e-19
 Match length 53
 % identity 85
 NCBI Description 17.5 KD CLASS II HEAT SHOCK PROTEIN >gi_100885_pir_S14998
 heat shock protein, 18K - maize >gi_22339_emb_CAA38013_
 (X54076) 18kDa heat shock protein [Zea mays]

Seq. No. 297502
 Seq. ID LIB3150-002-Q1-N1-C10
 Method BLASTX
 NCBI GI g462234
 BLAST score 243
 E value 6.0e-21
 Match length 63
 % identity 81
 NCBI Description HISTONE H2A >gi_419741_pir_S30155 histone H2A - Norway
 spruce >gi_297871_emb_CAA48030_ (X67819) histone H2A [Picea
 abies]

Seq. No. 297503
 Seq. ID LIB3150-002-Q1-N1-D12
 Method BLASTX
 NCBI GI g4519539
 BLAST score 150
 E value 5.0e-10
 Match length 53
 % identity 58
 NCBI Description (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
 domestica]

Seq. No. 297504
 Seq. ID LIB3150-002-Q1-N1-D2
 Method BLASTX
 NCBI GI g4049534
 BLAST score 266
 E value 1.0e-23
 Match length 69
 % identity 68
 NCBI Description (AL034564) 40s ribosomal protein [Schizosaccharomyces
 pombe] >gi_4481957_emb_CAB38515.1_ (AL035637) ribosomal
 protein subunit s18. [Schizosaccharomyces pombe]

Seq. No. 297505
 Seq. ID LIB3150-002-Q1-N1-D7
 Method BLASTX
 NCBI GI g3452497
 BLAST score 223
 E value 1.0e-18
 Match length 64
 % identity 67
 NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum]

Seq. No. 297506
 Seq. ID LIB3150-002-Q1-N1-E1
 Method BLASTX
 NCBI GI g480450

BLAST score 425
E value 6.0e-42
Match length 114
% identity 77
NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No. 297507
Seq. ID LIB3150-002-Q1-N1-E2
Method BLASTX
NCBI GI g4079809
BLAST score 180
E value 2.0e-13
Match length 114
% identity 5
NCBI Description (AF071172) HERC2 [Homo sapiens]

Seq. No. 297508
Seq. ID LIB3150-002-Q1-N1-G5
Method BLASTX
NCBI GI g3892056
BLAST score 241
E value 1.0e-20
Match length 62
% identity 76
NCBI Description (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]

Seq. No. 297509
Seq. ID LIB3150-002-Q1-N1-H2
Method BLASTX
NCBI GI g2811031
BLAST score 155
E value 5.0e-12
Match length 112
% identity 41
NCBI Description BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH) >gi_2109299_gb_AAB58165.1_ (AF000132) betaine aldehyde dehydrogenase [Amaranthus hypochondriacus]

Seq. No. 297510
Seq. ID LIB3150-003-Q1-N1-C1
Method BLASTX
NCBI GI g3236242
BLAST score 205
E value 1.0e-16
Match length 72
% identity 64
NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No. 297511
Seq. ID LIB3150-003-Q1-N1-D2
Method BLASTX
NCBI GI g118104
BLAST score 290
E value 1.0e-26

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Match length 74
% identity 77
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 297512
Seq. ID LIB3150-003-Q1-N1-D6
Method BLASTX
NCBI GI g3805954
BLAST score 207
E value 2.0e-16
Match length 72
% identity 53
NCBI Description (Y10414) stress protein [Rhizopus stolonifer]

Seq. No. 297513
Seq. ID LIB3150-003-Q1-N1-E4
Method BLASTN
NCBI GI g22119
BLAST score 43
E value 5.0e-15
Match length 66
% identity 91
NCBI Description Maize Adh1-F mRNA for alcohol dehydrogenase

Seq. No. 297514
Seq. ID LIB3150-003-Q1-N1-E6
Method BLASTX
NCBI GI g266346
BLAST score 198
E value 5.0e-22
Match length 91
% identity 67
NCBI Description KETOL-ACID REDUCTOISOMERASE PRECURSOR (ACETOHYDROXY-ACID
REDUCTOISOMERASE) (ALPHA-KETO-BETA-HYDROXYLACIL
REDUCTOISOMERASE) >gi_81509_pir_S17180 ketol-acid
reductoisomerase (EC 1.1.1.86) precursor - spinach
>gi_21234_emb_CAA40356_ (X57073) ketol-acid
reductoisomerase [Spinacia oleracea]

Seq. No. 297515
Seq. ID LIB3150-004-Q1-N1-A7
Method BLASTX
NCBI GI g548851
BLAST score 224
E value 2.0e-18
Match length 62
% identity 73
NCBI Description 40S RIBOSOMAL PROTEIN S20 >gi_481226_pir_S38356 ribosomal
protein S20 - rice >gi_391875_dbj_BAA02157_ (D12632) 40S
subunit ribosomal protein [Oryza sativa]

Seq. No. 297516
Seq. ID LIB3150-004-Q1-N1-B1

Method BLASTX
 NCBI GI g119355
 BLAST score 170
 E value 2.0e-12
 Match length 61
 % identity 59
 NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
 >gi_100869_pir_S16257 phosphopyruvate hydratase (EC
 4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
 [Zea mays]

Seq. No. 297517
 Seq. ID LIB3150-004-Q1-N1-B2
 Method BLASTX
 NCBI GI g2499932
 BLAST score 296
 E value 7.0e-27
 Match length 111
 % identity 59
 NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305
 (U22442) adenine phosphoribosyltransferase form 1 [Triticum
 aestivum]

Seq. No. 297518
 Seq. ID LIB3150-004-Q1-N1-B3
 Method BLASTX
 NCBI GI g2499932
 BLAST score 345
 E value 1.0e-32
 Match length 113
 % identity 60
 NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305
 (U22442) adenine phosphoribosyltransferase form 1 [Triticum
 aestivum]

Seq. No. 297519
 Seq. ID LIB3150-004-Q1-N1-B5
 Method BLASTX
 NCBI GI g112994
 BLAST score 258
 E value 9.0e-29
 Match length 87
 % identity 79
 NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
 >gi_82685_pir_S04536 embryonic abundant protein,
 glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
 ABA-inducible gene protein [Zea mays]
 >gi_226091_prf_1410284A abscisic acid inducible gene [Zea
 mays]

Seq. No. 297520
 Seq. ID LIB3150-004-Q1-N1-C4
 Method BLASTX
 NCBI GI g560150
 BLAST score 152
 E value 7.0e-10

Match length 95
% identity 38
NCBI Description (X74772) SF16 protein [Helianthus annuus]

Seq. No. 297521
Seq. ID LIB3150-004-Q1-N1-D4
Method BLASTX
NCBI GI g4191778
BLAST score 265
E value 4.0e-23
Match length 75
% identity 72
NCBI Description (AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No. 297522
Seq. ID LIB3150-004-Q1-N1-F9
Method BLASTN
NCBI GI g21796
BLAST score 33
E value 3.0e-09
Match length 65
% identity 88
NCBI Description Wheat histone H3 gene

Seq. No. 297523
Seq. ID LIB3150-005-Q1-N1-A1
Method BLASTX
NCBI GI g1168811
BLAST score 506
E value 2.0e-51
Match length 113
% identity 85
NCBI Description CELL DIVISION CONTROL PROTEIN 2 HOMOLOG B
>gi_282864_pir_S23096 protein kinase (EC 2.7.1.37) cdc2 homolog B - Arabidopsis thaliana >gi_217851_dbj_BAA01624_(D10851) p32 protein serine/threonine kinase-related protein [Arabidopsis thaliana]

Seq. No. 297524
Seq. ID LIB3150-005-Q1-N1-A3
Method BLASTX
NCBI GI g4588906
BLAST score 175
E value 8.0e-13
Match length 50
% identity 72
NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]

Seq. No. 297525
Seq. ID LIB3150-005-Q1-N1-C6
Method BLASTX
NCBI GI g1575130
BLAST score 161
E value 4.0e-11
Match length 47
% identity 72

NCBI Description (U58209) lumenal binding protein cBiPe3 [Zea mays]

Seq. No. 297526
Seq. ID LIB3150-005-Q1-N1-D5
Method BLASTX
NCBI GI g1561577
BLAST score 233
E value 1.0e-19
Match length 77
% identity 61
NCBI Description (Y08252) spermine synthase 1 [Datura stramonium]

Seq. No. 297527
Seq. ID LIB3150-005-Q1-N1-D7
Method BLASTX
NCBI GI g4467096
BLAST score 217
E value 1.0e-17
Match length 121
% identity 43
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 297528
Seq. ID LIB3150-005-Q1-N1-E11
Method BLASTX
NCBI GI g4056494
BLAST score 235
E value 8.0e-20
Match length 108
% identity 66
NCBI Description (AC005896) putative protein translocase [Arabidopsis thaliana]

Seq. No. 297529
Seq. ID LIB3150-005-Q1-N1-E3
Method BLASTX
NCBI GI g629843
BLAST score 268
E value 1.0e-23
Match length 75
% identity 68
NCBI Description heat shock protein hsp70-4 - maize (fragment)
>gi_498773_emb_CAA55183_ (X78414) heat shock protein 70 kDa
[Zea mays]

Seq. No. 297530
Seq. ID LIB3150-005-Q1-N1-H6
Method BLASTX
NCBI GI g119355
BLAST score 194
E value 4.0e-15
Match length 77
% identity 56
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
>gi_100869_pir_S16257 phosphopyruvate hydratase (EC
4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase

BIOCHIETRONIC

[Zea mays]

Seq. No. 297531
Seq. ID LIB3150-006-Q1-N1-C3
Method BLASTX
NCBI GI g2342685
BLAST score 236
E value 4.0e-27
Match length 109
% identity 59
NCBI Description (AC000106) Contains similarity to Rhodococcus amidase (gb_D16207). ESTs gb_T20504,gb_H36650,gb_N97423,gb_H36595 come from this gene. [Arabidopsis thaliana]

Seq. No. 297532
Seq. ID LIB3150-006-Q1-N1-D7
Method BLASTX
NCBI GI g4406816
BLAST score 394
E value 2.0e-38
Match length 113
% identity 72
NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 297533
Seq. ID LIB3150-006-Q1-N1-E1
Method BLASTN
NCBI GI g1184775
BLAST score 77
E value 1.0e-35
Match length 97
% identity 95
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4 (gpc4) mRNA, complete cds

Seq. No. 297534
Seq. ID LIB3150-006-Q1-N1-F6
Method BLASTN
NCBI GI g1658192
BLAST score 67
E value 3.0e-29
Match length 255
% identity 82
NCBI Description Sorghum bicolor obtusifoliol 14-alpha demethylase CYP51 (CYP51) mRNA, complete cds

Seq. No. 297535
Seq. ID LIB3150-006-Q1-N1-G8
Method BLASTX
NCBI GI g2493147
BLAST score 363
E value 1.0e-34
Match length 87
% identity 84
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_857574 (U27098) H+-ATPase [Oryza sativa]

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Seq. No.	297536
Seq. ID	LIB3150-007-Q1-N1-B11
Method	BLASTX
NCBI GI	g4586588
BLAST score	336
E value	1.0e-31
Match length	102
% identity	69
NCBI Description	(AB024998) translation elongation factor [Cicer arietinum]
Seq. No.	297537
Seq. ID	LIB3150-007-Q1-N1-D3
Method	BLASTX
NCBI GI	g1350783
BLAST score	236
E value	5.0e-20
Match length	91
% identity	30
NCBI Description	RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR >gi_282883_pir_S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana] >gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]
Seq. No.	297538
Seq. ID	LIB3150-007-Q1-N1-H2
Method	BLASTX
NCBI GI	g135398
BLAST score	485
E value	5.0e-49
Match length	90
% identity	99
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_82731_pir_S15773 tubulin alpha-1 chain - maize >gi_22147_emb_CAA33734_ (X15704) alpha1-tubulin [Zea mays]
Seq. No.	297539
Seq. ID	LIB3150-008-Q1-N1-B10
Method	BLASTX
NCBI GI	g3334320
BLAST score	456
E value	1.0e-45
Match length	92
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]
Seq. No.	297540
Seq. ID	LIB3150-008-Q1-N1-D1
Method	BLASTX
NCBI GI	g3201541
BLAST score	208
E value	1.0e-32
Match length	74
% identity	89
NCBI Description	(AJ005077). TCTR2 protein [Lycopersicon esculentum]

Seq. No. 297541
Seq. ID LIB3150-008-Q1-N1-D12
Method BLASTX
NCBI GI g2583129
BLAST score 264
E value 6.0e-23
Match length 72
% identity 64
NCBI Description (AC002387) putative methionine aminopeptidase [Arabidopsis thaliana]

Seq. No. 297542
Seq. ID LIB3150-008-Q1-N1-D7
Method BLASTX
NCBI GI g1841502
BLAST score 219
E value 6.0e-18
Match length 81
% identity 58
NCBI Description (Y11029) glutathione-dependent formaldehyde dehydrogenase [Zea mays]

Seq. No. 297543
Seq. ID LIB3150-008-Q1-N1-G9
Method BLASTX
NCBI GI g4206112
BLAST score 185
E value 2.0e-14
Match length 49
% identity 76
NCBI Description (AF097662) alpha tubulin [Mesembryanthemum crystallinum]

Seq. No. 297544
Seq. ID LIB3150-009-Q1-N1-A9
Method BLASTN
NCBI GI g168675
BLAST score 85
E value 5.0e-40
Match length 117
% identity 93
NCBI Description Maize mutant zein (zE19) gene, complete cds

Seq. No. 297545
Seq. ID LIB3150-009-Q1-N1-B8
Method BLASTX
NCBI GI g231683
BLAST score 229
E value 4.0e-19
Match length 81
% identity 62
NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir_JN0597 calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog [Arabidopsis thaliana]

Seq. No. 297546

Seq. ID LIB3150-009-Q1-N1-C10
 Method BLASTX
 NCBI GI g168691
 BLAST score 169
 E value 4.0e-20
 Match length 106
 % identity 59
 NCBI Description (M29628) zein [Zea mays]

Seq. No. 297547
 Seq. ID LIB3150-009-Q1-N1-C12
 Method BLASTX
 NCBI GI g141617
 BLAST score 273
 E value 1.0e-24
 Match length 73
 % identity 67
 NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
 >gi_100941_pir_S12140 zein Zc1 - maize
 >gi_100945_pir_B29017 zein 2 - maize
 >gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
 >gi_168666_(M16460) 16-kDa zein protein [Zea mays]

Seq. No. 297548
 Seq. ID LIB3150-009-Q1-N1-C5
 Method BLASTX
 NCBI GI g141617
 BLAST score 283
 E value 3.0e-25
 Match length 105
 % identity 52
 NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
 >gi_100941_pir_S12140 zein Zc1 - maize
 >gi_100945_pir_B29017 zein 2 - maize
 >gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
 >gi_168666_(M16460) 16-kDa zein protein [Zea mays]

Seq. No. 297549
 Seq. ID LIB3150-009-Q1-N1-D1
 Method BLASTX
 NCBI GI g118104
 BLAST score 283
 E value 2.0e-25
 Match length 74
 % identity 76
 NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
 (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
 >gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) - maize
 >gi_168461_(M55021) cyclophilin [Zea mays]
 >gi_829148_emb_CAA48638_(X68678) cyclophilin [Zea mays]

Seq. No. 297550
 Seq. ID LIB3150-009-Q1-N1-D10
 Method BLASTN
 NCBI GI g22514
 BLAST score 35
 E value 3.0e-10

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Match length 113
% identity 84
NCBI Description Maize Zcl gene for Zein Zcl (14 kD zein-2)

Seq. No. 297551
Seq. ID LIB3150-009-Q1-N1-D12
Method BLASTN
NCBI GI g168425
BLAST score 79
E value 2.0e-36
Match length 267
% identity 83
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 297552
Seq. ID LIB3150-009-Q1-N1-D4
Method BLASTX
NCBI GI g114420
BLAST score 183
E value 1.0e-13
Match length 73
% identity 56
NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
>gi_100882_pir_S11491 H+-transporting ATP synthase (EC
3.6.1.34) beta chain, mitochondrial - maize
>gi_22173_emb_CAA38140_ (X54233) ATPase F1 subunit protein
[Zea mays] >gi_897618_ (M36087) F-1-ATPase subunit 2 [Zea
mays]

Seq. No. 297553
Seq. ID LIB3150-009-Q1-N1-E1
Method BLASTX
NCBI GI g2286153
BLAST score 236
E value 4.0e-20
Match length 59
% identity 81
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 297554
Seq. ID LIB3150-009-Q1-N1-E11
Method BLASTX
NCBI GI g141603
BLAST score 446
E value 2.0e-44
Match length 110
% identity 87
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 297555
Seq. ID LIB3150-009-Q1-N1-E3
Method BLASTX
NCBI GI g3123264
BLAST score 239
E value 2.0e-20

DRAFT

Match length	68
% identity	72
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279 (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.	297556
Seq. ID	LIB3150-009-Q1-N1-E5
Method	BLASTX
NCBI GI	g4185308
BLAST score	183
E value	1.0e-13
Match length	103
% identity	47
NCBI Description	(AF090446) 22-kDa alpha zein protein 21 [Zea mays]
Seq. No.	297557
Seq. ID	LIB3150-009-Q1-N1-G12
Method	BLASTN
NCBI GI	g22528
BLAST score	35
E value	3.0e-10
Match length	75
% identity	87
NCBI Description	Zea mays mRNA encoding a zein (clone A20)
Seq. No.	297558
Seq. ID	LIB3150-009-Q1-N1-G9
Method	BLASTX
NCBI GI	g141599
BLAST score	155
E value	2.0e-10
Match length	55
% identity	58
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2) >gi_72316_pir_ZIZMA2 19K zein precursor (clone cZ19A2) - maize (fragment) >gi_168670 (M12142) 19 kDa zein protein [Zea mays]
Seq. No.	297559
Seq. ID	LIB3150-009-Q1-N1-H10
Method	BLASTX
NCBI GI	g141604
BLAST score	408
E value	7.0e-40
Match length	116
% identity	76
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1) >gi_72310_pir_ZIZM91 19K zein precursor (clone cZ19C1) - maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]
Seq. No.	297560
Seq. ID	LIB3150-009-Q1-N1-H11
Method	BLASTX
NCBI GI	g82654
BLAST score	273
E value	4.0e-24
Match length	77

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% identity 73
NCBI Description 10K zein precursor - maize >gi_22541_emb_CAA30409_ (X07535)
10kDa zein (AA 1 - 150) [Zea mays]

Seq. No. 297561
Seq. ID LIB3150-010-Q1-N1-A5
Method BLASTN
NCBI GI g22312
BLAST score 73
E value 4.0e-33
Match length 176
% identity 86
NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)

Seq. No. 297562
Seq. ID LIB3150-010-Q1-N1-B7
Method BLASTX
NCBI GI g1184774
BLAST score 431
E value 7.0e-43
Match length 94
% identity 89
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 297563
Seq. ID LIB3150-010-Q1-N1-D5
Method BLASTN
NCBI GI g22326
BLAST score 156
E value 1.0e-82
Match length 160
% identity 99
NCBI Description Z.mays gene for Hageman factor inhibitor

Seq. No. 297564
Seq. ID LIB3150-010-Q1-N1-F10
Method BLASTX
NCBI GI g141605
BLAST score 528
E value 6.0e-54
Match length 121
% identity 88
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cz19c2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 297565
Seq. ID LIB3150-010-Q1-N1-G1
Method BLASTN
NCBI GI g625147
BLAST score 123
E value 6.0e-63
Match length 231
% identity 88
NCBI Description Zea mays protein disulfide isomerase (pdi) mRNA, complete

D E S C R I P T O R

cds

Seq. No. 297566
Seq. ID LIB3150-010-Q1-N1-H9
Method BLASTX
NCBI GI g4191782
BLAST score 185
E value 7.0e-14
Match length 63
% identity 54
NCBI Description (AC005917) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No. 297567
Seq. ID LIB3150-011-Q1-N1-B10
Method BLASTX
NCBI GI g82696
BLAST score 301
E value 1.0e-27
Match length 74
% identity 78
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]

Seq. No. 297568
Seq. ID LIB3150-011-Q1-N1-B12
Method BLASTX
NCBI GI g1172836
BLAST score 378
E value 2.0e-36
Match length 95
% identity 75
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787)
small ras-related protein [Nicotiana tabacum]

Seq. No. 297569
Seq. ID LIB3150-012-Q1-N1-A4
Method BLASTX
NCBI GI g1184776
BLAST score 503
E value 3.0e-51
Match length 101
% identity 95
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC4 [Zea mays]

Seq. No. 297570
Seq. ID LIB3150-012-Q1-N1-A5
Method BLASTX
NCBI GI g82696
BLAST score 178
E value 1.0e-13
Match length 39
% identity 87
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]

Seq. No. 297571

DRAFT NUMBER

Seq. ID LIB3150-012-Q1-N1-B11
Method BLASTX
NCBI GI g131772
BLAST score 151
E value 5.0e-10
Match length 67
% identity 55
NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
>gi_82723_pir_A30097 ribosomal protein S14 (clone MCH1) - maize

Seq. No. 297572
Seq. ID LIB3150-012-Q1-N1-C10
Method BLASTX
NCBI GI g3915465
BLAST score 204
E value 4.0e-16
Match length 104
% identity 44
NCBI Description HYPOTHETICAL GTP-BINDING PROTEIN IN XSEA-HISS INTERGENIC REGION >gi_1788858 (AE000337) putative GTP-binding factor [Escherichia coli] >gi_1805570_dbj_BAA16397 (D90880) similar to [SwissProt Accession Number P44536] [Escherichia coli]

Seq. No. 297573
Seq. ID LIB3150-012-Q1-N1-D3
Method BLASTX
NCBI GI g118390
BLAST score 307
E value 2.0e-28
Match length 80
% identity 80
NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
>gi_2144526_pir_DCZMP pyruvate decarboxylase (EC 4.1.1.1) - maize >gi_22395_emb_CAA42120_ (X59546) pyruvate decarboxylase [Zea mays]

Seq. No. 297574
Seq. ID LIB3150-012-Q1-N1-F7
Method BLASTX
NCBI GI g132736
BLAST score 161
E value 3.0e-11
Match length 69
% identity 49
NCBI Description 60S RIBOSOMAL PROTEIN L19 (VEGETATIVE SPECIFIC PROTEIN V14) (22 KD CALMODULIN-BINDING PROTEIN) >gi_71266_pir_R5DO9E ribosomal protein L19.e - slime mold (*Dictyostelium discoideum*) >gi_295737_emb_CAA33443_ (X15383) V14 [*Dictyostelium discoideum*] >gi_443591 (L27657) ribosomal protein [*Dictyostelium discoideum*]

Seq. No. 297575
Seq. ID LIB3150-012-Q1-N1-H6
Method BLASTN
NCBI GI g2431766

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BLAST score	46
E value	3.0e-17
Match length	98
% identity	87
NCBI Description	Zea mays acidic ribosomal protein P3a (rpp3a) mRNA, complete cds
Seq. No.	297576
Seq. ID	LIB3150-013-Q1-N1-B10
Method	BLASTX
NCBI GI	g1848210
BLAST score	152
E value	5.0e-10
Match length	37
% identity	81
NCBI Description	(Y11208) histone H2B1 [Nicotiana tabacum]
Seq. No.	297577
Seq. ID	LIB3150-013-Q1-N1-F12
Method	BLASTX
NCBI GI	g3122053
BLAST score	176
E value	7.0e-13
Match length	110
% identity	41
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_1235582_emb_CAA65391_ (X96555) elongation factor 1-alpha [Pisum sativum]
Seq. No.	297578
Seq. ID	LIB3150-013-Q1-N1-G5
Method	BLASTN
NCBI GI	g22516
BLAST score	189
E value	1.0e-102
Match length	217
% identity	97
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.	297579
Seq. ID	LIB3150-014-Q1-N1-B11
Method	BLASTX
NCBI GI	g2281647
BLAST score	148
E value	1.0e-09
Match length	36
% identity	75
NCBI Description	(AF003104) AP2 domain containing protein RAP2.11 [Arabidopsis thaliana]
Seq. No.	297580
Seq. ID	LIB3150-014-Q1-N1-C2
Method	BLASTX
NCBI GI	g1658313
BLAST score	250
E value	1.0e-21
Match length	72

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% identity 62
NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 297581
Seq. ID LIB3150-014-Q1-N1-C9
Method BLASTX
NCBI GI g1184776
BLAST score 162
E value 2.0e-11
Match length 48
% identity 71
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]

Seq. No. 297582
Seq. ID LIB3150-014-Q1-N1-D10
Method BLASTN
NCBI GI g3747049
BLAST score 57
E value 1.0e-23
Match length 145
% identity 85
NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds

Seq. No. 297583
Seq. ID LIB3150-014-Q1-N1-D8
Method BLASTN
NCBI GI g168484
BLAST score 209
E value 1.0e-114
Match length 328
% identity 91
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 297584
Seq. ID LIB3150-014-Q1-N1-D9
Method BLASTX
NCBI GI g585876
BLAST score 188
E value 2.0e-14
Match length 67
% identity 63
NCBI Description 60S RIBOSOMAL PROTEIN L23A (L25) >gi_1084424_pir_S48026
ribosomal protein L25 - common tobacco >gi_310935 (L18908)
60S ribosomal protein L25 [Nicotiana tabacum]

Seq. No. 297585
Seq. ID LIB3150-014-Q1-N1-G2
Method BLASTX
NCBI GI g2230757
BLAST score 347
E value 9.0e-33
Match length 92
% identity 70
NCBI Description (Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No. 297586

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Seq. ID LIB3150-014-Q1-N1-H1
Method BLASTX
NCBI GI g629767
BLAST score 250
E value 1.0e-21
Match length 114
% identity 47
NCBI Description 11S globulin - oat >gi_472867_emb_CAA52764_ (X74741) 11S globulin [Avena sativa]

Seq. No. 297587
Seq. ID LIB3150-015-Q1-N1-A3
Method BLASTX
NCBI GI g1350680
BLAST score 300
E value 2.0e-27
Match length 102
% identity 60
NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 297588
Seq. ID LIB3150-015-Q1-N1-A4
Method BLASTX
NCBI GI g4582468
BLAST score 351
E value 1.0e-33
Match length 82
% identity 87
NCBI Description (AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No. 297589
Seq. ID LIB3150-015-Q1-N1-B1
Method BLASTX
NCBI GI g121569
BLAST score 373
E value 5.0e-36
Match length 104
% identity 70
NCBI Description IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG B70 (HEAT SHOCK PROTEIN 70 HOMOLOG) (B-70) >gi_484510_pir_JQ0966 immunoglobulin-binding protein homolog b70 - maize (fragment)

Seq. No. 297590
Seq. ID LIB3150-015-Q1-N1-C3
Method BLASTX
NCBI GI g2267597
BLAST score 189
E value 2.0e-14
Match length 75
% identity 59
NCBI Description (AF009413) 10 kDa chaperonin [Oryza sativa]

Seq. No. 297591
Seq. ID LIB3150-015-Q1-N1-D12
Method BLASTX

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NCBI GI	g3776564
BLAST score	253
E value	1.0e-21
Match length	66
% identity	68
NCBI Description	(AC005388) Similar to hypothetical protein T1D16.16 gi_3075397 from A. thaliana BAC gb_AC004484. [Arabidopsis thaliana]
Seq. No.	297592
Seq. ID	LIB3150-015-Q1-N1-D8
Method	BLASTX
NCBI GI	g1084457
BLAST score	259
E value	1.0e-22
Match length	80
% identity	66
NCBI Description	elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_ (D23674) elongation factor 1 beta [Oryza sativa]
Seq. No.	297593
Seq. ID	LIB3150-015-Q1-N1-D9
Method	BLASTX
NCBI GI	g1222552
BLAST score	607
E value	3.0e-63
Match length	141
% identity	78
NCBI Description	(U49330) pectin methylesterase [Lycopersicon esculentum]
Seq. No.	297594
Seq. ID	LIB3150-015-Q1-N1-E1
Method	BLASTX
NCBI GI	g1710551
BLAST score	281
E value	5.0e-25
Match length	51
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728_ (X95458) ribosomal protein L39 [Zea mays]
Seq. No.	297595
Seq. ID	LIB3150-015-Q1-N1-E3
Method	BLASTN
NCBI GI	g450548
BLAST score	68
E value	5.0e-30
Match length	168
% identity	86
NCBI Description	O.sativa (pRSAM-1) gene for S-adenosyl methionine synthetase
Seq. No.	297596
Seq. ID	LIB3150-015-Q1-N1-G2
Method	BLASTN
NCBI GI	g22324
BLAST score	38

E value 3.0e-12
Match length 46
% identity 96
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No. 297597
Seq. ID LIB3150-016-Q1-N1-A6
Method BLASTX
NCBI GI g131772
BLAST score 147
E value 2.0e-09
Match length 31
% identity 97
NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
>gi_82723_pir_A30097 ribosomal protein S14 (clone MCH1) - maize

Seq. No. 297598
Seq. ID LIB3150-016-Q1-N1-D10
Method BLASTX
NCBI GI g3746060
BLAST score 415
E value 9.0e-41
Match length 86
% identity 85
NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 297599
Seq. ID LIB3150-016-Q1-N1-D2
Method BLASTX
NCBI GI g419803
BLAST score 361
E value 1.0e-34
Match length 79
% identity 87
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 297600
Seq. ID LIB3150-016-Q1-N1-D7
Method BLASTX
NCBI GI g3915031
BLAST score 178
E value 4.0e-13
Match length 42
% identity 71
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
(STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232
(X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
[Gossypium hirsutum]

Seq. No. 297601
Seq. ID LIB3150-016-Q1-N1-E1
Method BLASTX
NCBI GI g4454464
BLAST score 211
E value 7.0e-17

Match length 64
% identity 59
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 297602
Seq. ID LIB3150-016-Q1-N1-G3
Method BLASTX
NCBI GI g122022
BLAST score 301
E value 2.0e-27
Match length 85
% identity 74
NCBI Description HISTONE H2B >gi_283025_pir_S22323 histone H2B - wheat
>gi_21801_emb_CAA42530_ (X59873) histone H2B [Triticum aestivum]

Seq. No. 297603
Seq. ID LIB3150-016-Q1-N1-G4
Method BLASTX
NCBI GI g1814403
BLAST score 186
E value 2.0e-14
Match length 57
% identity 67
NCBI Description (U84889) methionine synthase [Mesembryanthemum crystallinum]

Seq. No. 297604
Seq. ID LIB3150-016-Q1-N1-H4
Method BLASTX
NCBI GI g1922246
BLAST score 166
E value 9.0e-13
Match length 75
% identity 61
NCBI Description (Y10086) putative dehydrogenase [Arabidopsis thaliana]

Seq. No. 297605
Seq. ID LIB3150-017-Q1-N1-B11
Method BLASTX
NCBI GI g543711
BLAST score 170
E value 4.0e-13
Match length 97
% identity 49
NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796_pir_S30927 14-3-3
protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
brain specific protein [Oryza sativa]

Seq. No. 297606
Seq. ID LIB3150-017-Q1-N1-D6
Method BLASTX
NCBI GI g3914423
BLAST score 374
E value 4.0e-36
Match length 74
% identity 95

NCBI Description PROFILIN 4 >gi_2642324 (AF032370) profilin [Zea mays]

Seq. No. 297607
Seq. ID LIB3150-017-Q1-N1-E9
Method BLASTX
NCBI GI g1498382
BLAST score 158
E value 3.0e-11
Match length 65
% identity 55
NCBI Description (U60507) actin [Zea mays]

Seq. No. 297608
Seq. ID LIB3150-017-Q1-N1-F10
Method BLASTN
NCBI GI g1550813
BLAST score 67
E value 8.0e-30
Match length 119
% identity 89
NCBI Description Z.mays mRNA for acidic ribosomal protein P0

Seq. No. 297609
Seq. ID LIB3150-017-Q1-N1-H11
Method BLASTX
NCBI GI g2668742
BLAST score 250
E value 1.0e-21
Match length 69
% identity 72
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 297610
Seq. ID LIB3150-017-Q1-N1-H6
Method BLASTX
NCBI GI g4455207
BLAST score 293
E value 1.0e-26
Match length 88
% identity 72
NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 297611
Seq. ID LIB3150-018-Q1-N1-A1
Method BLASTN
NCBI GI g496267
BLAST score 41
E value 5.0e-14
Match length 81
% identity 88
NCBI Description Nicotiana tabacum GTP-binding protein (Ran-A1) mRNA, complete cds

Seq. No. 297612
Seq. ID LIB3150-018-Q1-N1-A7
Method BLASTX
NCBI GI g4154352

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BLAST score	187
E value	2.0e-14
Match length	78
% identity	53
NCBI Description	(AF110333) PrMC3 [Pinus radiata]
Seq. No.	297613
Seq. ID	LIB3150-018-Q1-N1-B4
Method	BLASTX
NCBI GI	g2865175
BLAST score	229
E value	4.0e-19
Match length	94
% identity	54
NCBI Description	(AB010945) AtRer1A [Arabidopsis thaliana]
Seq. No.	297614
Seq. ID	LIB3150-018-Q1-N1-F10
Method	BLASTX
NCBI GI	g995714
BLAST score	271
E value	6.0e-24
Match length	104
% identity	52
NCBI Description	(X91258) L3177 [Saccharomyces cerevisiae]
Seq. No.	297615
Seq. ID	LIB3150-019-Q1-N1-A1
Method	BLASTX
NCBI GI	g133867
BLAST score	259
E value	1.0e-22
Match length	72
% identity	72
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]
Seq. No.	297616
Seq. ID	LIB3150-019-Q1-N1-A12
Method	BLASTX
NCBI GI	g82718
BLAST score	309
E value	2.0e-28
Match length	88
% identity	68
NCBI Description	pyruvate,orthophosphate dikinase (EC 2.7.9.1) 2, cytosolic - maize (fragment) >gi_257810_bbs_117087 (S46967) orthophosphate dikinase, PPDK {N-terminal} [maize, Peptide Partial, 90 aa] [Zea mays]
Seq. No.	297617
Seq. ID	LIB3150-019-Q1-N1-A3
Method	BLASTX
NCBI GI	g66009
BLAST score	430
E value	9.0e-43

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Match length 93
% identity 86
NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,
cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH
(AA 1-337) [Zea mays]

Seq. No. 297618
Seq. ID LIB3150-019-Q1-N1-B4
Method BLASTN
NCBI GI g444046
BLAST score 66
E value 9.0e-29
Match length 293
% identity 83
NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor

Seq. No. 297619
Seq. ID LIB3150-019-Q1-N1-C4
Method BLASTX
NCBI GI g2827143
BLAST score 700
E value 3.0e-74
Match length 137
% identity 91
NCBI Description (AF027174) cellulose synthase catalytic subunit
[Arabidopsis thaliana]

Seq. No. 297620
Seq. ID LIB3150-019-Q1-N1-D9
Method BLASTX
NCBI GI g2996096
BLAST score 429
E value 2.0e-42
Match length 105
% identity 80
NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1
alpha [Oryza sativa]

Seq. No. 297621
Seq. ID LIB3150-019-Q1-N1-E11
Method BLASTX
NCBI GI g66615
BLAST score 237
E value 4.0e-20
Match length 79
% identity 65
NCBI Description glutathione transferase (EC 2.5.1.18) I - maize

Seq. No. 297622
Seq. ID LIB3150-019-Q1-N1-E12
Method BLASTX
NCBI GI g3318613
BLAST score 375
E value 4.0e-36
Match length 105
% identity 70
NCBI Description (AB016064) mitochondrial phosphate transporter [Zea mays]

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Seq. No. 297623
Seq. ID LIB3150-019-Q1-N1-E6
Method BLASTX
NCBI GI g1184776
BLAST score 278
E value 9.0e-25
Match length 101
% identity 54
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC4 [Zea mays]

Seq. No. 297624
Seq. ID LIB3150-019-Q1-N1-G12
Method BLASTX
NCBI GI g3036805
BLAST score 209
E value 1.0e-16
Match length 67
% identity 54
NCBI Description (AL022373) thaumatin-like protein [Arabidopsis thaliana]

Seq. No. 297625
Seq. ID LIB3150-019-Q1-N1-H11
Method BLASTX
NCBI GI g3868758
BLAST score 314
E value 6.0e-29
Match length 84
% identity 71
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 297626
Seq. ID LIB3150-020-Q1-N1-A2
Method BLASTX
NCBI GI g4006868
BLAST score 219
E value 6.0e-18
Match length 80
% identity 59
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 297627
Seq. ID LIB3150-020-Q1-N1-A8
Method BLASTN
NCBI GI g22549
BLAST score 155
E value 5.0e-82
Match length 239
% identity 91
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 297628
Seq. ID LIB3150-020-Q1-N1-C3
Method BLASTX
NCBI GI g3163946
BLAST score 509

E value 8.0e-52
Match length 94
% identity 100
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No. 297629
Seq. ID LIB3150-020-Q1-N1-D12
Method BLASTN
NCBI GI g829147
BLAST score 94
E value 8.0e-46
Match length 142
% identity 92
NCBI Description Z.mays gene for cyclophilin

Seq. No. 297630
Seq. ID LIB3150-020-Q1-N1-D6
Method BLASTX
NCBI GI g119150
BLAST score 206
E value 5.0e-27
Match length 111
% identity 66
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
>gi_82081_pir_S10507 translation elongation factor eEF-1
alpha chain - tomato >gi_19273_emb_CAA32618 (X14449) EF
1-alpha (AA 1-448) [Lycopersicon esculentum]
>gi_295810_emb_CAA37212 (X53043) elongation factor 1-alpha
[Lycopersicon esculentum]

Seq. No. 297631
Seq. ID LIB3150-020-Q1-N1-E11
Method BLASTN
NCBI GI g829147
BLAST score 37
E value 9.0e-12
Match length 97
% identity 85
NCBI Description Z.mays gene for cyclophilin

Seq. No. 297632
Seq. ID LIB3150-020-Q1-N1-G9
Method BLASTN
NCBI GI g2331300
BLAST score 52
E value 9.0e-21
Match length 140
% identity 85
NCBI Description Zea mays ribosomal protein S4 type I (rps4) mRNA, complete
cds

Seq. No. 297633
Seq. ID LIB3150-021-Q1-N1-C11
Method BLASTX
NCBI GI g100525
BLAST score 470
E value 2.0e-47

Match length 105
% identity 23
NCBI Description ubiquitin precursor UbB2 - common sunflower (fragment)
>gi_18803_emb_CAA40323_ (X57003) polyubiquitin protein
[Helianthus annuus]

Seq. No. 297634
Seq. ID LIB3150-021-Q1-N1-C9
Method BLASTN
NCBI GI g1864000
BLAST score 40
E value 3.0e-13
Match length 52
% identity 94
NCBI Description Maize DNA for Fd III, complete cds

Seq. No. 297635
Seq. ID LIB3150-021-Q1-N1-E1
Method BLASTN
NCBI GI g3747049
BLAST score 44
E value 6.0e-16
Match length 84
% identity 89
NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds

Seq. No. 297636
Seq. ID LIB3150-021-Q1-N1-G12
Method BLASTX
NCBI GI g3023812
BLAST score 176
E value 4.0e-13
Match length 48
% identity 73
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi_435046 (L26924) glyceraldehyde-phosphate dehydrogenase
[Ginkgo biloba]

Seq. No. 297637
Seq. ID LIB3150-021-Q1-N1-H12
Method BLASTN
NCBI GI g1184773
BLAST score 34
E value 4.0e-10
Match length 62
% identity 89
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3
(gpc3) mRNA, complete cds

Seq. No. 297638
Seq. ID LIB3150-021-Q1-N1-H6
Method BLASTN
NCBI GI g22338
BLAST score 64
E value 1.0e-27
Match length 155
% identity 86

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NCBI Description	Maize mRNA for an 18kDa heat shock protein
Seq. No.	297639
Seq. ID	LIB3150-022-Q1-N1-A3
Method	BLASTX
NCBI GI	g602958
BLAST score	231
E value	1.0e-19
Match length	81
% identity	58
NCBI Description	(U18102) Phalaenopsis sp. 'hybrid SM9108' actin [Phalaenopsis sp. 'hybrid SM9108']
Seq. No.	297640
Seq. ID	LIB3150-022-Q1-N1-D10
Method	BLASTX
NCBI GI	g2369714
BLAST score	272
E value	1.0e-24
Match length	67
% identity	75
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.	297641
Seq. ID	LIB3150-022-Q1-N1-E12
Method	BLASTX
NCBI GI	g2499489
BLAST score	212
E value	5.0e-17
Match length	118
% identity	48
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE BETA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483536_emb_CAA83683_ (Z32850) pyrophosphate-dependent phosphofructokinase beta subunit [Ricinus communis]
Seq. No.	297642
Seq. ID	LIB3150-022-Q1-N1-E5
Method	BLASTN
NCBI GI	g2811133
BLAST score	222
E value	1.0e-122
Match length	257
% identity	97
NCBI Description	Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA, partial cds
Seq. No.	297643
Seq. ID	LIB3150-022-Q1-N1-E9
Method	BLASTN
NCBI GI	g1498052
BLAST score	64
E value	2.0e-27
Match length	152
% identity	86

NCBI Description Zea mays ribosomal protein S8 mRNA, complete cds

Seq. No. 297644
Seq. ID LIB3150-022-Q1-N1-F6
Method BLASTX
NCBI GI g4176535
BLAST score 149
E value 1.0e-09
Match length 93
% identity 37
NCBI Description (AL035263) putative TFIIH subunit (transcription-repair factor) [Schizosaccharomyces pombe]

Seq. No. 297645
Seq. ID LIB3150-022-Q1-N1-H4
Method BLASTX
NCBI GI g2613143
BLAST score 231
E value 2.0e-19
Match length 82
% identity 61
NCBI Description (AF030548) tubulin [Oryza sativa]

Seq. No. 297646
Seq. ID LIB3150-022-Q1-N1-H9
Method BLASTX
NCBI GI g2833460
BLAST score 201
E value 1.0e-15
Match length 73
% identity 51
NCBI Description RIBOFLAVIN-SPECIFIC DEAMINASE >gi_1001153_dbj_BAA10295_(D64001) riboflavin biosynthesis protein [Synechocystis sp.]

Seq. No. 297647
Seq. ID LIB3150-023-Q1-N1-A11
Method BLASTX
NCBI GI g1169528
BLAST score 156
E value 1.0e-10
Match length 44
% identity 73
NCBI Description ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi_602253 (U17973)
enolase [Zea mays]

Seq. No. 297648
Seq. ID LIB3150-023-Q1-N1-A6
Method BLASTX
NCBI GI g4263519
BLAST score 272
E value 5.0e-24
Match length 55
% identity 95
NCBI Description (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]

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Seq. No.	297649
Seq. ID	LIB3150-023-Q1-N1-C8
Method	BLASTX
NCBI GI	g135060
BLAST score	370
E value	8.0e-36
Match length	76
% identity	97
NCBI Description	SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1) (SHRUNKEN-1) >gi_66570_pir_YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382) sucrose synthase [Zea mays]
Seq. No.	297650
Seq. ID	LIB3150-023-Q1-N1-D4
Method	BLASTX
NCBI GI	g4589852
BLAST score	270
E value	5.0e-24
Match length	97
% identity	52
NCBI Description	(AB025968) cycloartenol synthase [Glycyrrhiza glabra]
Seq. No.	297651
Seq. ID	LIB3150-023-Q1-N1-E3
Method	BLASTX
NCBI GI	g4588012
BLAST score	162
E value	1.0e-11
Match length	40
% identity	75
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]
Seq. No.	297652
Seq. ID	LIB3150-023-Q1-N1-F1
Method	BLASTX
NCBI GI	g731707
BLAST score	277
E value	1.0e-24
Match length	115
% identity	47
NCBI Description	SET1 PROTEIN >gi_626647_pir_S48961 hypothetical protein YHR119w - yeast (Saccharomyces cerevisiae) >gi_529135 (U00059) Set1p [Saccharomyces cerevisiae]
Seq. No.	297653
Seq. ID	LIB3150-023-Q1-N1-F6
Method	BLASTN
NCBI GI	g22549
BLAST score	159
E value	2.0e-84
Match length	203
% identity	95
NCBI Description	Maize gene for a 27kDa storage protein, zein

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Seq. No.	297654
Seq. ID	LIB3150-023-Q1-N1-G6
Method	BLASTX
NCBI GI	g1519251
BLAST score	591
E value	2.0e-61
Match length	131
% identity	90
NCBI Description	(U65957) GF14-c protein [Oryza sativa]
Seq. No.	297655
Seq. ID	LIB3150-023-Q1-N1-H11
Method	BLASTN
NCBI GI	g22272
BLAST score	57
E value	9.0e-24
Match length	73
% identity	95
NCBI Description	Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
Seq. No.	297656
Seq. ID	LIB3150-025-Q1-N1-A9
Method	BLASTX
NCBI GI	g3355468
BLAST score	153
E value	3.0e-10
Match length	109
% identity	44
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]
Seq. No.	297657
Seq. ID	LIB3150-025-Q1-N1-C11
Method	BLASTX
NCBI GI	g3834321
BLAST score	302
E value	1.0e-27
Match length	98
% identity	59
NCBI Description	(AC005679) Strong similarity to F13P17.9 gi_3337356 transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]
Seq. No.	297658
Seq. ID	LIB3150-025-Q1-N1-F9
Method	BLASTX
NCBI GI	g3043428
BLAST score	252
E value	5.0e-22
Match length	77
% identity	68
NCBI Description	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
Seq. No.	297659
Seq. ID	LIB3150-026-Q1-N1-C10

Method BLASTX
NCBI GI g2369714
BLAST score 168
E value 5.0e-13
Match length 90
% identity 51
NCBI Description (297178) elongation factor 2 [Beta vulgaris]

Seq. No. 297660
Seq. ID LIB3150-026-Q1-N1-E7
Method BLASTN
NCBI GI g22119
BLAST score 58
E value 5.0e-24
Match length 173
% identity 84
NCBI Description Maize Adh1-F mRNA for alcohol dehydrogenase

Seq. No. 297661
Seq. ID LIB3150-026-Q1-N1-F1
Method BLASTX
NCBI GI g1172977
BLAST score 146
E value 9.0e-10
Match length 32
% identity 88
NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 297662
Seq. ID LIB3150-026-Q1-N1-F5
Method BLASTN
NCBI GI g1519250
BLAST score 37
E value 1.0e-11
Match length 73
% identity 88
NCBI Description Oryza sativa GF14-c protein mRNA, complete cds

Seq. No. 297663
Seq. ID LIB3150-026-Q1-N1-F9
Method BLASTN
NCBI GI g22338
BLAST score 70
E value 2.0e-31
Match length 110
% identity 92
NCBI Description Maize mRNA for an 18kDa heat shock protein

Seq. No. 297664
Seq. ID LIB3150-026-Q1-N1-G1
Method BLASTX
NCBI GI g1706253
BLAST score 165
E value 1.0e-11
Match length 83
% identity 43

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NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 7 (PPIASE) (ROTAMASE)
(CYCLOPHILIN-7) >gi_863016 (U27559) cyclophilin
[Caenorhabditis elegans]

Seq. No. 297665
Seq. ID LIB3150-026-Q1-N1-G4
Method BLASTX
NCBI GI g113621
BLAST score 432
E value 8.0e-43
Match length 91
% identity 90
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
>gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366 (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A
cytoplasmic aldolase [Zea mays]

Seq. No. 297666
Seq. ID LIB3150-026-Q1-N1-G5
Method BLASTX
NCBI GI g4467125
BLAST score 441
E value 7.0e-44
Match length 106
% identity 74
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 297667
Seq. ID LIB3150-026-Q1-N1-G8
Method BLASTN
NCBI GI g22312
BLAST score 96
E value 9.0e-47
Match length 244
% identity 88
NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA =
abscisic acid)

Seq. No. 297668
Seq. ID LIB3150-026-Q1-N1-H8
Method BLASTX
NCBI GI g2443388
BLAST score 248
E value 2.0e-21
Match length 85
% identity 66
NCBI Description (D38452) calcium-dependent protein kinase-related kinase
[Zea mays]

Seq. No. 297669
Seq. ID LIB3150-027-Q1-N1-A12
Method BLASTX
NCBI GI g2130032
BLAST score 261
E value 1.0e-22

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Match length 117
% identity 49
NCBI Description catechol O-methyltransferase (EC 2.1.1.6) - barley

Seq. No. 297670
Seq. ID LIB3150-027-Q1-N1-A3
Method BLASTN
NCBI GI g602605
BLAST score 44
E value 1.0e-15
Match length 56
% identity 95
NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin

Seq. No. 297671
Seq. ID LIB3150-027-Q1-N1-A7
Method BLASTX
NCBI GI g2384758
BLAST score 330
E value 4.0e-31
Match length 92
% identity 72
NCBI Description (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza sativa]

Seq. No. 297672
Seq. ID LIB3150-027-Q1-N1-B10
Method BLASTX
NCBI GI g1350986
BLAST score 291
E value 2.0e-26
Match length 83
% identity 72
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
>gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]

Seq. No. 297673
Seq. ID LIB3150-027-Q1-N1-B3
Method BLASTX
NCBI GI g4033424
BLAST score 301
E value 2.0e-27
Match length 100
% identity 68
NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic pyrophosphatase [Zea mays]

Seq. No. 297674
Seq. ID LIB3150-027-Q1-N1-C1
Method BLASTX
NCBI GI g4587553
BLAST score 214
E value 3.0e-17
Match length 79
% identity 54
NCBI Description (AC006577) F15I1.20 [Arabidopsis thaliana]

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Seq. No.	297675
Seq. ID	LIB3150-027-Q1-N1-C2
Method	BLASTN
NCBI GI	g556685
BLAST score	57
E value	1.0e-23
Match length	89
% identity	91
NCBI Description	Z.mays mRNA for ADP-ribosylation factor
Seq. No.	297676
Seq. ID	LIB3150-027-Q1-N1-E11
Method	BLASTX
NCBI GI	g320130
BLAST score	221
E value	4.0e-18
Match length	87
% identity	53
NCBI Description	acetolactate synthase (EC 4.1.3.18) (clone pSOG109) - maize >gi_22141_emb_CAA45117_ (X63554) acetohydroxyacid synthase [Zea mays]
Seq. No.	297677
Seq. ID	LIB3150-027-Q1-N1-E2
Method	BLASTX
NCBI GI	g4587553
BLAST score	192
E value	1.0e-14
Match length	66
% identity	58
NCBI Description	(AC006577) F15I1.20 [Arabidopsis thaliana]
Seq. No.	297678
Seq. ID	LIB3150-027-Q1-N1-F6
Method	BLASTX
NCBI GI	g3986695
BLAST score	165
E value	9.0e-12
Match length	61
% identity	61
NCBI Description	(AF101423) ribosomal protein L12 [Cichorium intybus]
Seq. No.	297679
Seq. ID	LIB3150-028-Q1-N1-A4
Method	BLASTX
NCBI GI	g2244797
BLAST score	167
E value	7.0e-12
Match length	94
% identity	43
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.	297680
Seq. ID	LIB3150-028-Q1-N1-C8
Method	BLASTN
NCBI GI	g4416300

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BLAST score 88
E value 8.0e-42
Match length 235
% identity 58
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No. 297681
Seq. ID LIB3150-028-Q1-N1-D11
Method BLASTX
NCBI GI g113621
BLAST score 340
E value 3.0e-32
Match length 80
% identity 86
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
>gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366 (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A cytoplasmic aldolase [Zea mays]

Seq. No. 297682
Seq. ID LIB3150-028-Q1-N1-E11
Method BLASTX
NCBI GI g3747046
BLAST score 358
E value 4.0e-34
Match length 77
% identity 91
NCBI Description (AF093538) voltage-dependent anion-selective channel protein [Zea mays]

Seq. No. 297683
Seq. ID LIB3150-028-Q1-N1-E9
Method BLASTN
NCBI GI g485376
BLAST score 35
E value 1.0e-10
Match length 71
% identity 87
NCBI Description Zea mays alpha-3-tubulin gene, complete cds

Seq. No. 297684
Seq. ID LIB3150-028-Q1-N1-F10
Method BLASTX
NCBI GI g2832648
BLAST score 138
E value 6.0e-09
Match length 80
% identity 44
NCBI Description (AL021710) membrane-bound small GTP-binding - like protein [Arabidopsis thaliana]

Seq. No. 297685
Seq. ID LIB3150-028-Q1-N1-F2
Method BLASTN

NCBI GI g22312
 BLAST score 226
 E value 1.0e-124
 Match length 374
 % identity 90
 NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)

Seq. No. 297686
 Seq. ID LIB3150-028-Q1-N1-G5
 Method BLASTX
 NCBI GI g2342678
 BLAST score 137
 E value 9.0e-09
 Match length 57
 % identity 53
 NCBI Description (AC000106) Similar to Arabidopsis luminal binding protein (gb_D89342). [Arabidopsis thaliana]

Seq. No. 297687
 Seq. ID LIB3150-028-Q1-N1-G6
 Method BLASTX
 NCBI GI g2511531
 BLAST score 220
 E value 4.0e-18
 Match length 82
 % identity 57
 NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]
 >gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
 [Eleusine indica]

Seq. No. 297688
 Seq. ID LIB3150-028-Q1-N1-H9
 Method BLASTX
 NCBI GI g4646206
 BLAST score 247
 E value 4.0e-21
 Match length 119
 % identity 44
 NCBI Description (AC007230) Contains similarity to gb_D13630 KIAA0005 gene from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene.
 [Arabidopsis thaliana]

Seq. No. 297689
 Seq. ID LIB3150-029-Q1-N1-A4
 Method BLASTX
 NCBI GI g1703380
 BLAST score 298
 E value 4.0e-27
 Match length 67
 % identity 88
 NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760)
 ADP-ribosylation factor [Oryza sativa]

Seq. No. 297690
 Seq. ID LIB3150-029-Q1-N1-A6

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Method	BLASTX
NCBI GI	g3915826
BLAST score	375
E value	4.0e-36
Match length	96
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L5
Seq. No.	297691
Seq. ID	LIB3150-029-Q1-N1-E7
Method	BLASTX
NCBI GI	g266567
BLAST score	198
E value	1.0e-20
Match length	111
% identity	53
NCBI Description	MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II) >gi_421956_pir_S23558 mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - potato >gi_21493_emb_CAA46990_ (X66284) mitochondrial processing peptidase [Solanum tuberosum]
Seq. No.	297692
Seq. ID	LIB3150-029-Q1-N1-F9
Method	BLASTX
NCBI GI	g542125
BLAST score	149
E value	6.0e-10
Match length	53
% identity	62
NCBI Description	translation elongation factor eEF-1 alpha chain - barley >gi_396134_emb_CAA80666_ (Z23130) protein synthesis elongation factor-1 alpha [Hordeum vulgare]
Seq. No.	297693
Seq. ID	LIB3150-029-Q1-N1-G1
Method	BLASTN
NCBI GI	g1550813
BLAST score	59
E value	1.0e-24
Match length	107
% identity	89
NCBI Description	Z.mays mRNA for acidic ribosomal protein P0
Seq. No.	297694
Seq. ID	LIB3150-030-Q1-N1-A4
Method	BLASTN
NCBI GI	g22514
BLAST score	121
E value	1.0e-61
Match length	249
% identity	87
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.	297695
Seq. ID	LIB3150-030-Q1-N1-B4

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Method	BLASTN
NCBI GI	g22312
BLAST score	121
E value	7.0e-62
Match length	165
% identity	93
NCBI Description	Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)
Seq. No.	297696
Seq. ID	LIB3150-030-Q1-N1-B7
Method	BLASTX
NCBI GI	g4033424
BLAST score	297
E value	3.0e-27
Match length	62
% identity	94
NCBI Description	SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic pyrophosphatase [Zea mays]
Seq. No.	297697
Seq. ID	LIB3150-030-Q1-N1-C6
Method	BLASTX
NCBI GI	g1732511
BLAST score	506
E value	2.0e-51
Match length	116
% identity	78
NCBI Description	(U62742) Ran binding protein 1 homolog [Arabidopsis thaliana]
Seq. No.	297698
Seq. ID	LIB3150-030-Q1-N1-D1
Method	BLASTX
NCBI GI	g113621
BLAST score	155
E value	7.0e-11
Match length	36
% identity	89
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366 (X12872) fructose bisphosphatase aldolase [Zea mays] >gi_225624_prf_1307278A cytoplasmic aldolase [Zea mays]
Seq. No.	297699
Seq. ID	LIB3150-030-Q1-N1-D2
Method	BLASTX
NCBI GI	g2654208
BLAST score	163
E value	8.0e-12
Match length	60
% identity	63
NCBI Description	(AF035456) heat shock 70 protein [Spinacia oleracea] >gi_2773050 (AF039083) heat shock 70 protein [Spinacia

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oleracea]

Seq. No. 297700
Seq. ID LIB3150-030-Q1-N1-E2
Method BLASTN
NCBI GI g1658312
BLAST score 47
E value 1.0e-17
Match length 99
% identity 88
NCBI Description O.sativa osr40g2 gene

Seq. No. 297701
Seq. ID LIB3150-030-Q1-N1-E4
Method BLASTN
NCBI GI g829147
BLAST score 72
E value 2.0e-32
Match length 96
% identity 94
NCBI Description Z.mays gene for cyclophilin

Seq. No. 297702
Seq. ID LIB3150-030-Q1-N1-F2
Method BLASTX
NCBI GI g1709920
BLAST score 240
E value 2.0e-20
Match length 72
% identity 62
NCBI Description PHOSPHORIBOSYLAMINE--GLYCINE LIGASE PRECURSOR (GARS)
(GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE)
(PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE)
>gi_1019915_emb_CAA52778_ (X74766) glycinamide
ribonucleotide synthetase [Arabidopsis thaliana]

Seq. No. 297703
Seq. ID LIB3150-030-Q1-N1-F3
Method BLASTX
NCBI GI g120670
BLAST score 381
E value 4.0e-37
Match length 84
% identity 87
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi_100879_pir_S06879 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) C - maize
>gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]

Seq. No. 297704
Seq. ID LIB3150-030-Q1-N1-G3
Method BLASTN
NCBI GI g1895083
BLAST score 43
E value 2.0e-15
Match length 51
% identity 96

BIOLOGICAL ASPECTS

NCBI Description Zea mays golgi associated protein se-wap41 mRNA, complete cds
Seq. No. 297705
Seq. ID LIB3150-030-Q1-N1-H6
Method BLASTX
NCBI GI g4467128
BLAST score 320
E value 7.0e-31
Match length 96
% identity 71
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
Seq. No. 297706
Seq. ID LIB3150-031-Q1-N1-A11
Method BLASTN
NCBI GI g747916
BLAST score 62
E value 1.0e-26
Match length 110
% identity 89
NCBI Description Z.mays CaM2 mRNA for calmodulin
Seq. No. 297707
Seq. ID LIB3150-031-Q1-N1-A7
Method BLASTX
NCBI GI g113621
BLAST score 268
E value 1.0e-23
Match length 95
% identity 93
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
>gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphatase aldolase [Zea mays] >gi_225624_prf_1307278A
cytoplasmic aldolase [Zea mays]
Seq. No. 297708
Seq. ID LIB3150-031-Q1-N1-B4
Method BLASTX
NCBI GI g2909846
BLAST score 181
E value 2.0e-13
Match length 55
% identity 65
NCBI Description (AF045570) (S)-adenosyl-L-methionine:delta 24-sterol
methyltransferase [Zea mays]
Seq. No. 297709
Seq. ID LIB3150-031-Q1-N1-D10
Method BLASTX
NCBI GI g1685091
BLAST score 337
E value 1.0e-31
Match length 98
% identity 68

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NCBI Description (U45243) diphenol oxidase [Nicotiana tabacum]
Seq. No. 297710
Seq. ID LIB3150-031-Q1-N1-D12
Method BLASTX
NCBI GI g3163946
BLAST score 261
E value 5.0e-38
Match length 102
% identity 72
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]
Seq. No. 297711
Seq. ID LIB3150-031-Q1-N1-F1
Method BLASTX
NCBI GI g1076626
BLAST score 491
E value 1.0e-49
Match length 97
% identity 93
NCBI Description glycine rich protein - common tobacco
>gi_790473_emb_CAA58702_(X83731) soluble, glycine rich
protein [Nicotiana tabacum]
Seq. No. 297712
Seq. ID LIB3150-031-Q1-N1-H5
Method BLASTX
NCBI GI g4588003
BLAST score 238
E value 7.0e-20
Match length 65
% identity 74
NCBI Description (AF085279) hypothetical EIF-2-Alpha [Arabidopsis thaliana]
Seq. No. 297713
Seq. ID LIB3150-031-Q1-N1-H9
Method BLASTX
NCBI GI g4455293
BLAST score 213
E value 4.0e-17
Match length 88
% identity 61
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]
Seq. No. 297714
Seq. ID LIB3150-032-Q1-N1-C8
Method BLASTX
NCBI GI g3402679
BLAST score 184
E value 3.0e-14
Match length 81
% identity 52
NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]
Seq. No. 297715
Seq. ID LIB3150-032-Q1-N1-D6
Method BLASTX

NCBI GI g118104
 BLAST score 566
 E value 2.0e-58
 Match length 125
 % identity 86
 NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
 (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
 >gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
 maize >gi_168461 (M55021) cyclophilin [Zea mays]
 >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 297716
 Seq. ID LIB3150-032-Q1-N1-F4
 Method BLASTX
 NCBI GI g1174583
 BLAST score 201
 E value 1.0e-15
 Match length 104
 % identity 40
 NCBI Description TRANSALDOLASE >gi_1074653_pir_D64167 hypothetical protein
 HII125 - Haemophilus influenzae (strain Rd KW20)
 >gi_1574680 (U32792) transaldolase B (talB) [Haemophilus
 influenzae Rd]

Seq. No. 297717
 Seq. ID LIB3150-032-Q1-N1-G3
 Method BLASTX
 NCBI GI g2407800
 BLAST score 308
 E value 4.0e-28
 Match length 98
 % identity 62
 NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No. 297718
 Seq. ID LIB3150-032-Q1-N1-H1
 Method BLASTX
 NCBI GI g1172811
 BLAST score 285
 E value 4.0e-26
 Match length 59
 % identity 83
 NCBI Description 60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPPRESSOR SC34)
 >gi_1076751_pir_S49575 ribosomal protein L10.e, cytosolic
 - rice >gi_575355_emb_CAA57339_ (X81691) putative tumor
 supresser [Oryza sativa]

Seq. No. 297719
 Seq. ID LIB3150-033-Q1-N1-D10
 Method BLASTX
 NCBI GI g2253583
 BLAST score 151
 E value 6.0e-10
 Match length 46
 % identity 74
 NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297720
Seq. ID LIB3150-033-Q1-N1-D2
Method BLASTX
NCBI GI g2832700
BLAST score 174
E value 8.0e-13
Match length 81
% identity 42
NCBI Description (AL021713) unknown protein [Arabidopsis thaliana]

Seq. No. 297721
Seq. ID LIB3150-033-Q1-N1-F3
Method BLASTX
NCBI GI g861170
BLAST score 176
E value 3.0e-13
Match length 48
% identity 77
NCBI Description (X03697) heat shock protein 70 [Zea mays]

Seq. No. 297722
Seq. ID LIB3150-033-Q1-N1-F6
Method BLASTX
NCBI GI g3183094
BLAST score 238
E value 3.0e-20
Match length 94
% identity 47
NCBI Description ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE)
(ORNITHINE TRANSCARBAMYLASE) >gi_971168 (U13684) ornithine carbamoyltransferase [Pisum sativum]

Seq. No. 297723
Seq. ID LIB3150-033-Q1-N1-G12
Method BLASTX
NCBI GI g2459421
BLAST score 426
E value 4.0e-42
Match length 118
% identity 64
NCBI Description (AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No. 297724
Seq. ID LIB3150-033-Q1-N1-G5
Method BLASTX
NCBI GI g1184774
BLAST score 484
E value 6.0e-49
Match length 95
% identity 98
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 297725
Seq. ID LIB3150-033-Q1-N1-G8
Method BLASTN

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INDEXED
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NCBI GI	g3015620
BLAST score	120
E value	5.0e-61
Match length	240
% identity	88
NCBI Description	Zea mays low molecular weight heat shock protein precursor (hsp22) mRNA, nuclear gene encoding mitochondrial protein, complete cds
Seq. No.	297726
Seq. ID	LIB3150-034-Q1-N1-A11
Method	BLASTX
NCBI GI	g82696
BLAST score	207
E value	9.0e-17
Match length	57
% identity	75
NCBI Description	glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]
Seq. No.	297727
Seq. ID	LIB3150-034-Q1-N1-B6
Method	BLASTX
NCBI GI	g1184774
BLAST score	149
E value	5.0e-15
Match length	94
% identity	51
NCBI Description	(U45856) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]
Seq. No.	297728
Seq. ID	LIB3150-034-Q1-N1-G5
Method	BLASTX
NCBI GI	g2792208
BLAST score	272
E value	5.0e-24
Match length	124
% identity	45
NCBI Description	(AF032682) NBS-LRR type resistance protein [Hordeum vulgare]
Seq. No.	297729
Seq. ID	LIB3150-034-Q1-N1-G7
Method	BLASTX
NCBI GI	g418777
BLAST score	269
E value	8.0e-24
Match length	101
% identity	57
NCBI Description	phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain (clone EP7) - Arabidopsis thaliana (fragment)
Seq. No.	297730
Seq. ID	LIB3150-035-Q1-N1-B4
Method	BLASTX
NCBI GI	g2081612

BLAST score	289
E value	5.0e-26
Match length	68
% identity	81
NCBI Description	(D49714) delta-pyrroline-5-carboxylate synthetase [Oryza sativa]
Seq. No.	297731
Seq. ID	LIB3150-035-Q1-N1-B8
Method	BLASTX
NCBI GI	g231536
BLAST score	378
E value	2.0e-36
Match length	128
% identity	64
NCBI Description	CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir_S22399 leucyl aminopeptidase (EC 3.4.11.1) - <i>Arabidopsis thaliana</i> >gi_16394_emb_CAA45040 (X63444) leucine aminopeptidase [<i>Arabidopsis thaliana</i>] >gi_4115380 (AC005967) putative leucine aminopeptidase [<i>Arabidopsis thaliana</i>]
Seq. No.	297732
Seq. ID	LIB3150-035-Q1-N1-B9
Method	BLASTN
NCBI GI	g998429
BLAST score	45
E value	4.0e-16
Match length	126
% identity	52
NCBI Description	GRF1=general regulatory factor [Zea mays, XL80, Genomic, 5348 nt]
Seq. No.	297733
Seq. ID	LIB3150-035-Q1-N1-D9
Method	BLASTX
NCBI GI	g4510346
BLAST score	273
E value	4.0e-24
Match length	73
% identity	71
NCBI Description	(AC006921) hypothetical protein [<i>Arabidopsis thaliana</i>]
Seq. No.	297734
Seq. ID	LIB3150-035-Q1-N1-E12
Method	BLASTX
NCBI GI	g1708777
BLAST score	148
E value	1.0e-09
Match length	101
% identity	37
NCBI Description	(Z83202) potassium channel [<i>Arabidopsis thaliana</i>] >gi_3063705_emb_CAA18596.1 (AL022537) potassium channel protein [<i>Arabidopsis thaliana</i>] >gi_4090537 (U73325) K ⁺ inward rectifying channel protein [<i>Arabidopsis thaliana</i>] >gi_4098949 (U81239) K ⁺ inward rectifying channel

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[Arabidopsis thaliana]

Seq. No. 297735
Seq. ID LIB3150-035-Q1-N1-E3
Method BLASTN
NCBI GI g1296954
BLAST score 48
E value 5.0e-18
Match length 83
% identity 89
NCBI Description O.sativa mRNA for novel protein, osr40cl

Seq. No. 297736
Seq. ID LIB3150-035-Q1-N1-E4
Method BLASTX
NCBI GI g1658313
BLAST score 227
E value 7.0e-19
Match length 86
% identity 41
NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 297737
Seq. ID LIB3150-035-Q1-N1-E9
Method BLASTX
NCBI GI g118104
BLAST score 283
E value 3.0e-25
Match length 109
% identity 56
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 297738
Seq. ID LIB3150-035-Q1-N1-F10
Method BLASTX
NCBI GI g2828012
BLAST score 255
E value 3.0e-22
Match length 67
% identity 67
NCBI Description (AF036891) starch synthase I precursor [Zea mays]

Seq. No. 297739
Seq. ID LIB3150-035-Q1-N1-G3
Method BLASTN
NCBI GI g168704
BLAST score 59
E value 9.0e-25
Match length 86
% identity 95
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 297740

Q9E2E
E2E2E
E2E2E
E2E2E
E2E2E

Seq. ID LIB3150-036-Q1-N1-A8
Method BLASTX
NCBI GI g2668742
BLAST score 239
E value 9.0e-26
Match length 70
% identity 91
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 297741
Seq. ID LIB3150-036-Q1-N1-B1
Method BLASTX
NCBI GI g1666234
BLAST score 157
E value 1.0e-10
Match length 40
% identity 80
NCBI Description (U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin [Pisum sativum]

Seq. No. 297742
Seq. ID LIB3150-036-Q1-N1-E6
Method BLASTX
NCBI GI g4558664
BLAST score 441
E value 7.0e-44
Match length 122
% identity 63
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297743
Seq. ID LIB3150-036-Q1-N1-G12
Method BLASTX
NCBI GI g4160346
BLAST score 218
E value 1.0e-17
Match length 84
% identity 51
NCBI Description (AL035216) nucleolar protein involved in pre-rRNA processing [Schizosaccharomyces pombe]

Seq. No. 297744
Seq. ID LIB3150-037-Q1-N1-A6
Method BLASTX
NCBI GI g135535
BLAST score 452
E value 2.0e-45
Match length 110
% identity 82
NCBI Description T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
(CCT-ALPHA) >gi_322602_pir_JN0448 t-complex polypeptide
Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955
(D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana]

Seq. No. 297745

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Seq. ID LIB3150-037-Q1-N1-B4
Method BLASTN
NCBI GI g2645165
BLAST score 69
E value 1.0e-30
Match length 85
% identity 95
NCBI Description Oryza sativa mRNA, similar to ribosomal protein

Seq. No. 297746
Seq. ID LIB3150-037-Q1-N1-B5
Method BLASTX
NCBI GI g3395430
BLAST score 154
E value 2.0e-10
Match length 87
% identity 34
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297747
Seq. ID LIB3150-037-Q1-N1-C1
Method BLASTX
NCBI GI g4512659
BLAST score 409
E value 4.0e-40
Match length 116
% identity 70
NCBI Description (AC006931) putative protein kinase [Arabidopsis thaliana]
>gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [Arabidopsis thaliana]

Seq. No. 297748
Seq. ID LIB3150-037-Q1-N1-H1
Method BLASTX
NCBI GI g2624328
BLAST score 150
E value 6.0e-10
Match length 65
% identity 45
NCBI Description (AJ002894) OsGRP2 [Oryza sativa]

Seq. No. 297749
Seq. ID LIB3150-037-Q1-N1-H8
Method BLASTX
NCBI GI g1184774
BLAST score 199
E value 6.0e-16
Match length 55
% identity 73
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 297750
Seq. ID LIB3150-038-Q1-N1-A7
Method BLASTX
NCBI GI g1351974
BLAST score 326

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E value	2.0e-30
Match length	89
% identity	76
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1076788_pir_S49325 ADP-ribosylation factor - maize >gi_1076789_pir_S53486 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_(X80042) ADP-ribosylation factor [Zea mays]
Seq. No.	297751
Seq. ID	LIB3150-038-Q1-N1-C5
Method	BLASTX
NCBI GI	g462243
BLAST score	325
E value	4.0e-30
Match length	88
% identity	77
NCBI Description	HISTONE H4 >gi_421921_pir_S32769 histone H4 - tomato >gi_297150_emb_CAA48923_(X69179) histone H4 [Lycopersicon esculentum] >gi_297152_emb_CAA48924_(X69180) histone H4 [Lycopersicon esculentum] >gi_2746721 (AF038387) histone H4 [Capsicum annuum]
Seq. No.	297752
Seq. ID	LIB3150-038-Q1-N1-C6
Method	BLASTX
NCBI GI	g140496
BLAST score	152
E value	6.0e-10
Match length	117
% identity	30
NCBI Description	HYPOTHETICAL 42.5 KD PROTEIN IN TSM1-ARE1 INTERGENIC REGION >gi_83226_pir_S19457 probable membrane protein YCR044c - yeast (Saccharomyces cerevisiae) >gi_1907186_emb_CAA42292_(X59720) YCR044c, len:357 [Saccharomyces cerevisiae]
Seq. No.	297753
Seq. ID	LIB3150-038-Q1-N1-D5
Method	BLASTX
NCBI GI	g3914423
BLAST score	207
E value	6.0e-17
Match length	54
% identity	74
NCBI Description	PROFILIN 4 >gi_2642324 (AF032370) profilin [Zea mays]
Seq. No.	297754
Seq. ID	LIB3150-038-Q1-N1-F3
Method	BLASTX
NCBI GI	g2642159
BLAST score	191
E value	9.0e-15
Match length	86
% identity	49
NCBI Description	(AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]

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Seq. No. 297755
Seq. ID LIB3150-038-Q1-N1-F5
Method BLASTX
NCBI GI g4581156
BLAST score 192
E value 2.0e-17
Match length 109
% identity 52
NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]

Seq. No. 297756
Seq. ID LIB3150-038-Q1-N1-F8
Method BLASTX
NCBI GI g533082
BLAST score 288
E value 6.0e-26
Match length 103
% identity 56
NCBI Description (U07552) delta-9 stearoyl-acyl carrier protein desaturase [Thunbergia alata]

Seq. No. 297757
Seq. ID LIB3150-038-Q1-N1-H9
Method BLASTX
NCBI GI g3413717
BLAST score 160
E value 5.0e-11
Match length 65
% identity 46
NCBI Description (AC004747) unknown protein [Arabidopsis thaliana]
>gi_3643590 (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 297758
Seq. ID LIB3150-039-Q1-N1-A12
Method BLASTX
NCBI GI g2668742
BLAST score 330
E value 5.0e-31
Match length 79
% identity 86
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 297759
Seq. ID LIB3150-039-Q1-N1-B6
Method BLASTN
NCBI GI g22272
BLAST score 63
E value 4.0e-27
Match length 175
% identity 84
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 297760
Seq. ID LIB3150-039-Q1-N1-E10
Method BLASTX

SEQUENCE DEDUCTION

NCBI GI	g2459445
BLAST score	168
E value	7.0e-12
Match length	66
% identity	41
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]
Seq. No.	297761
Seq. ID	LIB3150-039-Q1-N1-E11
Method	BLASTX
NCBI GI	g1184776
BLAST score	530
E value	3.0e-54
Match length	132
% identity	79
NCBI Description	(U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]
Seq. No.	297762
Seq. ID	LIB3150-039-Q1-N1-E2
Method	BLASTX
NCBI GI	g3249113
BLAST score	157
E value	6.0e-11
Match length	66
% identity	52
NCBI Description	(AC003114) Strong similarity to kinesin homolog IG002P16.12 gb_2191180 from A. thaliana BAC gb_AF007270. [Arabidopsis thaliana]
Seq. No.	297763
Seq. ID	LIB3150-039-Q1-N1-F1
Method	BLASTX
NCBI GI	g4104321
BLAST score	168
E value	5.0e-12
Match length	101
% identity	34
NCBI Description	(AF034582) vesicle associated protein [Rattus norvegicus]
Seq. No.	297764
Seq. ID	LIB3150-040-Q1-N1-A10
Method	BLASTX
NCBI GI	g3913804
BLAST score	274
E value	3.0e-24
Match length	105
% identity	58
NCBI Description	HISTONE H2B.3 >gi_577825_emb_CAA49584_ (X69960) H2B histone [Zea mays]
Seq. No.	297765
Seq. ID	LIB3150-040-Q1-N1-B9
Method	BLASTX
NCBI GI	g2827524
BLAST score	198

09680
E value 2.0e-15
Match length 51
% identity 67
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 297766
Seq. ID LIB3150-040-Q1-N1-D8
Method BLASTX
NCBI GI g3341685
BLAST score 191
E value 1.0e-14
Match length 95
% identity 48
NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 297767
Seq. ID LIB3150-040-Q1-N1-F4
Method BLASTX
NCBI GI g1143864
BLAST score 193
E value 1.0e-14
Match length 108
% identity 43
NCBI Description (U28047) beta-glucosidase [Oryza sativa]

Seq. No. 297768
Seq. ID LIB3150-041-Q1-N1-A4
Method BLASTX
NCBI GI g1345588
BLAST score 222
E value 1.0e-31
Match length 127
% identity 61
NCBI Description 14-3-3-LIKE PROTEIN GF14-12 >gi_998432_bbs_164524
GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays,
XL80, Peptide, 261 aa]

Seq. No. 297769
Seq. ID LIB3150-041-Q1-N1-B9
Method BLASTN
NCBI GI g2511540
BLAST score 50
E value 2.0e-19
Match length 130
% identity 85
NCBI Description Oryza sativa DNA-binding protein GBP16 (Rgbp16) mRNA,
complete cds

Seq. No. 297770
Seq. ID LIB3150-041-Q1-N1-D7
Method BLASTX
NCBI GI g3335336
BLAST score 266
E value 2.0e-25
Match length 127
% identity 54
NCBI Description (AC004512) Contains similarity to DnaJ gene YM8520.10

gb_825566 from from S. cerevisiae cosmid gb_Z49705. ESTs
gb_Z47720 and gb_Z29879 come from this gene. [Arabidopsis
thaliana]

Seq. No. 297771
Seq. ID LIB3150-041-Q1-N1-H8
Method BLASTX
NCBI GI g3915826
BLAST score 166
E value 1.0e-11
Match length 33
% identity 94
NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 297772
Seq. ID LIB3150-042-Q1-N1-B2
Method BLASTX
NCBI GI g3024738
BLAST score 277
E value 2.0e-24
Match length 135
% identity 43
NCBI Description TYPE II DNA TOPOISOMERASE VI SUBUNIT A
>gi_1926404_emb_CAA71605 (Y10582) type II DNA
topoisomerase subunit A [Sulfolobus shibatae]

Seq. No. 297773
Seq. ID LIB3150-042-Q1-N1-B9
Method BLASTX
NCBI GI g3080437
BLAST score 176
E value 1.0e-12
Match length 112
% identity 43
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 297774
Seq. ID LIB3150-042-Q1-N1-C10
Method BLASTX
NCBI GI g4519539
BLAST score 320
E value 8.0e-30
Match length 98
% identity 64
NCBI Description (AB016256) NAD-dependent sorbitol dehydrogenase [Malus
domestica]

Seq. No. 297775
Seq. ID LIB3150-042-Q1-N1-C11
Method BLASTX
NCBI GI g82694
BLAST score 336
E value 1.0e-31
Match length 106
% identity 69
NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) 2 -
maize (fragment) >gi_293889 (L13432)

glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 297776
Seq. ID LIB3150-042-Q1-N1-C8
Method BLASTX
NCBI GI g2459420
BLAST score 200
E value 5.0e-16
Match length 53
% identity 79
NCBI Description (AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]

Seq. No. 297777
Seq. ID LIB3150-042-Q1-N1-D4
Method BLASTX
NCBI GI g3201611
BLAST score 145
E value 5.0e-09
Match length 42
% identity 64
NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]

Seq. No. 297778
Seq. ID LIB3150-042-Q1-N1-E2
Method BLASTX
NCBI GI g135411
BLAST score 305
E value 2.0e-52
Match length 106
% identity 98
NCBI Description TUBULIN ALPHA-2 CHAIN >gi_82732_pir_S15772 tubulin alpha-2 chain - maize >gi_22148_emb_CAA33733_ (X15704)
alpha2-tubulin [Zea mays]

Seq. No. 297779
Seq. ID LIB3150-042-Q1-N1-E3
Method BLASTX
NCBI GI g141616
BLAST score 254
E value 6.0e-22
Match length 88
% identity 57
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 297780
Seq. ID LIB3150-042-Q1-N1-E4
Method BLASTX
NCBI GI g100925
BLAST score 155
E value 9.0e-11
Match length 49
% identity 59
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_ (X58197) 27kDa storage protein, zein [Zea mays]

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Seq. No.	297781
Seq. ID	LIB3150-042-Q1-N1-E9
Method	BLASTX
NCBI GI	g1346109
BLAST score	254
E value	4.0e-22
Match length	91
% identity	59
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231) RWD [Oryza sativa]
Seq. No.	297782
Seq. ID	LIB3150-042-Q1-N1-G10
Method	BLASTX
NCBI GI	g310317
BLAST score	330
E value	8.0e-31
Match length	110
% identity	59
NCBI Description	(L19598) beta-tubulin [Oryza sativa]
Seq. No.	297783
Seq. ID	LIB3150-042-Q1-N1-G11
Method	BLASTX
NCBI GI	g4415992
BLAST score	182
E value	1.0e-24
Match length	99
% identity	65
NCBI Description	(AF059288) beta-tubulin 2 [Eleusine indica]
Seq. No.	297784
Seq. ID	LIB3150-042-Q1-N1-H9
Method	BLASTN
NCBI GI	g2773153
BLAST score	62
E value	2.0e-26
Match length	90
% identity	92
NCBI Description	Oryza sativa abscisic acid- and stress-inducible protein (Asrl1) mRNA, complete cds
Seq. No.	297785
Seq. ID	LIB3150-043-Q1-N1-C10
Method	BLASTX
NCBI GI	g122070
BLAST score	388
E value	9.0e-38
Match length	82
% identity	95
NCBI Description	HISTONE H3 >gi_82483_pir_A25564 histone H3 - rice >gi_169793 (M15664) histone 3 [Oryza sativa] >gi_940018 (U25664) histone H3 [Oryza sativa]
Seq. No.	297786
Seq. ID	LIB3150-043-Q1-N1-E10

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Method	BLASTX
NCBI GI	g2554835
BLAST score	277
E value	3.0e-25
Match length	65
% identity	80
NCBI Description	Chain I, Acetohydroxy Acid Isomeroreductase Complexed With Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropylloxamate) >gi_2554836_pdb_1YVE_J Chain J, Acetohydroxy Acid Isomeroreductase Complexed With Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropylloxamate) >gi_2554837_pdb_1YVE_K Chain K, Acetohydroxy Acid Isomeroreductase Complexed With Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropylloxamate) >gi_2554838_pdb_1YVE_L Chain L, Acetohydroxy Acid Isomeroreductase Complexed With Nadph, Magnesium And Inhibitor Ipoha (N-Hydroxy-N-Isopropylloxamate)
Seq. No.	297787
Seq. ID	LIB3150-043-Q1-N1-E5
Method	BLASTX
NCBI GI	g121472
BLAST score	225
E value	1.0e-18
Match length	104
% identity	44
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea mays] >gi_168485_(M16066) glutelin-2 [Zea mays]
Seq. No.	297788
Seq. ID	LIB3150-043-Q1-N1-F3
Method	BLASTX
NCBI GI	g3927831
BLAST score	281
E value	5.0e-25
Match length	91
% identity	55
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]
Seq. No.	297789
Seq. ID	LIB3150-043-Q1-N1-G10
Method	BLASTX
NCBI GI	g1711567
BLAST score	194
E value	7.0e-25
Match length	92
% identity	62
NCBI Description	ELONGATION FACTOR 1-ALPHA 2 (EF-1-ALPHA-2) (STATIN S1) >gi_112321_pir_A40389 translation elongation factor eEF-1 alpha chain (clone pS1) - rat >gi_1083500_pir_JC2445 translation elongation factor eEF-1 alpha-like protein S1 -

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mouse >gi_206438 (M62751) statin-related protein [Rattus norvegicus] >gi_1220410 (L26479) elongation factor-1 alpha [Mus musculus]

Seq. No. 297790
Seq. ID LIB3150-043-Q1-N1-G7
Method BLASTX
NCBI GI g135411
BLAST score 441
E value 5.0e-44
Match length 106
% identity 82
NCBI Description TUBULIN ALPHA-2 CHAIN >gi_82732_pir_S15772 tubulin alpha-2 chain - maize >gi_22148_emb_CAA33733_ (X15704)
alpha2-tubulin [Zea mays]

Seq. No. 297791
Seq. ID LIB3150-044-Q1-N1-B10
Method BLASTN
NCBI GI g2104711
BLAST score 307
E value 1.0e-172
Match length 323
% identity 99
NCBI Description Zea mays endosperm specific protein mRNA, complete cds

Seq. No. 297792
Seq. ID LIB3150-044-Q1-N1-B11
Method BLASTN
NCBI GI g2104711
BLAST score 126
E value 1.0e-64
Match length 194
% identity 92
NCBI Description Zea mays endosperm specific protein mRNA, complete cds

Seq. No. 297793
Seq. ID LIB3150-044-Q1-N1-D11
Method BLASTX
NCBI GI g3163946
BLAST score 383
E value 7.0e-40
Match length 81
% identity 91
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No. 297794
Seq. ID LIB3150-044-Q1-N1-E5
Method BLASTX
NCBI GI g1173218
BLAST score 196
E value 1.0e-21
Match length 81
% identity 71
NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No. 297795
Seq. ID LIB3150-044-Q1-N1-E7
Method BLASTN
NCBI GI g168484
BLAST score 212
E value 1.0e-116
Match length 300
% identity 93
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 297796
Seq. ID LIB3150-044-Q1-N1-F3
Method BLASTX
NCBI GI g606751
BLAST score 172
E value 3.0e-12
Match length 60
% identity 57
NCBI Description (L34934) RNA binding protein [Drosophila melanogaster]

Seq. No. 297797
Seq. ID LIB3150-044-Q1-N1-F7
Method BLASTX
NCBI GI g129916
BLAST score 164
E value 1.0e-17
Match length 64
% identity 70
NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir_TVWTGY
phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
>gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
(AA 1 - 401) [Triticum aestivum]

Seq. No. 297798
Seq. ID LIB3150-045-Q1-N1-B1
Method BLASTN
NCBI GI g531057
BLAST score 41
E value 8.0e-14
Match length 85
% identity 87
NCBI Description Wheat mRNA for protein H2B-8, complete cds

Seq. No. 297799
Seq. ID LIB3150-045-Q1-N1-D2
Method BLASTX
NCBI GI g113621
BLAST score 150
E value 3.0e-10
Match length 45
% identity 69
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
>gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A

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cytoplasmic aldolase [Zea mays]

Seq. No. 297800
Seq. ID LIB3150-045-Q1-N1-D3
Method BLASTX
NCBI GI g3024506
BLAST score 200
E value 1.0e-15
Match length 79
% identity 54
NCBI Description RAS-RELATED PROTEIN RAB11A >gi_623582 (L29271) Nt-Rab11a gene product [Nicotiana tabacum]

Seq. No. 297801
Seq. ID LIB3150-045-Q1-N1-F1
Method BLASTN
NCBI GI g2345153
BLAST score 36
E value 6.0e-11
Match length 88
% identity 86
NCBI Description Zea mays ribosomal protein S4 (rps4) mRNA, complete cds

Seq. No. 297802
Seq. ID LIB3150-045-Q1-N1-F7
Method BLASTN
NCBI GI g434325
BLAST score 60
E value 3.0e-25
Match length 152
% identity 85
NCBI Description Z.mays mRNA gs1-2 for glutamine synthetase

Seq. No. 297803
Seq. ID LIB3150-045-Q1-N1-H2
Method BLASTN
NCBI GI g168425
BLAST score 35
E value 1.0e-10
Match length 59
% identity 90
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 297804
Seq. ID LIB3150-045-Q1-N1-H9
Method BLASTX
NCBI GI g1946355
BLAST score 210
E value 7.0e-30
Match length 122
% identity 57
NCBI Description (U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 297805
Seq. ID LIB3150-046-Q1-N1-A6

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Method	BLASTX
NCBI GI	g118104
BLAST score	188
E value	1.0e-14
Match length	37
% identity	97
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) - maize >gi_168461 (M55021) cyclophilin [Zea mays] >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
Seq. No.	297806
Seq. ID	LIB3150-046-Q1-N1-A9
Method	BLASTX
NCBI GI	g3845207
BLAST score	147
E value	2.0e-09
Match length	75
% identity	45
NCBI Description	(AE001400) asparaginyl-tRNA synthetase (OO, TP) [Plasmodium falciparum]
Seq. No.	297807
Seq. ID	LIB3150-046-Q1-N1-B1
Method	BLASTX
NCBI GI	g141616
BLAST score	215
E value	2.0e-24
Match length	107
% identity	62
NCBI Description	ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3) >gi_168662 (M12147) 15 kDa zein protein [Zea mays]
Seq. No.	297808
Seq. ID	LIB3150-046-Q1-N1-B8
Method	BLASTX
NCBI GI	g4204309
BLAST score	255
E value	6.0e-22
Match length	94
% identity	56
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]
Seq. No.	297809
Seq. ID	LIB3150-046-Q1-N1-C3
Method	BLASTX
NCBI GI	g1184774
BLAST score	524
E value	2.0e-53
Match length	119
% identity	88
NCBI Description	(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]
Seq. No.	297810

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Seq. ID LIB3150-046-Q1-N1-E6
Method BLASTX
NCBI GI g3413165
BLAST score 193
E value 2.0e-15
Match length 74
% identity 62
NCBI Description (AJ010224) glyceraldehyde 3-phosphate dehydrogenase, cytosolic [Cicer arietinum]

Seq. No. 297811
Seq. ID LIB3150-046-Q1-N1-H11
Method BLASTN
NCBI GI g22516
BLAST score 97
E value 4.0e-47
Match length 177
% identity 89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 297812
Seq. ID LIB3150-046-Q1-N1-H3
Method BLASTN
NCBI GI g4874248
BLAST score 39
E value 2.0e-12
Match length 51
% identity 94
NCBI Description Zea mays defender against cell death 1 (dad1) mRNA, partial cds

Seq. No. 297813
Seq. ID LIB3150-047-Q1-N1-E9
Method BLASTX
NCBI GI g2498077
BLAST score 154
E value 2.0e-23
Match length 87
% identity 76
NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase [Saccharum officinarum]

Seq. No. 297814
Seq. ID LIB3150-047-Q1-N1-F11
Method BLASTX
NCBI GI g123620
BLAST score 174
E value 6.0e-13
Match length 98
% identity 52
NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir_S14950
heat shock cognate protein 70 - tomato
>gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate 70 [Lycopersicon esculentum]

Seq. No. 297815

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Seq. ID	LIB3150-047-Q1-N1-F4
Method	BLASTX
NCBI GI	g3122386
BLAST score	254
E value	4.0e-22
Match length	62
% identity	79
NCBI Description	WD-40 REPEAT PROTEIN MSI1 >gi_2394227 (AF016845) WD-40 repeat protein [Lycopersicon esculentum]
Seq. No.	297816
Seq. ID	LIB3150-047-Q1-N1-H7
Method	BLASTX
NCBI GI	g4586111
BLAST score	194
E value	8.0e-15
Match length	82
% identity	57
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]
Seq. No.	297817
Seq. ID	LIB3150-048-Q1-N1-B10
Method	BLASTX
NCBI GI	g2245136
BLAST score	154
E value	9.0e-11
Match length	64
% identity	44
NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]
Seq. No.	297818
Seq. ID	LIB3150-048-Q1-N1-C7
Method	BLASTX
NCBI GI	g1184776
BLAST score	271
E value	3.0e-24
Match length	67
% identity	82
NCBI Description	(U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]
Seq. No.	297819
Seq. ID	LIB3150-048-Q1-N1-C9
Method	BLASTX
NCBI GI	g1184774
BLAST score	248
E value	6.0e-32
Match length	78
% identity	95
NCBI Description	(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]
Seq. No.	297820
Seq. ID	LIB3150-048-Q1-N1-D1
Method	BLASTN
NCBI GI	g168606

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BLAST score	53
E value	3.0e-21
Match length	104
% identity	88
NCBI Description	Zea mays mitochondrial Rieske Fe-S protein mRNA, complete cds
Seq. No.	297821
Seq. ID	LIB3150-048-Q1-N1-F2
Method	BLASTX
NCBI GI	g4104060
BLAST score	316
E value	3.0e-29
Match length	112
% identity	55
NCBI Description	(AF031231) S222 [Triticum aestivum]
Seq. No.	297822
Seq. ID	LIB3150-048-Q1-N1-H10
Method	BLASTN
NCBI GI	g168419
BLAST score	64
E value	1.0e-27
Match length	108
% identity	90
NCBI Description	Maize (Z.mays) aldolase mRNA, complete cds
Seq. No.	297823
Seq. ID	LIB3150-048-Q1-N1-H5
Method	BLASTX
NCBI GI	g1076800
BLAST score	317
E value	3.0e-29
Match length	68
% identity	90
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme - maize >gi_600116_emb_CAA84406 (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi_1096503_prf_2111423A ascorbate peroxidase [Zea mays]
Seq. No.	297824
Seq. ID	LIB3150-049-Q1-N1-A3
Method	BLASTX
NCBI GI	g2944417
BLAST score	318
E value	2.0e-29
Match length	98
% identity	64
NCBI Description	(AF049881) peroxidase FLXPER4 [Linum usitatissimum]
Seq. No.	297825
Seq. ID	LIB3150-049-Q1-N1-A5
Method	BLASTX
NCBI GI	g1184776
BLAST score	377
E value	3.0e-36
Match length	107

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% identity 75
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC4 [Zea mays]

Seq. No. 297826
Seq. ID LIB3150-049-Q1-N1-C7
Method BLASTX
NCBI GI g2286151
BLAST score 326
E value 2.0e-30
Match length 111
% identity 64
NCBI Description (AF007580) translation initiation factor [Zea mays]

Seq. No. 297827
Seq. ID LIB3150-049-Q1-N1-C9
Method BLASTX
NCBI GI g1345587
BLAST score 324
E value 4.0e-32
Match length 97
% identity 79
NCBI Description 14-3-3-LIKE PROTEIN GF14-6 >gi_998430_bbs_164522 (S77133)
GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261
aa] [Zea mays]

Seq. No. 297828
Seq. ID LIB3150-049-Q1-N1-D4
Method BLASTX
NCBI GI g118104
BLAST score 479
E value 3.0e-48
Match length 123
% identity 76
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 297829
Seq. ID LIB3150-049-Q1-N1-E1
Method BLASTX
NCBI GI g2464864
BLAST score 242
E value 1.0e-20
Match length 96
% identity 47
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 297830
Seq. ID LIB3150-049-Q1-N1-E12
Method BLASTX
NCBI GI g4539006
BLAST score 424
E value 7.0e-42
Match length 123

Q10920
Q10921
Q10922
Q10923
Q10924
Q10925
Q10926
Q10927
Q10928

% identity 67
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 297831
Seq. ID LIB3150-049-Q1-N1-E7
Method BLASTX
NCBI GI g135411
BLAST score 514
E value 2.0e-52
Match length 109
% identity 90
NCBI Description TUBULIN ALPHA-2 CHAIN >gi_82732_pir_S15772 tubulin alpha-2 chain - maize >gi_22148_emb_CAA33733_ (X15704)
alpha2-tubulin [Zea mays]

Seq. No. 297832
Seq. ID LIB3150-049-Q1-N1-F11
Method BLASTX
NCBI GI g4193320
BLAST score 405
E value 1.0e-39
Match length 119
% identity 67
NCBI Description (AF045473) histone deacetylase [Zea mays]

Seq. No. 297833
Seq. ID LIB3150-049-Q1-N1-F9
Method BLASTX
NCBI GI g134598
BLAST score 471
E value 2.0e-47
Match length 98
% identity 100
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)

Seq. No. 297834
Seq. ID LIB3150-049-Q1-N1-G4
Method BLASTX
NCBI GI g4039155
BLAST score 162
E value 4.0e-11
Match length 110
% identity 44
NCBI Description (AF104258) putative copper-inducible 35.6 kDa protein
[Festuca rubra]

Seq. No. 297835
Seq. ID LIB3150-049-Q1-N1-G5
Method BLASTX
NCBI GI g112994
BLAST score 262
E value 8.0e-23
Match length 82
% identity 71
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
>gi_82685_pir_S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

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ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 297836
Seq. ID LIB3150-050-Q1-N1-B9
Method BLASTX
NCBI GI g3242789
BLAST score 472
E value 2.0e-47
Match length 130
% identity 62
NCBI Description (AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]

Seq. No. 297837
Seq. ID LIB3150-050-Q1-N1-C11
Method BLASTX
NCBI GI g1709619
BLAST score 259
E value 1.0e-22
Match length 99
% identity 56
NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
(GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
>gi_2146814_pir_S69181 protein disulfide isomerase (EC
5.3.4.1) precursor - maize >gi_625148 (L39014) protein
disulfide isomerase [Zea mays]

Seq. No. 297838
Seq. ID LIB3150-050-Q1-N1-D11
Method BLASTX
NCBI GI g1321661
BLAST score 265
E value 2.0e-23
Match length 60
% identity 85
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 297839
Seq. ID LIB3150-050-Q1-N1-D8
Method BLASTX
NCBI GI g1350986
BLAST score 202
E value 5.0e-16
Match length 69
% identity 64
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
>gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]

Seq. No. 297840
Seq. ID LIB3150-050-Q1-N1-D9
Method BLASTX
NCBI GI g629861
BLAST score 209
E value 3.0e-21

Q36301-36302

Match length 76
% identity 80
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 297841
Seq. ID LIB3150-050-Q1-N1-E6
Method BLASTX
NCBI GI g4585900
BLAST score 228
E value 7.0e-19
Match length 76
% identity 68
NCBI Description (AC007133) putative histone H2A [Arabidopsis thaliana]

Seq. No. 297842
Seq. ID LIB3150-050-Q1-N1-F1
Method BLASTN
NCBI GI g3015620
BLAST score 39
E value 1.0e-12
Match length 63
% identity 90
NCBI Description Zea mays low molecular weight heat shock protein precursor
(hsp22) mRNA, nuclear gene encoding mitochondrial protein,
complete cds

Seq. No. 297843
Seq. ID LIB3150-050-Q1-N1-F7
Method BLASTX
NCBI GI g4455283
BLAST score 178
E value 1.0e-17
Match length 97
% identity 55
NCBI Description (AL035527) L1 specific homeobox gene ATML1/ovule-specific
homeobox protein A20 [Arabidopsis thaliana]

Seq. No. 297844
Seq. ID LIB3150-050-Q1-N1-G10
Method BLASTX
NCBI GI g1658313
BLAST score 206
E value 2.0e-23
Match length 85
% identity 34
NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 297845
Seq. ID LIB3150-050-Q1-N1-G11
Method BLASTN
NCBI GI g260552
BLAST score 34
E value 1.0e-09
Match length 38
% identity 97
NCBI Description Wx (wx-B2) {transposable element Tourist-Zm1} [Zea

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mays=corn, Transposon Mutant, 150 nt]

Seq. No.	297846
Seq. ID	LIB3150-050-Q1-N1-H11
Method	BLASTX
NCBI GI	g1885348
BLAST score	159
E value	3.0e-11
Match length	47
% identity	77
NCBI Description	(X91515) histone.H4 [Trichogramma caceociae]
Seq. No.	297847
Seq. ID	LIB3150-050-Q1-N1-H9
Method	BLASTX
NCBI GI	g1346251
BLAST score	208
E value	2.0e-16
Match length	53
% identity	79
NCBI Description	HISTONE H2B.4 >gi_577819_emb_CAA49585_ (X69961) H2B histone [Zea mays]
Seq. No.	297848
Seq. ID	LIB3150-051-Q1-N1-B9
Method	BLASTX
NCBI GI	g1709000
BLAST score	422
E value	1.0e-41
Match length	88
% identity	92
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine synthetase [Hordeum vulgare]
Seq. No.	297849
Seq. ID	LIB3150-051-Q1-N1-C10
Method	BLASTX
NCBI GI	g133961
BLAST score	260
E value	1.0e-22
Match length	68
% identity	78
NCBI Description	40S RIBOSOMAL PROTEIN S4 (OMNIPOTENT SUPPRESSOR PROTEIN SUP44) (RP12) (S2E) >gi_70888_pir_R3BYS2 ribosomal protein S2.e - yeast (Saccharomyces cerevisiae) >gi_172793_ (M59375) ribosomal protein S4 [Saccharomyces cerevisiae] >gi_1322683_emb_CAA96831_ (Z72645) ORF YGL123w [Saccharomyces cerevisiae] >gi_1628451_emb_CAA63835_ (X94106) SUP44 [Saccharomyces cerevisiae]
Seq. No.	297850
Seq. ID	LIB3150-051-Q1-N1-C7
Method	BLASTX
NCBI GI	g3334756
BLAST score	224

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E value	2.0e-18
Match length	88
% identity	57
NCBI Description	(Y16672) putative arginine/serine-rich splicing factor [Medicago sativa]
Seq. No.	297851
Seq. ID	LIB3150-051-Q1-N1-D5
Method	BLASTX
NCBI GI	g730536
BLAST score	529
E value	2.0e-54
Match length	103
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal protein subunit L17 [Nicotiana tabacum]
Seq. No.	297852
Seq. ID	LIB3150-051-Q1-N1-G3
Method	BLASTX
NCBI GI	g1184776
BLAST score	598
E value	3.0e-62
Match length	114
% identity	100
NCBI Description	(U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]
Seq. No.	297853
Seq. ID	LIB3150-051-Q1-N1-H6
Method	BLASTX
NCBI GI	g2293566
BLAST score	185
E value	2.0e-16
Match length	53
% identity	96
NCBI Description	(AF012896) ADP-ribosylation factor 1 [Oryza sativa]
Seq. No.	297854
Seq. ID	LIB3150-052-Q1-N1-B2
Method	BLASTX
NCBI GI	g122087
BLAST score	471
E value	3.0e-47
Match length	120
% identity	81
NCBI Description	HISTONE H3 >gi_81849_pir_S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir_A26014 histone H3 - wheat >gi_19607_emb_CAA31964 (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965 (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451 (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]
Seq. No.	297855
Seq. ID	LIB3150-052-Q1-N1-B5

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Method	BLASTX
NCBI GI	g1184774
BLAST score	594
E value	1.0e-61
Match length	114
% identity	99
NCBI Description	(U45856) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]
Seq. No.	297856
Seq. ID	LIB3150-052-Q1-N1-C2
Method	BLASTN
NCBI GI	g22144
BLAST score	171
E value	1.0e-91
Match length	218
% identity	96
NCBI Description	Maize anaerobically regulated gene for fructose bisphosphate aldolase (EC 4.1.2.13)
Seq. No.	297857
Seq. ID	LIB3150-052-Q1-N1-E12
Method	BLASTX
NCBI GI	g131772
BLAST score	378
E value	2.0e-36
Match length	109
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) >gi_82723_pir_A30097 ribosomal protein S14 (clone MCH1) - maize
Seq. No.	297858
Seq. ID	LIB3150-052-Q1-N1-G11
Method	BLASTX
NCBI GI	g122022
BLAST score	157
E value	1.0e-10
Match length	60
% identity	60
NCBI Description	HISTONE H2B >gi_283025_pir_S22323 histone H2B - wheat >gi_21801_emb_CAA42530_ (X59873) histone H2B [Triticum aestivum]
Seq. No.	297859
Seq. ID	LIB3150-052-Q1-N1-G3
Method	BLASTX
NCBI GI	g133867
BLAST score	493
E value	6.0e-50
Match length	120
% identity	78
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]
Seq. No.	297860

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Seq. ID	LIB3150-053-Q1-N1-A6
Method	BLASTX
NCBI GI	g70644
BLAST score	592
E value	1.0e-61
Match length	125
% identity	18
NCBI Description	ubiquitin precursor - common sunflower (fragment)
Seq. No.	297861
Seq. ID	LIB3150-053-Q1-N1-A7
Method	BLASTX
NCBI GI	g3914402
BLAST score	247
E value	3.0e-21
Match length	97
% identity	57
NCBI Description	PROTOPORPHYRINOGEN OXIDASE, CHLOROPLAST PRECURSOR (PPO I) (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME I) (PPX I) >gi_2370333_emb_CAA73865_ (Y13465) protoporphyrinogen oxidase [Nicotiana tabacum]
Seq. No.	297862
Seq. ID	LIB3150-053-Q1-N1-D10
Method	BLASTX
NCBI GI	g120670
BLAST score	495
E value	3.0e-50
Match length	121
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_100879_pir_S06879 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C - maize >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]
Seq. No.	297863
Seq. ID	LIB3150-053-Q1-N1-D8
Method	BLASTX
NCBI GI	g266398
BLAST score	169
E value	3.0e-12
Match length	62
% identity	55
NCBI Description	TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR INHIBITOR) (CHFI) >gi_68849_pir_TIZM1 trypsin/factor XIIa inhibitor precursor - maize >gi_22327_emb_CAA37998_ (X54064) corn Hageman factor inhibitor [Zea mays]
Seq. No.	297864
Seq. ID	LIB3150-053-Q1-N1-E12
Method	BLASTX
NCBI GI	g2864625
BLAST score	522
E value	2.0e-53
Match length	112
% identity	86
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Q36304704

Seq. No. 297865
Seq. ID LIB3150-053-Q1-N1-E9
Method BLASTX
NCBI GI g70644
BLAST score 291
E value 1.0e-26
Match length 94
% identity 13
NCBI Description ubiquitin precursor - common sunflower (fragment)

Seq. No. 297866
Seq. ID LIB3150-054-Q1-N1-A10
Method BLASTX
NCBI GI g4506491
BLAST score 281
E value 4.0e-25
Match length 89
% identity 63
NCBI Description replication factor C (activator 1) 4 (37kD)
>gi_1703052_sp_P35249_AC12_HUMAN ACTIVATOR 1 37 KD SUBUNIT
(REPLICATION FACTOR C 37 KD SUBUNIT) (A1 37 KD SUBUNIT)
(RFC-C 37 KD SUBUNIT) (RFC37) >gi_1498256 (M87339)
replication factor C, 37-kDa subunit [Homo sapiens]

Seq. No. 297867
Seq. ID LIB3150-054-Q1-N1-B2
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 297868
Seq. ID LIB3150-054-Q1-N1-D7
Method BLASTX
NCBI GI g1654140
BLAST score 340
E value 5.0e-32
Match length 101
% identity 57
NCBI Description (U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No. 297869
Seq. ID LIB3150-054-Q1-N1-D8
Method BLASTX
NCBI GI g3548802
BLAST score 149
E value 4.0e-10
Match length 41
% identity 66
NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]
>gi_4335769_gb_AAD17446_ (AC006284) putative axil protein
[Nicotiana tabacum] [Arabidopsis thaliana]

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Seq. No.	297870
Seq. ID	LIB3150-054-Q1-N1-G11
Method	BLASTX
NCBI GI	g399854
BLAST score	241
E value	2.0e-20
Match length	71
% identity	73
NCBI Description	HISTONE H2B.2 >gi_283042_pir_S28049 histone H2B - maize >gi_22325_emb_CAA40565_(X57313) H2B histone [Zea mays]
Seq. No.	297871
Seq. ID	LIB3150-054-Q1-N1-G5
Method	BLASTX
NCBI GI	g2492504
BLAST score	156
E value	1.0e-10
Match length	108
% identity	41
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_1669660_emb_CAA70565_(Y09396) protein of AAA family [Capsicum annuum]
Seq. No.	297872
Seq. ID	LIB3150-054-Q1-N1-G6
Method	BLASTX
NCBI GI	g3608145
BLAST score	186
E value	6.0e-14
Match length	62
% identity	63
NCBI Description	(AC005314) hypothetical protein [Arabidopsis thaliana]
Seq. No.	297873
Seq. ID	LIB3150-054-Q1-N1-H10
Method	BLASTX
NCBI GI	g4519539
BLAST score	182
E value	1.0e-13
Match length	64
% identity	56
NCBI Description	(AB016256) NAD-dependent sorbitol dehydrogenase [Malus domestica]
Seq. No.	297874
Seq. ID	LIB3150-055-Q1-N1-A9
Method	BLASTX
NCBI GI	g2266666
BLAST score	380
E value	1.0e-36
Match length	82
% identity	83
NCBI Description	(Y14202) hypothetical protein [Hordeum vulgare]
Seq. No.	297875
Seq. ID	LIB3150-055-Q1-N1-D10
Method	BLASTN

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NCBI GI	g1256711
BLAST score	74
E value	1.0e-33
Match length	224
% identity	82
NCBI Description	Zea mays O-methyltransferase (OMT) gene, complete cds
Seq. No.	297876
Seq. ID	LIB3150-056-Q1-N1-A3
Method	BLASTN
NCBI GI	g340933
BLAST score	60
E value	3.0e-25
Match length	72
% identity	96
NCBI Description	Zea mays 10-kDa zein gene, complete cds
Seq. No.	297877
Seq. ID	LIB3150-056-Q1-N1-B6
Method	BLASTX
NCBI GI	g1666173
BLAST score	430
E value	1.0e-42
Match length	92
% identity	90
NCBI Description	(Y09106) transcription factor [Nicotiana plumbaginifolia]
Seq. No.	297878
Seq. ID	LIB3150-056-Q1-N1-D3
Method	BLASTX
NCBI GI	g119355
BLAST score	495
E value	3.0e-50
Match length	99
% identity	99
NCBI Description	ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1) >gi_100869_pir_S16257 phosphopyruvate hydratase (EC 4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase [Zea mays]
Seq. No.	297879
Seq. ID	LIB3150-056-Q1-N1-D9
Method	BLASTX
NCBI GI	g464705
BLAST score	162
E value	3.0e-11
Match length	32
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S13 >gi_419802_pir_S30146 ribosomal protein S13.e - maize >gi_288059_emb_CAA44311_ (X62455) cytoplasmatic ribosomal protein S13 [Zea mays]
Seq. No.	297880
Seq. ID	LIB3150-057-Q1-N1-A6
Method	BLASTX
NCBI GI	g1632831

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BLAST score	171
E value	1.0e-12
Match length	36
% identity	89
NCBI Description	(Z49698) orf [Ricinus communis]
Seq. No.	297881
Seq. ID	LIB3150-057-Q1-N1-B5
Method	BLASTX
NCBI GI	g2642648
BLAST score	289
E value	4.0e-26
Match length	67
% identity	88
NCBI Description	(AF033852) cytosolic heat shock 70 protein; HSC70-3 [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617) cytosolic heat shock 70 protein [Spinacia oleracea]
Seq. No.	297882
Seq. ID	LIB3150-057-Q1-N1-B6
Method	BLASTX
NCBI GI	g4580990
BLAST score	170
E value	2.0e-14
Match length	96
% identity	48
NCBI Description	(AF120335) putative transposase [Arabidopsis thaliana]
Seq. No.	297883
Seq. ID	LIB3150-057-Q1-N1-B9
Method	BLASTX
NCBI GI	g2911067
BLAST score	160
E value	3.0e-11
Match length	80
% identity	46
NCBI Description	(AL021960) UV-damaged DNA-binding protein-like [Arabidopsis thaliana]
Seq. No.	297884
Seq. ID	LIB3150-057-Q1-N1-G10
Method	BLASTX
NCBI GI	g4056502
BLAST score	170
E value	3.0e-12
Match length	53
% identity	62
NCBI Description	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.	297885
Seq. ID	LIB3150-057-Q1-N1-H9
Method	BLASTX
NCBI GI	g2340947
BLAST score	301
E value	5.0e-28
Match length	59

% identity 100
 NCBI Description (X98497) ESR1g1 [Zea mays] >gi_2340951_emb_CAA68230_
 (X99968) ESR1g2 [Zea mays]

Seq. No. 297886
 Seq. ID LIB3150-058-Q1-N1-A3
 Method BLASTX
 NCBI GI g100857
 BLAST score 571
 E value 5.0e-59
 Match length 115
 % identity 97
 NCBI Description Bronze-2 protein - Maize

Seq. No. 297887
 Seq. ID LIB3150-058-Q1-N1-B1
 Method BLASTX
 NCBI GI g118104
 BLAST score 371
 E value 1.0e-35
 Match length 95
 % identity 76
 NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
 (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
 >gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
 maize >gi_168461 (M55021) cyclophilin [Zea mays]
 >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 297888
 Seq. ID LIB3150-058-Q1-N1-B11
 Method BLASTX
 NCBI GI g1620753
 BLAST score 156
 E value 2.0e-10
 Match length 63
 % identity 48
 NCBI Description (U72942) proteinase inhibitor [Oryza sativa]
 >gi_2829212_gb_AAC00503_ (AF044059) proteinase inhibitor
 [Oryza sativa]

Seq. No. 297889
 Seq. ID LIB3150-058-Q1-N1-C10
 Method BLASTX
 NCBI GI g3790100
 BLAST score 213
 E value 3.0e-17
 Match length 112
 % identity 49
 NCBI Description (AF095520) pyrophosphate-dependent phosphofructokinase beta
 subunit [Citrus X paradisi]

Seq. No. 297890
 Seq. ID LIB3150-058-Q1-N1-E11
 Method BLASTX
 NCBI GI g1184776
 BLAST score 176
 E value 5.0e-20

Match length 91
% identity 65
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC4 [Zea mays]

Seq. No. 297891
Seq. ID LIB3150-058-Q1-N1-F3
Method BLASTN
NCBI GI g3851527
BLAST score 54
E value 2.0e-21
Match length 141
% identity 85
NCBI Description Hordeum vulgare cultivar Bomi starch branching enzyme IIb
(sbeIIb) gene, nuclear gene encoding plastid protein,
partial cds

Seq. No. 297892
Seq. ID LIB3150-058-Q1-N1-G6
Method BLASTX
NCBI GI g2282584
BLAST score 457
E value 7.0e-46
Match length 103
% identity 83
NCBI Description (U76259) elongation factor 1-alpha [Zea mays]

Seq. No. 297893
Seq. ID LIB3150-059-Q1-N1-A8
Method BLASTX
NCBI GI g82705
BLAST score 264
E value 3.0e-23
Match length 74
% identity 80
NCBI Description lipid body-associated major protein L3 - maize (fragment)
>gi_168513 (M17225) major protein L3 [Zea mays]

Seq. No. 297894
Seq. ID LIB3150-059-Q1-N1-B10
Method BLASTX
NCBI GI g118104
BLAST score 341
E value 4.0e-34
Match length 97
% identity 77
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 297895
Seq. ID LIB3150-059-Q1-N1-C10
Method BLASTX
NCBI GI g1184776
BLAST score 569

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E value 7.0e-59
Match length 108
% identity 100
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]

Seq. No. 297896
Seq. ID LIB3150-059-Q1-N1-C11
Method BLASTX
NCBI GI g133867
BLAST score 258
E value 1.0e-22
Match length 83
% identity 64
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No. 297897
Seq. ID LIB3150-059-Q1-N1-C8
Method BLASTX
NCBI GI g134613
BLAST score 321
E value 9.0e-30
Match length 74
% identity 84
NCBI Description SUPEROXIDE DISMUTASE-2 (CU-ZN) >gi_82727_pir_A29077 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 2 - maize >gi_168620 (M54936) superoxide dismutase 2 [Zea mays] >gi_168622 (M15175) SOD2 protein [Zea mays]

Seq. No. 297898
Seq. ID LIB3150-059-Q1-N1-D10
Method BLASTX
NCBI GI g129916
BLAST score 238
E value 3.0e-20
Match length 60
% identity 80
NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir_TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum]

Seq. No. 297899
Seq. ID LIB3150-059-Q1-N1-D11
Method BLASTX
NCBI GI g3334138
BLAST score 269
E value 5.0e-28
Match length 94
% identity 66
NCBI Description CALnexin HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin [Glycine max]

Seq. No. 297900
Seq. ID LIB3150-059-Q1-N1-D12

Method BLASTX
NCBI GI g3983663
BLAST score 554
E value 4.0e-57
Match length 124
% identity 85
NCBI Description (AB011270) importin-beta1 [Oryza sativa]

Seq. No. 297901
Seq. ID LIB3150-059-Q1-N1-D6
Method BLASTN
NCBI GI g899607
BLAST score 50
E value 1.0e-19
Match length 94
% identity 58
NCBI Description Zea mays polyubiquitin (MubC5) mRNA, complete cds

Seq. No. 297902
Seq. ID LIB3150-060-Q1-N1-C2
Method BLASTX
NCBI GI g4056483
BLAST score 146
E value 1.0e-09
Match length 71
% identity 48
NCBI Description (AC005896) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297903
Seq. ID LIB3150-060-Q1-N1-C6
Method BLASTX
NCBI GI g2914700
BLAST score 261
E value 3.0e-23
Match length 58
% identity 84
NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No. 297904
Seq. ID LIB3150-060-Q1-N1-D10
Method BLASTX
NCBI GI g1184776
BLAST score 177
E value 1.0e-17
Match length 61
% identity 85
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]

Seq. No. 297905
Seq. ID LIB3150-060-Q1-N1-F8
Method BLASTX
NCBI GI g2642213
BLAST score 159
E value 2.0e-14
Match length 45

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% identity 93
NCBI Description (AF030385) nitrate-induced NOI protein [Zea mays]
>gi_2895781 (AF045033) nitrate-induced NOI protein [Zea mays]

Seq. No. 297906
Seq. ID LIB3150-060-Q1-N1-H10
Method BLASTX
NCBI GI g1184776
BLAST score 151
E value 4.0e-10
Match length 58
% identity 47
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]

Seq. No. 297907
Seq. ID LIB3150-061-Q1-N1-D1
Method BLASTX
NCBI GI g135398
BLAST score 272
E value 2.0e-34
Match length 94
% identity 76
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir_S15773 tubulin alpha-1 chain - maize >gi_22147_emb_CAA33734_ (X15704) alphal-tubulin [Zea mays]

Seq. No. 297908
Seq. ID LIB3150-063-P2-K1-A8
Method BLASTN
NCBI GI g1575127
BLAST score 92
E value 2.0e-44
Match length 136
% identity 92
NCBI Description Zea mays luminal binding protein cBiPe2 mRNA, complete cds

Seq. No. 297909
Seq. ID LIB3150-063-P2-K1-H6
Method BLASTN
NCBI GI g1037129
BLAST score 59
E value 8.0e-25
Match length 83
% identity 93
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 297910
Seq. ID LIB3150-064-P1-N1-A5
Method BLASTX
NCBI GI g1708107
BLAST score 312
E value 1.0e-28
Match length 87
% identity 76

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NCBI Description HISTONE H2B >gi_473605 (U08226) histone H2B [Zea mays]
Seq. No. 297911
Seq. ID LIB3150-064-P1-N1-B8
Method BLASTX
NCBI GI g2828280
BLAST score 400
E value 5.0e-39
Match length 101
% identity 72
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]
>gi_2832633_emb_CAA16762_ (AL021711) putative protein
[Arabidopsis thaliana]

Seq. No. 297912
Seq. ID LIB3150-064-P1-N1-H1
Method BLASTX
NCBI GI g113460
BLAST score 291
E value 3.0e-26
Match length 84
% identity 70
NCBI Description ADP,ATP CARRIER PROTEIN 2 PRECURSOR (ADP/ATP TRANSLOCASE 2)
(ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2)
>gi_100851_pir_S16568 ADP,ATP carrier protein precursor -
maize >gi_22164_emb_CAA41812_ (X59086) adenine nucleotide
translocator [Zea mays]

Seq. No. 297913
Seq. ID LIB3150-064-P2-K1-B5
Method BLASTN
NCBI GI g902585
BLAST score 38
E value 3.0e-12
Match length 46
% identity 96
NCBI Description Zea mays clone MuBG9 ubiquitin gene, complete cds

Seq. No. 297914
Seq. ID LIB3150-064-P2-K1-B7
Method BLASTN
NCBI GI g2340954
BLAST score 193
E value 1.0e-104
Match length 213
% identity 98
NCBI Description Z.mays ESR3g2 gene, clone L42a4

Seq. No. 297915
Seq. ID LIB3150-064-P2-K1-D8
Method BLASTX
NCBI GI g4519539
BLAST score 153
E value 5.0e-14
Match length 124
% identity 39
NCBI Description (AB016256) NAD-dependent sorbitol dehydrogenase [Malus

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domestica]

Seq. No. 297916
Seq. ID LIB3150-064-P2-K1-F4
Method BLASTX
NCBI GI g2829869
BLAST score 249
E value 3.0e-21
Match length 69
% identity 65
NCBI Description (AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No. 297917
Seq. ID LIB3150-064-P2-K1-G2
Method BLASTN
NCBI GI g1184775
BLAST score 40
E value 2.0e-13
Match length 72
% identity 89
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4 (gpc4) mRNA, complete cds

Seq. No. 297918
Seq. ID LIB3150-064-P2-K1-H6
Method BLASTN
NCBI GI g606969
BLAST score 35
E value 2.0e-10
Match length 71
% identity 87
NCBI Description Arabidopsis thaliana cytoplasmic ribosomal protein L18 mRNA, complete cds

Seq. No. 297919
Seq. ID LIB3150-065-P2-K1-A3
Method BLASTX
NCBI GI g1321661
BLAST score 154
E value 3.0e-10
Match length 39
% identity 79
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 297920
Seq. ID LIB3150-065-P2-K1-B10
Method BLASTN
NCBI GI g3851000
BLAST score 151
E value 2.0e-79
Match length 267
% identity 90
NCBI Description Zea mays pyruvate dehydrogenase E1 beta subunit isoform 2 mRNA, nuclear gene encoding mitochondrial protein, complete cds

CDS/EST Database

Seq. No.	297921
Seq. ID	LIB3150-065-P2-K1-B7
Method	BLASTX
NCBI GI	g2459446
BLAST score	232
E value	1.0e-19
Match length	90
% identity	52
NCBI Description	(AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]
Seq. No.	297922
Seq. ID	LIB3150-065-P2-K1-C11
Method	BLASTX
NCBI GI	g1350983
BLAST score	211
E value	1.0e-16
Match length	86
% identity	51
NCBI Description	40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
Seq. No.	297923
Seq. ID	LIB3150-065-P2-K1-C6
Method	BLASTN
NCBI GI	g168584
BLAST score	80
E value	5.0e-37
Match length	215
% identity	92
NCBI Description	Corn pyruvate,orthophosphate dikinase gene, exons 2-19
Seq. No.	297924
Seq. ID	LIB3150-065-P2-K1-D5
Method	BLASTX
NCBI GI	g2129553
BLAST score	319
E value	2.0e-29
Match length	79
% identity	72
NCBI Description	calcium-dependent protein kinase 6 - Arabidopsis thaliana
Seq. No.	297925
Seq. ID	LIB3150-065-P2-K1-F4
Method	BLASTN
NCBI GI	g168419
BLAST score	82
E value	2.0e-38
Match length	155
% identity	89
NCBI Description	Maize (Z.mays) aldolase mRNA, complete cds
Seq. No.	297926
Seq. ID	LIB3150-065-P2-K1-G3
Method	BLASTN
NCBI GI	g1917018
BLAST score	80
E value	6.0e-37

Match length 136
% identity 90
NCBI Description Zea mays ribosomal protein S6 RPS6-1 (rps6-1) mRNA,
complete cds

Seq. No. 297927
Seq. ID LIB3150-065-P2-K1-G8
Method BLASTN
NCBI GI g22312
BLAST score 52
E value 2.0e-20
Match length 180
% identity 83
NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA =
abscisic acid)

Seq. No. 297928
Seq. ID LIB3150-066-P1-N1-A10
Method BLASTX
NCBI GI g2181180
BLAST score 144
E value 3.0e-09
Match length 80
% identity 35
NCBI Description (Z84377) xylosidase [Aspergillus niger]

Seq. No. 297929
Seq. ID LIB3150-066-P1-N1-B3
Method BLASTX
NCBI GI g1184774
BLAST score 326
E value 1.0e-30
Match length 69
% identity 91
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC3 [Zea mays]

Seq. No. 297930
Seq. ID LIB3150-066-P1-N1-F1
Method BLASTN
NCBI GI g1276936
BLAST score 52
E value 1.0e-20
Match length 76
% identity 92
NCBI Description Zea mays USDA Ames 8212 ITS1, 5.8S ribosomal RNA, ITS2

Seq. No. 297931
Seq. ID LIB3150-066-P1-N1-G4
Method BLASTX
NCBI GI g1658315
BLAST score 347
E value 7.0e-33
Match length 99
% identity 69
NCBI Description (Y08988) osr40g3 [Oryza sativa]

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Seq. No.	297932
Seq. ID	LIB3150-066-P2-K1-A6
Method	BLASTX
NCBI GI	g1498064
BLAST score	251
E value	2.0e-21
Match length	81
% identity	63
NCBI Description	(U64825) AtE1 [Arabidopsis thaliana]
Seq. No.	297933
Seq. ID	LIB3150-066-P2-K1-G10
Method	BLASTN
NCBI GI	g2282583
BLAST score	84
E value	2.0e-39
Match length	152
% identity	89
NCBI Description	Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete cds
Seq. No.	297934
Seq. ID	LIB3150-066-P2-K1-G4
Method	BLASTN
NCBI GI	g296203
BLAST score	43
E value	6.0e-15
Match length	79
% identity	89
NCBI Description	P. miliaceum mRNA for alanine aminotransferase
Seq. No.	297935
Seq. ID	LIB3150-066-P2-K1-H2
Method	BLASTX
NCBI GI	g464707
BLAST score	283
E value	3.0e-25
Match length	70
% identity	77
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir_S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]
Seq. No.	297936
Seq. ID	LIB3150-067-P1-N1-E2

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Method BLASTX
NCBI GI g82512
BLAST score 171
E value 2.0e-12
Match length 37
% identity 47
NCBI Description ubiquitin precursor - rice (fragment)
>gi_218189_dbj_BAA02241_ (D12776) poly-ubiquitin [Oryza sativa]

Seq. No. 297937
Seq. ID LIB3150-067-P1-N1-G4
Method BLASTN
NCBI GI g22176
BLAST score 163
E value 1.0e-86
Match length 289
% identity 89
NCBI Description Z.mays P gene

Seq. No. 297938
Seq. ID LIB3150-067-P2-K1-A6
Method BLASTX
NCBI GI g2511531
BLAST score 197
E value 9.0e-16
Match length 49
% identity 73
NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]
>gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1 [Eleusine indica]

Seq. No. 297939
Seq. ID LIB3150-067-P2-K1-B12
Method BLASTN
NCBI GI g2286150
BLAST score 151
E value 3.0e-79
Match length 331
% identity 85
NCBI Description Zea mays translation initiation factor (eIF-4A) mRNA, complete cds

Seq. No. 297940
Seq. ID LIB3150-067-P2-K1-D4
Method BLASTN
NCBI GI g168482
BLAST score 95
E value 3.0e-46
Match length 159
% identity 91
NCBI Description Corn starch branching enzyme II mRNA, complete cds

Seq. No. 297941
Seq. ID LIB3150-067-P2-K1-D6
Method BLASTN
NCBI GI g2668741

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BLAST score 165
E value 7.0e-88
Match length 248
% identity 92
NCBI Description Zea mays glycine-rich RNA binding protein (GRP) mRNA, complete cds

Seq. No. 297942
Seq. ID LIB3150-067-P2-K1-F3
Method BLASTX
NCBI GI g1172836
BLAST score 169
E value 3.0e-12
Match length 46
% identity 76
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787)
small ras-related protein [Nicotiana tabacum]

Seq. No. 297943
Seq. ID LIB3150-067-P2-K1-G2
Method BLASTX
NCBI GI g4096786
BLAST score 168
E value 7.0e-12
Match length 35
% identity 94
NCBI Description (U39958) NADP-malic enzyme [Zea mays]

Seq. No. 297944
Seq. ID LIB3150-068-P1-N1-B6
Method BLASTX
NCBI GI g4467099
BLAST score 221
E value 4.0e-18
Match length 72
% identity 71
NCBI Description (AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No. 297945
Seq. ID LIB3150-068-P1-N1-C2
Method BLASTX
NCBI GI g1184774
BLAST score 271
E value 5.0e-24
Match length 74
% identity 78
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 297946
Seq. ID LIB3150-068-P1-N1-C5
Method BLASTX
NCBI GI g1709619
BLAST score 280
E value 5.0e-25
Match length 57

% identity 95
 NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
 DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
 (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
 >gi_2146814_pir_S69181 protein disulfide isomerase (EC
 5.3.4.1) precursor - maize >gi_625148 (L39014) protein
 disulfide isomerase [Zea mays]

Seq. No. 297947
 Seq. ID LIB3150-068-P1-N1-F4
 Method BLASTX
 NCBI GI g1835729
 BLAST score 159
 E value 8.0e-11
 Match length 38
 % identity 87
 NCBI Description (U86017) ribosomal protein [Oryza sativa]

Seq. No. 297948
 Seq. ID LIB3150-068-P1-N1-F8
 Method BLASTX
 NCBI GI g136632
 BLAST score 250
 E value 5.0e-22
 Match length 61
 % identity 82
 NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 1 >gi_100841_pir_A38373
 ubiquitin--protein ligase (EC 6.3.2.19) E1 - wheat
 >gi_285451_pir_A42873 ubiquitin-activating enzyme E1, UBA1
 - Wheat >gi_170780 (M55604) ubiquitin-activating enzyme E1
 [Triticum aestivum]

Seq. No. 297949
 Seq. ID LIB3150-068-P1-N1-H6
 Method BLASTN
 NCBI GI g22101
 BLAST score 41
 E value 6.0e-14
 Match length 132
 % identity 83
 NCBI Description Maize 7SL RNA of signal recognition particle

Seq. No. 297950
 Seq. ID LIB3150-068-P2-K1-B11
 Method BLASTX
 NCBI GI g1350777
 BLAST score 237
 E value 7.0e-20
 Match length 71
 % identity 66
 NCBI Description 60S RIBOSOMAL PROTEIN L9 >gi_971282_dbj_BAA07209_ (D38012)
 ribosomal protein L9 [Oryza sativa]

Seq. No. 297951
 Seq. ID LIB3150-068-P2-K1-C7
 Method BLASTN
 NCBI GI g22144

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BLAST score	244
E value	1.0e-135
Match length	260
% identity	98
NCBI Description	Maize anaerobically regulated gene for fructose bisphosphate aldolase (EC 4.1.2.13)
Seq. No.	297952
Seq. ID	LIB3150-068-P2-K1-F12
Method	BLASTX
NCBI GI	g1350777
BLAST score	234
E value	1.0e-19
Match length	53
% identity	85
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_971282_dbj_BAA07209_ (D38012) ribosomal protein L9 [Oryza sativa]
Seq. No.	297953
Seq. ID	LIB3150-068-P2-K1-G2
Method	BLASTX
NCBI GI	g1707017
BLAST score	272
E value	6.0e-24
Match length	66
% identity	74
NCBI Description	(U78721) RNA helicase isolog [Arabidopsis thaliana]
Seq. No.	297954
Seq. ID	LIB3150-068-P2-K1-H3
Method	BLASTX
NCBI GI	g556401
BLAST score	146
E value	3.0e-09
Match length	55
% identity	51
NCBI Description	(M28159) glutelin [Oryza sativa]
Seq. No.	297955
Seq. ID	LIB3150-068-P2-K1-H8
Method	BLASTX
NCBI GI	g3970823
BLAST score	288
E value	9.0e-26
Match length	56
% identity	98
NCBI Description	(X17555) pyruvate decarboxylase [Zea mays]
Seq. No.	297956
Seq. ID	LIB3150-069-P1-N1-B6
Method	BLASTX
NCBI GI	g118104
BLAST score	184
E value	3.0e-14
Match length	39
% identity	92
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 297957
Seq. ID LIB3150-069-P1-N1-D8
Method BLASTX
NCBI GI g232031
BLAST score 142
E value 3.0e-09
Match length 36
% identity 75
NCBI Description ELONGATION FACTOR 1 BETA' >gi_322851_pir_S29224
translation elongation factor eEF-1 beta' chain - rice
>gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
[Oryza sativa]

Seq. No. 297958
Seq. ID LIB3150-069-P1-N1-F1
Method BLASTX
NCBI GI g2244990
BLAST score 187
E value 4.0e-14
Match length 37
% identity 100
NCBI Description (Z97340) similarity to LIM homeobox protein -
Caenorhabditis [Arabidopsis thaliana]

Seq. No. 297959
Seq. ID LIB3150-069-P1-N1-F7
Method BLASTX
NCBI GI g1350783
BLAST score 160
E value 5.0e-11
Match length 97
% identity 39
NCBI Description RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR
>gi_282883_pir_S27756 receptor-like protein kinase
precursor - Arabidopsis thaliana >gi_166850 (M84660)
receptor-like protein kinase [Arabidopsis thaliana]
>gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein
kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No. 297960
Seq. ID LIB3150-069-P1-N1-H6
Method BLASTX
NCBI GI g1173055
BLAST score 152
E value 4.0e-22
Match length 94
% identity 60
NCBI Description 60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir_S42497
ribosomal protein L11.e - alfalfa >gi_1076504_pir_S51819
RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_
(X78284) RL5 ribosomal protein [Medicago sativa]

Seq. No. 297961
Seq. ID LIB3150-069-P2-K1-C11
Method BLASTN
NCBI GI g1037129
BLAST score 58
E value 4.0e-24
Match length 86
% identity 92
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 297962
Seq. ID LIB3150-069-P2-K1-D8
Method BLASTN
NCBI GI g22272
BLAST score 80
E value 4.0e-37
Match length 167
% identity 87
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 297963
Seq. ID LIB3150-069-P2-K1-F2
Method BLASTX
NCBI GI g567890
BLAST score 153
E value 5.0e-10
Match length 129
% identity 38
NCBI Description (L37352) beta-galactosidase-complementation protein [Cloning vector]

Seq. No. 297964
Seq. ID LIB3150-069-P2-K1-F4
Method BLASTX
NCBI GI g135417
BLAST score 225
E value 1.0e-18
Match length 74
% identity 66
NCBI Description TUBULIN ALPHA-3 CHAIN >gi_100946_pir_JN0105 tubulin alpha-3 chain - maize >gi_22150_emb_CAA44861_ (X63176) Alpha-tubulin #3 [Zea mays] >gi_485377_(M60171) alpha-3 tubulin [Zea mays]

Seq. No. 297965
Seq. ID LIB3150-069-P2-K1-G9
Method BLASTX
NCBI GI g464706
BLAST score 156
E value 2.0e-10
Match length 43
% identity 77
NCBI Description 40S RIBOSOMAL PROTEIN S15 (S12) >gi_1078669_pir_A53793 ribosomal protein S12, cytosolic - Podospora anserina >gi_401841_emb_CAA80805_ (Z23267) cytoplasmic ribosomal protein S12 [Podospora anserina]

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Seq. No. 297966
Seq. ID LIB3150-070-P1-N1-B9
Method BLASTX
NCBI GI g1084457
BLAST score 158
E value 7.0e-11
Match length 51
% identity 65
NCBI Description elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_(D23674) elongation factor 1 beta [Oryza sativa]

Seq. No. 297967
Seq. ID LIB3150-070-P1-N1-D10
Method BLASTN
NCBI GI g829147
BLAST score 51
E value 4.0e-20
Match length 139
% identity 84
NCBI Description Z.mays gene for cyclophilin

Seq. No. 297968
Seq. ID LIB3150-071-P1-N1-C7
Method BLASTX
NCBI GI g82696
BLAST score 187
E value 2.0e-14
Match length 46
% identity 78
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]

Seq. No. 297969
Seq. ID LIB3150-071-P1-N1-D11
Method BLASTX
NCBI GI g399414
BLAST score 245
E value 7.0e-21
Match length 78
% identity 65
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
>gi_322865_pir_JC1454 translation elongation factor eEF-1
alpha chain - wheat >gi_170776 (M90077) translation
elongation factor 1 alpha-subunit [Triticum aestivum]
>gi_949878_emb_CAA90651_ (Z50789) elongation factor 1-alpha
[Hordeum vulgare]

Seq. No. 297970
Seq. ID LIB3150-071-P1-N1-D6
Method BLASTX
NCBI GI g1184776
BLAST score 265
E value 2.0e-23
Match length 76
% identity 75
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC4 [Zea mays]

Seq. No. 297971
 Seq. ID LIB3150-071-P1-N1-E12
 Method BLASTN
 NCBI GI g22172
 BLAST score 61
 E value 6.0e-26
 Match length 61
 % identity 100
 NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit

Seq. No. 297972
 Seq. ID LIB3150-071-P1-N1-E2
 Method BLASTX
 NCBI GI g122007
 BLAST score 142
 E value 5.0e-09
 Match length 38
 % identity 79
 NCBI Description HISTONE H2A >gi_100161_pir_S11498 histone H2A - parsley
 >gi_20448_emb_CAA37828_(X53831) H2A histone protein (AA 1
 - 149) [Petroselinum crispum]

Seq. No. 297973
 Seq. ID LIB3150-071-P1-N1-E9
 Method BLASTX
 NCBI GI g4038461
 BLAST score 187
 E value 3.0e-14
 Match length 72
 % identity 51
 NCBI Description (AF107772) TcSTI1 [Trypanosoma cruzi]

Seq. No. 297974
 Seq. ID LIB3150-071-P1-N1-F1
 Method BLASTX
 NCBI GI g2723473
 BLAST score 155
 E value 2.0e-23
 Match length 94
 % identity 67
 NCBI Description (D89726) defender against apoptotic death 1 protein [Oryza sativa] >gi_2723883_dbj_BAA24104_ (D89727) defender against apoptotic death 1 protein [Oryza sativa]

Seq. No. 297975
 Seq. ID LIB3150-071-P1-N1-F2
 Method BLASTX
 NCBI GI g2642158
 BLAST score 221
 E value 5.0e-18
 Match length 83
 % identity 55
 NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No. 297976

Seq. ID LIB3150-071-P1-N1-F7
 Method BLASTX
 NCBI GI g3122071
 BLAST score 419
 E value 2.0e-42
 Match length 106
 % identity 84
 NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
 >gi_2130148_pir_S66339 translation elongation factor eEF-1
 alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408)
 alpha subunit of tlanslation elongation factor 1 [Zea mays]

Seq. No. 297977
 Seq. ID LIB3150-071-P1-N1-F8
 Method BLASTN
 NCBI GI g4185305
 BLAST score 44
 E value 1.0e-15
 Match length 60
 % identity 48
 NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
 protein, polyprotein, and copia protein genes, complete
 cds; and unknown genes

Seq. No. 297978
 Seq. ID LIB3150-071-P1-N1-G10
 Method BLASTX
 NCBI GI g121446
 BLAST score 251
 E value 1.0e-21
 Match length 70
 % identity 76
 NCBI Description FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE PRECURSOR
 (FD-GOGAT) >gi_100877_pir_A38596 glutamate synthase
 (ferredoxin) (EC 1.4.7.1) - maize >gi_168477 (M59190)
 ferredoxin-dependent glutamate synthase [Zea mays]

Seq. No. 297979
 Seq. ID LIB3150-072-P2-K1-A9
 Method BLASTX
 NCBI GI g3779021
 BLAST score 149
 E value 1.0e-09
 Match length 87
 % identity 37
 NCBI Description (AC005171) putative reverse transcriptase [Arabidopsis
 thaliana]

Seq. No. 297980
 Seq. ID LIB3150-072-P2-K1-D3
 Method BLASTX
 NCBI GI g2191131
 BLAST score 209
 E value 2.0e-16
 Match length 87
 % identity 47

NCBI Description (AF007269) A_IG002N01.8 gene product [Arabidopsis thaliana]

Seq. No. 297981
Seq. ID LIB3150-073-P1-N1-A11
Method BLASTX
NCBI GI g3342821
BLAST score 188
E value 2.0e-21
Match length 90
% identity 56

NCBI Description (AF076954) eukaryotic translation initiation factor small subunit [Zea mays]

Seq. No. 297982
Seq. ID LIB3150-073-P1-N1-E10
Method BLASTX
NCBI GI g1350720
BLAST score 235
E value 8.0e-20
Match length 73
% identity 63

NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 297983
Seq. ID LIB3150-073-P1-N1-E5
Method BLASTX
NCBI GI g3413700
BLAST score 168
E value 2.0e-12
Match length 37
% identity 86

NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No. 297984
Seq. ID LIB3150-073-P1-N1-E8
Method BLASTX
NCBI GI g1326372
BLAST score 153
E value 2.0e-10
Match length 68
% identity 51

NCBI Description (U58750) Similar to Histone. [Caenorhabditis elegans]

Seq. No. 297985
Seq. ID LIB3150-073-P1-N1-F3
Method BLASTX
NCBI GI g1381676
BLAST score 236
E value 9.0e-20
Match length 73
% identity 68

NCBI Description (U58853) small GTP-binding protein [Glycine max]

Seq. No. 297986
Seq. ID LIB3150-073-P1-N1-G2
Method BLASTX
NCBI GI g2244834

Seq. No. 297987
 Seq. ID LIB3150-073-P1-N1-G5
 Method BLASTX
 NCBI GI g3608481
 BLAST score 272
 E value 3.0e-24
 Match length 68
 % identity 75
 NCBI Description (AF088913) ribosomal protein L27a [Petunia x hybrida]

Seq. No. 297988
 Seq. ID LIB3150-073-P2-K1-A1
 Method BLASTN
 NCBI GI g644491
 BLAST score 56
 E value 8.0e-23
 Match length 152
 % identity 85
 NCBI Description Corn mRNA for elongation factor 1A

Seq. No. 297989
 Seq. ID LIB3150-073-P2-K1-A11
 Method BLASTX
 NCBI GI g1172816
 BLAST score 194
 E value 7.0e-15
 Match length 70
 % identity 60
 NCBI Description 60S RIBOSOMAL PROTEIN L11A (L16A) >gi_624938_emb_CAA57395_(X81799) ribosomal protein L16 [Arabidopsis thaliana]

Seq. No. 297990
 Seq. ID LIB3150-073-P2-K1-A7
 Method BLASTX
 NCBI GI g136063
 BLAST score 261
 E value 9.0e-23
 Match length 53
 % identity 100
 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
 >gi_68426_pir_ISZMT triose-phosphate isomerase (EC
 5.3.1.1) - maize >gi_168647 (L00371) triosephosphate
 isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)
 triosephosphate isomerase [Zea mays]

Seq. No. 297991
 Seq. ID LIB3150-073-P2-K1-A9
 Method BLASTX
 NCBI GI g1172874
 BLAST score 145
 E value 5.0e-09

Match length 102
 % identity 35
 NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
 >gi_479589_pir_S34823 dehydration-induced protein RD22 -
Arabidopsis thaliana >gi_391608_dbj_BAA01546 (D10703) rd22
 [Arabidopsis thaliana] >gi_447134_prf_1913421A rd22 gene
 [Arabidopsis thaliana]

Seq. No. 297992
 Seq. ID LIB3150-073-P2-K1-B10
 Method BLASTN
 NCBI GI g4185305
 BLAST score 43
 E value 6.0e-15
 Match length 207
 % identity 81
 NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
 protein, polyprotein, and copia protein genes, complete
 cds; and unknown genes

Seq. No. 297993
 Seq. ID LIB3150-073-P2-K1-B3
 Method BLASTX
 NCBI GI g3745759
 BLAST score 195
 E value 6.0e-15
 Match length 56
 % identity 70
 NCBI Description Chain B, X-Ray Structure Of The Nucleosome Core Particle At
 2.8 A Resolution >gi_3745763_pdb_1AOI_F Chain F, X-Ray
 Structure Of The Nucleosome Core Particle At 2.8 A
 Resolution

Seq. No. 297994
 Seq. ID LIB3150-073-P2-K1-B8
 Method BLASTN
 NCBI GI g2286150
 BLAST score 263
 E value 1.0e-146
 Match length 275
 % identity 99
 NCBI Description Zea mays translation initiation factor (eIF-4A) mRNA,
 complete cds

Seq. No. 297995
 Seq. ID LIB3150-073-P2-K1-C4
 Method BLASTX
 NCBI GI g2182029
 BLAST score 233
 E value 2.0e-19
 Match length 89
 % identity 57
 NCBI Description (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]

Seq. No. 297996
 Seq. ID LIB3150-073-P2-K1-C9

DRAFT Sequence

Method	BLASTN
NCBI GI	g22324
BLAST score	71
E value	1.0e-31
Match length	151
% identity	87
NCBI Description	Z.mays mRNA for H2B histone (clone cH2B221)
Seq. No.	297997
Seq. ID	LIB3150-073-P2-K1-F11
Method	BLASTN
NCBI GI	g602605
BLAST score	72
E value	3.0e-32
Match length	254
% identity	63
NCBI Description	Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
Seq. No.	297998
Seq. ID	LIB3150-074-P1-N1-D2
Method	BLASTX
NCBI GI	g1321661
BLAST score	186
E value	3.0e-14
Match length	52
% identity	71
NCBI Description	(D45423) ascorbate peroxidase [Oryza sativa]
Seq. No.	297999
Seq. ID	LIB3150-074-P1-N1-E2
Method	BLASTX
NCBI GI	g3126967
BLAST score	358
E value	1.0e-34
Match length	99
% identity	14
NCBI Description	(AF061807) polyubiquitin [Elaeagnus umbellata]
Seq. No.	298000
Seq. ID	LIB3150-074-P1-N1-F12
Method	BLASTN
NCBI GI	g642120
BLAST score	48
E value	3.0e-18
Match length	76
% identity	91
NCBI Description	Oryza sativa small GTP-binding protein (ORRab-2) mRNA, complete cds
Seq. No.	298001
Seq. ID	LIB3150-074-P1-N1-H6
Method	BLASTX
NCBI GI	g2144183
BLAST score	156
E value	5.0e-11
Match length	53
% identity	53

NCBI Description DNA-directed RNA polymerase (EC 2.7.7.6) chain III -
 Ecotype Columbia >gi_1184686 (U35049) RNA polymerase I(A)
 and III(C) 14 kDa subunit [Arabidopsis thaliana]
 >gi_1184688 (U35050) Arabidopsis thaliana RNA polymerase
 I(A) and III(C) 14 kDa subunit [Arabidopsis thaliana]
 >gi_3980382 (AC004561) RNA polymerase I(A) and III(C) 14
 kDa subunit (AtRPAC14) [Arabidopsis thaliana]

Seq. No. 298002
 Seq. ID LIB3150-074-P2-K1-G7
 Method BLASTN
 NCBI GI g602605
 BLAST score 43
 E value 5.0e-15
 Match length 75
 % identity 89
 NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin

Seq. No. 298003
 Seq. ID LIB3150-074-P2-K1-H4
 Method BLASTN
 NCBI GI g902585
 BLAST score 67
 E value 2.0e-29
 Match length 219
 % identity 83
 NCBI Description Zea mays clone MuBG9 ubiquitin gene, complete cds

Seq. No. 298004
 Seq. ID LIB3150-074-P2-K1-H7
 Method BLASTN
 NCBI GI g393400
 BLAST score 71
 E value 8.0e-32
 Match length 156
 % identity 85
 NCBI Description Z.mays mRNA for alpha-tubulin

Seq. No. 298005
 Seq. ID LIB3150-075-P1-N1-D1
 Method BLASTX
 NCBI GI g4588906
 BLAST score 195
 E value 2.0e-15
 Match length 49
 % identity 80
 NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]

Seq. No. 298006
 Seq. ID LIB3150-075-P1-N1-E10
 Method BLASTN
 NCBI GI g540534
 BLAST score 58
 E value 6.0e-24
 Match length 82
 % identity 93
 NCBI Description Rice mRNA for q group of receptor for activated C-kinase,

complete cds

Seq. No. 298007
Seq. ID LIB3150-075-P1-N1-E7
Method BLASTX
NCBI GI g1184774
BLAST score 165
E value 2.0e-20
Match length 59
% identity 92
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC3 [Zea mays]

Seq. No. 298008
Seq. ID LIB3150-075-P1-N1-F7
Method BLASTX
NCBI GI g1053047
BLAST score 301
E value 1.0e-27
Match length 68
% identity 90
NCBI Description (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
[Glycine max]

Seq. No. 298009
Seq. ID LIB3150-075-P1-N1-G7
Method BLASTX
NCBI GI g729676
BLAST score 204
E value 2.0e-18
Match length 75
% identity 72
NCBI Description HISTONE H3.1 >gi_542444_pir_S41499 histone H3.1 -
Tetrahymena thermophila (SGC5) >gi_161788 (M87304) histone
H3 [Tetrahymena thermophila] >gi_161790 (M87504) histone H3
[Tetrahymena thermophila]

Seq. No. 298010
Seq. ID LIB3150-075-P2-N2-A3
Method BLASTX
NCBI GI g113621
BLAST score 332
E value 5.0e-31
Match length 67
% identity 97
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
>gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366 (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A
cytoplasmic aldolase [Zea mays]

Seq. No. 298011
Seq. ID LIB3150-075-P2-N2-B1
Method BLASTX
NCBI GI g2982289

BLAST score 397
E value 1.0e-38
Match length 78
% identity 97
NCBI Description (AF051229) 60S ribosomal protein L17 [Picea mariana]

Seq. No. 298012
Seq. ID LIB3150-075-P2-N2-B3
Method BLASTN
NCBI GI g22272
BLAST score 140
E value 6.0e-73
Match length 219
% identity 91
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298013
Seq. ID LIB3150-075-P2-N2-D1
Method BLASTX
NCBI GI g2507281
BLAST score 246
E value 1.0e-24
Match length 66
% identity 91
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_(X97380) atran2 [Arabidopsis thaliana]

Seq. No. 298014
Seq. ID LIB3150-075-P2-N2-D8
Method BLASTX
NCBI GI g401238
BLAST score 536
E value 4.0e-55
Match length 131
% identity 82
NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 3 >gi_170686 (M90664) ubiquitin activating enzyme [Triticum aestivum]

Seq. No. 298015
Seq. ID LIB3150-075-P2-N2-F2
Method BLASTN
NCBI GI g22100
BLAST score 33
E value 3.0e-09
Match length 57
% identity 89
NCBI Description Z.mays 27kDa zein locus DNA

Seq. No. 298016
Seq. ID LIB3150-075-P2-N2-H10
Method BLASTX
NCBI GI g4220445
BLAST score 320
E value 3.0e-32
Match length 132
% identity 22
NCBI Description (AC006216) Similar to gi_3004555 F19F24.14 salt inducible

protein homolog from *Arabidopsis thaliana* BAC gb_AC003673.
[*Arabidopsis thaliana*]

Seq. No. 298017
Seq. ID LIB3150-075-P2-N2-H11
Method BLASTX
NCBI GI g4220445
BLAST score 171
E value 1.0e-12
Match length 73
% identity 47
NCBI Description (AC006216) Similar to gi_3004555 F19F24.14 salt inducible protein homolog from *Arabidopsis thaliana* BAC gb_AC003673.
[*Arabidopsis thaliana*]

Seq. No. 298018
Seq. ID LIB3150-075-P2-N2-H12
Method BLASTX
NCBI GI g1730666
BLAST score 169
E value 7.0e-12
Match length 70
% identity 54
NCBI Description HYPOTHETICAL 32.2 KD PROTEIN IN ARE2-SWP73 INTERGENIC REGION >gi_2131968_pir_S63351 hypothetical protein YNR020c - yeast (*Saccharomyces cerevisiae*)
>gi_1302506_emb_CAA96299_ (Z71635) ORF YNR020c
[*Saccharomyces cerevisiae*]

Seq. No. 298019
Seq. ID LIB3150-076-P1-N1-F3
Method BLASTX
NCBI GI g4582468
BLAST score 150
E value 7.0e-10
Match length 64
% identity 47
NCBI Description (AC007071) putative 40S ribosomal protein; contains C-terminal domain [*Arabidopsis thaliana*]

Seq. No. 298020
Seq. ID LIB3150-076-P1-N1-G3
Method BLASTX
NCBI GI g1184776
BLAST score 280
E value 4.0e-25
Match length 71
% identity 79
NCBI Description (U45857) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC4 [*Zea mays*]

Seq. No. 298021
Seq. ID LIB3150-076-P2-N2-A7
Method BLASTX
NCBI GI g3337352
BLAST score 331
E value 4.0e-31

Match length 101
 % identity 66
 NCBI Description (AC004481) putative chromatin structural protein Supt5hp
 [Arabidopsis thaliana]

Seq. No. 298022
 Seq. ID LIB3150-076-P2-N2-A9
 Method BLASTN
 NCBI GI g1839582
 BLAST score 47
 E value 9.0e-18
 Match length 63
 % identity 94
 NCBI Description polyubiquitin homolog {clone CHEM 6} [Zea mays=maize, cv.
 INRA 258, mercuric chloride-treated, leaves, mRNA Partial,
 199 nt, segment 1 of 2]

Seq. No. 298023
 Seq. ID LIB3150-076-P2-N2-C6
 Method BLASTX
 NCBI GI g2117937
 BLAST score 623
 E value 4.0e-65
 Match length 123
 % identity 94
 NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
 barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
 pyrophosphorylase [Hordeum vulgare]

Seq. No. 298024
 Seq. ID LIB3150-076-P2-N2-E8
 Method BLASTN
 NCBI GI g4185305
 BLAST score 84
 E value 2.0e-39
 Match length 304
 % identity 83
 NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
 protein, polyprotein, and copia protein genes, complete
 cds; and unknown genes

Seq. No. 298025
 Seq. ID LIB3150-076-P2-N2-F1
 Method BLASTX
 NCBI GI g1351974
 BLAST score 390
 E value 8.0e-38
 Match length 105
 % identity 77
 NCBI Description ADP-RIBOSYLATION FACTOR >gi_1076788_pir_S49325
 ADP-ribosylation factor - maize >gi_1076789_pir_S53486
 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_
 (X80042) ADP-ribosylation factor [Zea mays]

Seq. No. 298026
 Seq. ID LIB3150-076-P2-N2-G4

Method BLASTN
 NCBI GI g22312
 BLAST score 70
 E value 4.0e-31
 Match length 97
 % identity 94
 NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)

Seq. No. 298027
 Seq. ID LIB3150-076-P2-N2-H12
 Method BLASTX
 NCBI GI g2286153
 BLAST score 372
 E value 9.0e-36
 Match length 75
 % identity 100
 NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 298028
 Seq. ID LIB3150-076-P2-N2-H5
 Method BLASTX
 NCBI GI g913865
 BLAST score 153
 E value 1.0e-10
 Match length 49
 % identity 61
 NCBI Description branching enzyme II BEII [Zea mays, cultivar B73, endosperms, Peptide, 738 aa]

Seq. No. 298029
 Seq. ID LIB3150-077-P1-N1-A12
 Method BLASTX
 NCBI GI g4038471
 BLAST score 349
 E value 5.0e-33
 Match length 86
 % identity 80
 NCBI Description (AF111029) 40S ribosomal protein S27 homolog [Zea mays]

Seq. No. 298030
 Seq. ID LIB3150-077-P1-N1-E5
 Method BLASTX
 NCBI GI g417154
 BLAST score 168
 E value 2.0e-18
 Match length 84
 % identity 79
 NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock protein 82 - rice (strain Taichung Native One)
 >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No. 298031
 Seq. ID LIB3150-077-P1-N1-E7
 Method BLASTX
 NCBI GI g122022

BLAST score 142
 E value 8.0e-09
 Match length 94
 % identity 44
 NCBI Description HISTONE H2B >gi_283025_pir_S22323 histone H2B - wheat
 >gi_21801_emb_CAA42530_ (X59873) histone H2B [Triticum aestivum]

 Seq. No. 298032
 Seq. ID LIB3150-077-P1-N1-F2
 Method BLASTX
 NCBI GI g3294469
 BLAST score 165
 E value 2.0e-21
 Match length 101
 % identity 63
 NCBI Description (U89342) phosphoglucomutase 2 [Zea mays]

 Seq. No. 298033
 Seq. ID LIB3150-077-P1-N1-F4
 Method BLASTX
 NCBI GI g4567275
 BLAST score 248
 E value 8.0e-27
 Match length 108
 % identity 61
 NCBI Description (AC006841) hypothetical protein [Arabidopsis thaliana]

 Seq. No. 298034
 Seq. ID LIB3150-077-P1-N1-G3
 Method BLASTN
 NCBI GI g3015620
 BLAST score 55
 E value 3.0e-22
 Match length 291
 % identity 80
 NCBI Description Zea mays low molecular weight heat shock protein precursor (hsp22) mRNA, nuclear gene encoding mitochondrial protein, complete cds

 Seq. No. 298035
 Seq. ID LIB3150-077-P1-N1-H8
 Method BLASTX
 NCBI GI g119355
 BLAST score 340
 E value 5.0e-32
 Match length 95
 % identity 77
 NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
 (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
 >gi_100869_pir_S16257 phosphopyruvate hydratase (EC
 4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
 [Zea mays]

 Seq. No. 298036
 Seq. ID LIB3150-077-P2-N2-C4
 Method BLASTN

NCBI GI g22272
BLAST score 99
E value 2.0e-48
Match length 205
% identity 88
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298037
Seq. ID LIB3150-077-P2-N2-E2
Method BLASTN
NCBI GI g1808693
BLAST score 132
E value 5.0e-68
Match length 224
% identity 90
NCBI Description S. stapfianus pSD.34 mRNA

Seq. No. 298038
Seq. ID LIB3150-077-P2-N2-E5
Method BLASTX
NCBI GI g118104
BLAST score 547
E value 3.0e-56
Match length 121
% identity 87
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 298039
Seq. ID LIB3150-077-P2-N2-E6
Method BLASTX
NCBI GI g1185556
BLAST score 159
E value 2.0e-11
Match length 37
% identity 92
NCBI Description (U45859) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 298040
Seq. ID LIB3150-077-P2-N2-F9
Method BLASTN
NCBI GI g1037129
BLAST score 191
E value 1.0e-103
Match length 219
% identity 65
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298041
Seq. ID LIB3150-077-P2-N2-G9
Method BLASTX
NCBI GI g2865661

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BLAST score 146
 E value 2.0e-09
 Match length 55
 % identity 58
 NCBI Description (AF045548) alcohol dehydrogenase 1 [Tripsacum dactyloides]

 Seq. No. 298042
 Seq. ID LIB3150-077-P2-N2-H4
 Method BLASTX
 NCBI GI g2511541
 BLAST score 287
 E value 7.0e-26
 Match length 77
 % identity 73
 NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]

 Seq. No. 298043
 Seq. ID LIB3150-078-P1-N1-A8
 Method BLASTX
 NCBI GI g3334138
 BLAST score 152
 E value 2.0e-10
 Match length 41
 % identity 63
 NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin
 [Glycine max]

 Seq. No. 298044
 Seq. ID LIB3150-078-P1-N1-B6
 Method BLASTX
 NCBI GI g1351904
 BLAST score 288
 E value 2.0e-26
 Match length 70
 % identity 83
 NCBI Description ASPARTOKINASE 1 / HOMOSERINE DEHYDROGENASE 1 CHLOROPLAST
 PRECURSOR (AK-HSDH 1) (AKHSDH1) >gi_500851 (L33912)
 aspartate kinase-homoserine dehydrogenase [Zea mays]

 Seq. No. 298045
 Seq. ID LIB3150-078-P1-N1-C1
 Method BLASTX
 NCBI GI g4218535
 BLAST score 211
 E value 3.0e-17
 Match length 79
 % identity 58
 NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

 Seq. No. 298046
 Seq. ID LIB3150-078-P1-N1-D2
 Method BLASTX
 NCBI GI g3367522
 BLAST score 418
 E value 4.0e-41
 Match length 142
 % identity 55

NCBI Description (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No. 298047
Seq. ID LIB3150-078-P1-N1-F1
Method BLASTX
NCBI GI g112994
BLAST score 321
E value 7.0e-30
Match length 71
% identity 92
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
>gi_82685_pir_S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 298048
Seq. ID LIB3150-078-P1-N1-F3
Method BLASTX
NCBI GI g4432866
BLAST score 147
E value 2.0e-09
Match length 80
% identity 39
NCBI Description (AC006300) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No. 298049
Seq. ID LIB3150-078-P1-N1-F8
Method BLASTX
NCBI GI g2282584
BLAST score 484
E value 7.0e-49
Match length 104
% identity 88
NCBI Description (U76259) elongation factor 1-alpha [Zea mays]

Seq. No. 298050
Seq. ID LIB3150-078-P1-N1-G3
Method BLASTX
NCBI GI g112994
BLAST score 427
E value 3.0e-42
Match length 91
% identity 93
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
>gi_82685_pir_S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 298051
Seq. ID LIB3150-078-P1-N1-H7
Method BLASTN

O
B
S
E
R
C
H
O
D
E
R

NCBI GI g303854
BLAST score 54
E value 1.0e-21
Match length 162
% identity 85
NCBI Description Rice mRNA for ribosomal protein L7A, complete cds

Seq. No. 298052
Seq. ID LIB3150-078-P2-N2-A3
Method BLASTX
NCBI GI g4580398
BLAST score 349
E value 6.0e-34
Match length 111
% identity 65
NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis thaliana]

Seq. No. 298053
Seq. ID LIB3150-078-P2-N2-B8
Method BLASTX
NCBI GI g3747050
BLAST score 328
E value 1.0e-30
Match length 69
% identity 96
NCBI Description (AF093540) ribosomal protein L26 [Zea mays]

Seq. No. 298054
Seq. ID LIB3150-078-P2-N2-B9
Method BLASTN
NCBI GI g3747049
BLAST score 35
E value 1.0e-10
Match length 83
% identity 86
NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds

Seq. No. 298055
Seq. ID LIB3150-078-P2-N2-D5
Method BLASTN
NCBI GI g293886
BLAST score 52
E value 6.0e-21
Match length 96
% identity 89
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase mRNA, 3' end, (clone GACP3)

Seq. No. 298056
Seq. ID LIB3150-078-P2-N2-D8
Method BLASTN
NCBI GI g21800
BLAST score 106
E value 1.0e-52
Match length 196
% identity 89

NCBI Description T.aestivum L mRNA for histone H2B

Seq. No. 298057
Seq. ID LIB3150-079-P1-N1-A11
Method BLASTX
NCBI GI g113621
BLAST score 163
E value 3.0e-11
Match length 68
% identity 57
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
>gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A
cytoplasmic aldolase [Zea mays]

Seq. No. 298058
Seq. ID LIB3150-079-P1-N1-A8
Method BLASTX
NCBI GI g232029
BLAST score 238
E value 3.0e-20
Match length 70
% identity 70
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
>gi_100154_pir_S21989 translation elongation factor eEF-1
alpha chain - carrot >gi_18339_emb_CAA42843_ (X60302)
elongation factor 1A [Daucus carota]

Seq. No. 298059
Seq. ID LIB3150-079-P1-N1-D2
Method BLASTX
NCBI GI g2760349
BLAST score 232
E value 9.0e-20
Match length 68
% identity 14
NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]

Seq. No. 298060
Seq. ID LIB3150-079-P1-N1-E2
Method BLASTX
NCBI GI g1184776
BLAST score 405
E value 2.0e-39
Match length 78
% identity 95
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC4 [Zea mays]

Seq. No. 298061
Seq. ID LIB3150-079-P1-N1-E3
Method BLASTX
NCBI GI g4510368
BLAST score 276
E value 2.0e-24

Match length 131
% identity 56
NCBI Description (AC007017) putative transcription factor E2F5 [Arabidopsis thaliana]

Seq. No. 298062
Seq. ID LIB3150-079-P1-N1-E7
Method BLASTX
NCBI GI g730558
BLAST score 225
E value 6.0e-28
Match length 96
% identity 74
NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_1076636_pir_S48027 ribosomal protein L34 - common tobacco >gi_2129964_pir_S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi_436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi_436032 (L27107) 60S ribosomal protein L34 [Nicotiana tabacum]

Seq. No. 298063
Seq. ID LIB3150-079-P2-N2-A11
Method BLASTN
NCBI GI g3318612
BLAST score 78
E value 6.0e-36
Match length 190
% identity 84
NCBI Description Zea mays mRNA for mitochondrial phosphate transporter, complete cds

Seq. No. 298064
Seq. ID LIB3150-079-P2-N2-B1
Method BLASTN
NCBI GI g416263
BLAST score 37
E value 2.0e-11
Match length 65
% identity 89
NCBI Description Rice mRNA for ribosomal protein S28, partial sequence

Seq. No. 298065
Seq. ID LIB3150-079-P2-N2-E4
Method BLASTN
NCBI GI g1213278
BLAST score 60
E value 3.0e-25
Match length 100
% identity 90
NCBI Description Z.mays ZEMb gene

Seq. No. 298066
Seq. ID LIB3150-079-P2-N2-F3
Method BLASTX
NCBI GI g3805847
BLAST score 315
E value 5.0e-29

Match length 111
% identity 58
NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 298067
Seq. ID LIB3150-079-P2-N2-H5
Method BLASTN
NCBI GI g886739
BLAST score 70
E value 3.0e-31
Match length 245
% identity 84
NCBI Description Z.mays histone H4 gene

Seq. No. 298068
Seq. ID LIB3150-080-P2-N2-G2
Method BLASTN
NCBI GI g1550813
BLAST score 102
E value 3.0e-50
Match length 181
% identity 90
NCBI Description Z.mays mRNA for acidic ribosomal protein P0

Seq. No. 298069
Seq. ID LIB3150-081-P1-N1-C6
Method BLASTX
NCBI GI g2137285
BLAST score 145
E value 4.0e-09
Match length 75
% identity 40
NCBI Description estrogen-responsive finger protein - mouse
>gi_1088467_dbj_BAA09941_(D63902) estrogen-responsive
finger protein [Mus musculus]

Seq. No. 298070
Seq. ID LIB3150-081-P1-N1-E1
Method BLASTX
NCBI GI g425194
BLAST score 448
E value 9.0e-45
Match length 87
% identity 99
NCBI Description (L26243) heat shock protein [Spinacia oleracea] >gi_2660772
(AF034618) cytosolic heat shock 70 protein [Spinacia
oleracea]

Seq. No. 298071
Seq. ID LIB3150-081-P1-N1-G2
Method BLASTX
NCBI GI g3913804
BLAST score 260
E value 1.0e-22
Match length 65
% identity 83
NCBI Description HISTONE H2B.3 >gi_577825_emb_CAA49584_ (X69960) H2B histone

[Zea mays]

Seq. No. 298072
Seq. ID LIB3150-081-P1-N1-H3
Method BLASTX
NCBI GI g118104
BLAST score 477
E value 4.0e-48
Match length 98
% identity 91
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 298073
Seq. ID LIB3150-081-P2-N2-D11
Method BLASTN
NCBI GI g168425
BLAST score 186
E value 1.0e-100
Match length 255
% identity 93
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 298074
Seq. ID LIB3150-081-P2-N2-F8
Method BLASTX
NCBI GI g520544
BLAST score 251
E value 1.0e-21
Match length 46
% identity 96
NCBI Description (U12195) betaine aldehyde dehydrogenase [Sorghum bicolor]

Seq. No. 298075
Seq. ID LIB3150-082-P1-N1-A5
Method BLASTX
NCBI GI g168586
BLAST score 147
E value 7.0e-10
Match length 43
% identity 70
NCBI Description (M58656) pyruvate,orthophosphate dikinase [Zea mays]

Seq. No. 298076
Seq. ID LIB3150-082-P1-N1-B8
Method BLASTN
NCBI GI g2811133
BLAST score 100
E value 4.0e-49
Match length 189
% identity 88
NCBI Description Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA,
partial cds

Seq. No. 298077
 Seq. ID LIB3150-082-P1-N1-C4
 Method BLASTX
 NCBI GI g168407
 BLAST score 173
 E value 2.0e-12
 Match length 57
 % identity 70
 NCBI Description (M32984) alcohol dehydrogenase [Zea mays]

Seq. No. 298078
 Seq. ID LIB3150-082-P2-N2-B4
 Method BLASTN
 NCBI GI g829147
 BLAST score 44
 E value 5.0e-16
 Match length 56
 % identity 95
 NCBI Description Z.mays gene for cyclophilin

Seq. No. 298079
 Seq. ID LIB3150-083-P1-N1-A1
 Method BLASTN
 NCBI GI g1143704
 BLAST score 97
 E value 3.0e-47
 Match length 125
 % identity 94
 NCBI Description Z.mays mRNA for homeobox 2a protein

Seq. No. 298080
 Seq. ID LIB3150-083-P1-N1-A2
 Method BLASTX
 NCBI GI g126896
 BLAST score 340
 E value 1.0e-37
 Match length 93
 % identity 86
 NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
 >gi_319831_pir_DEPUMW malate dehydrogenase (EC 1.1.1.37)
 precursor, mitochondrial - watermelon
 >gi_18297_emb_CAA35239_ (X17362) precursor protein (AA -27
 to 320) [Citrullus lanatus]

Seq. No. 298081
 Seq. ID LIB3150-083-P1-N1-B3
 Method BLASTX
 NCBI GI g4206112
 BLAST score 175
 E value 3.0e-13
 Match length 71
 % identity 61
 NCBI Description (AF097662) alpha tubulin [Mesembryanthemum crystallinum]

Seq. No. 298082
 Seq. ID LIB3150-083-P1-N1-B5
 Method BLASTX

NCBI GI g4206112
BLAST score 159
E value 2.0e-11
Match length 59
% identity 59
NCBI Description (AF097662) alpha tubulin [Mesembryanthemum crystallinum]

Seq. No. 298083
Seq. ID LIB3150-083-P1-N1-C1
Method BLASTX
NCBI GI g1279206
BLAST score 190
E value 1.0e-14
Match length 68
% identity 62
NCBI Description (X97446) alpha-tubulin [Avena sativa]

Seq. No. 298084
Seq. ID LIB3150-083-P1-N1-E11
Method BLASTX
NCBI GI g1883028
BLAST score 231
E value 2.0e-19
Match length 72
% identity 68
NCBI Description (X91511) histone H4 [Diprion pini]

Seq. No. 298085
Seq. ID LIB3150-083-P1-N1-F2
Method BLASTN
NCBI GI g577824
BLAST score 146
E value 1.0e-76
Match length 170
% identity 96
NCBI Description Z.mays gene for H2B histone (gH2B3)

Seq. No. 298086
Seq. ID LIB3150-083-P1-N1-G4
Method BLASTX
NCBI GI g3935184
BLAST score 384
E value 3.0e-37
Match length 115
% identity 65
NCBI Description (AC004557) F17L21.27 [Arabidopsis thaliana]

Seq. No. 298087
Seq. ID LIB3150-083-P1-N1-H8
Method BLASTX
NCBI GI g3122071
BLAST score 304
E value 4.0e-28
Match length 62
% identity 95
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
>gi_2130148_pir_S66339 translation elongation factor eEF-1

alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408)
alpha subunit of translation elongation factor 1 [Zea mays]

Seq. No. 298088
Seq. ID LIB3150-083-P2-N2-A10
Method BLASTX
NCBI GI g4406372
BLAST score 188
E value 3.0e-14
Match length 43
% identity 77
NCBI Description (AF109156) thiosulfate sulfurtransferase [Datisca glomerata]

Seq. No. 298089
Seq. ID LIB3150-083-P2-N2-C12
Method BLASTN
NCBI GI g1575127
BLAST score 220
E value 1.0e-120
Match length 280
% identity 94
NCBI Description Zea mays luminal binding protein cBiPe2 mRNA, complete cds

Seq. No. 298090
Seq. ID LIB3150-083-P2-N2-D11
Method BLASTN
NCBI GI g531055
BLAST score 64
E value 1.0e-27
Match length 72
% identity 97
NCBI Description Wheat mRNA for protein H2B-6, complete cds

Seq. No. 298091
Seq. ID LIB3150-083-P2-N2-F12
Method BLASTX
NCBI GI g2760321
BLAST score 309
E value 2.0e-28
Match length 108
% identity 59
NCBI Description (AC002130) F1N21.6 [Arabidopsis thaliana]

Seq. No. 298092
Seq. ID LIB3150-083-P2-N2-G11
Method BLASTX
NCBI GI g480450
BLAST score 158
E value 1.0e-10
Match length 34
% identity 91
NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No. 298093

Seq. ID LIB3150-083-P2-N2-H5
Method BLASTN
NCBI GI g2642323
BLAST score 89
E value 2.0e-42
Match length 222
% identity 86
NCBI Description Zea mays profilin (PRO4) mRNA, complete cds

Seq. No. 298094
Seq. ID LIB3150-084-P2-N2-F6
Method BLASTN
NCBI GI g498772
BLAST score 39
E value 1.0e-12
Match length 67
% identity 91
NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein

Seq. No. 298095
Seq. ID LIB3150-084-P2-N2-G10
Method BLASTX
NCBI GI g1335862
BLAST score 403
E value 2.0e-39
Match length 88
% identity 86
NCBI Description (U42608) clathrin heavy chain [Glycine max]

Seq. No. 298096
Seq. ID LIB3150-085-P1-N1-B3
Method BLASTX
NCBI GI g312179
BLAST score 264
E value 2.0e-33
Match length 81
% identity 95
NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 298097
Seq. ID LIB3150-085-P1-N1-D2
Method BLASTX
NCBI GI g2624328
BLAST score 207
E value 2.0e-16
Match length 63
% identity 65
NCBI Description (AJ002894) OsGRP2 [Oryza sativa]

Seq. No. 298098
Seq. ID LIB3150-085-P1-N1-F1
Method BLASTX
NCBI GI g1172833

Seq. No. 298099
 Seq. ID LIB3150-085-P1-N1-G1
 Method BLASTN
 NCBI GI g4099507
 BLAST score 66
 E value 6.0e-29
 Match length 141
 % identity 87
 NCBI Description Zea mays proliferating cell nuclear antigen (ZmPCNA2) mRNA, complete cds

Seq. No. 298100
 Seq. ID LIB3150-085-P1-N1-G2
 Method BLASTX
 NCBI GI g1262171
 BLAST score 203
 E value 6.0e-16
 Match length 61
 % identity 72
 NCBI Description (U21557) phosphoprotein phosphatase 2A, regulatory subunit A [Arabidopsis thaliana]

Seq. No. 298101
 Seq. ID LIB3150-086-P1-N1-C1
 Method BLASTX
 NCBI GI g3024018
 BLAST score 165
 E value 5.0e-12
 Match length 38
 % identity 87
 NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
 >gi_1546919_emb_CAA69225_(Y07920) translation initiation factor 5A [Zea mays] >gi_2668738_(AF034943) translation initiation factor 5A [Zea mays]

Seq. No. 298102
 Seq. ID LIB3150-086-P1-N1-D4
 Method BLASTN
 NCBI GI g168484
 BLAST score 50
 E value 1.0e-19
 Match length 114
 % identity 86
 NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298103
 Seq. ID LIB3150-086-P1-N1-E8
 Method BLASTX

NCBI GI g1184776
BLAST score 293
E value 2.0e-26
Match length 63
% identity 90
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]

Seq. No. 298104
Seq. ID LIB3150-087-P2-K1-C3
Method BLASTN
NCBI GI g498774
BLAST score 74
E value 9.0e-34
Match length 197
% identity 85
NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein

Seq. No. 298105
Seq. ID LIB3150-087-P2-K1-D6
Method BLASTN
NCBI GI g927571
BLAST score 51
E value 2.0e-20
Match length 62
% identity 97
NCBI Description Z.mays mRNA for calreticulin precursor

Seq. No. 298106
Seq. ID LIB3150-087-P2-K1-E8
Method BLASTX
NCBI GI g861170
BLAST score 298
E value 5.0e-27
Match length 76
% identity 78
NCBI Description (X03697) heat shock protein 70 [Zea mays]

Seq. No. 298107
Seq. ID LIB3150-087-P2-K1-F1
Method BLASTN
NCBI GI g22516
BLAST score 114
E value 2.0e-57
Match length 198
% identity 89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298108
Seq. ID LIB3150-087-P2-K1-F11
Method BLASTN
NCBI GI g2282583
BLAST score 38
E value 6.0e-12
Match length 134
% identity 83
NCBI Description Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete

cds

Seq. No. 298109
Seq. ID LIB3150-087-P2-K1-G2
Method BLASTN
NCBI GI g22121
BLAST score 191
E value 1.0e-103
Match length 243
% identity 95
NCBI Description Maize alcohol dehydrogenase 1 gene (Adh1-1F)

Seq. No. 298110
Seq. ID LIB3150-088-P2-K1-A4
Method BLASTN
NCBI GI g22272
BLAST score 105
E value 7.0e-52
Match length 328
% identity 82
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298111
Seq. ID LIB3150-088-P2-K1-B10
Method BLASTX
NCBI GI g3928086
BLAST score 157
E value 2.0e-10
Match length 45
% identity 58
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 298112
Seq. ID LIB3150-088-P2-K1-D11
Method BLASTX
NCBI GI g4586035
BLAST score 147
E value 3.0e-10
Match length 89
% identity 48
NCBI Description (AC007109) putative prohibitin protein [Arabidopsis thaliana]

Seq. No. 298113
Seq. ID LIB3150-088-P2-K1-F2
Method BLASTX
NCBI GI g4115937
BLAST score 226
E value 2.0e-18
Match length 51
% identity 75
NCBI Description (AF118223) contains similarity to human PCF11p homolog (GB:AF046935) [Arabidopsis thaliana]

Seq. No. 298114
Seq. ID LIB3150-089-P1-N1-B10
Method BLASTX

DRAFT

NCBI GI g417154
BLAST score 316
E value 2.0e-29
Match length 76
% identity 84
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock protein 82 - rice (strain Taichung Native One)
>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No. 298115
Seq. ID LIB3150-089-P1-N1-B2
Method BLASTX
NCBI GI g417154
BLAST score 288
E value 5.0e-30
Match length 104
% identity 71
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock protein 82 - rice (strain Taichung Native One)
>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No. 298116
Seq. ID LIB3150-089-P1-N1-F12
Method BLASTX
NCBI GI g2129626
BLAST score 360
E value 2.0e-34
Match length 88
% identity 76
NCBI Description J-domain protein - Arabidopsis thaliana
>gi_928936_emb_CAA89204_ (Z49238) J-domain protein [Arabidopsis thaliana] >gi_1585434_prf_2124427A diamide resistance gene [Arabidopsis thaliana]

Seq. No. 298117
Seq. ID LIB3150-089-P1-N1-G6
Method BLASTX
NCBI GI g3355475
BLAST score 177
E value 6.0e-13
Match length 81
% identity 53
NCBI Description (AC004218) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No. 298118
Seq. ID LIB3150-089-P1-N1-H2
Method BLASTN
NCBI GI g2623247
BLAST score 51
E value 3.0e-20
Match length 107
% identity 88
NCBI Description Zea mays SU1 isoamylase (sugary1) gene, complete cds

Seq. No. 298119

DRAFT

Seq. ID	LIB3150-089-P1-N1-H6
Method	BLASTX
NCBI GI	g1711036
BLAST score	264
E value	3.0e-23
Match length	95
% identity	63
NCBI Description	(U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]
Seq. No.	298120
Seq. ID	LIB3150-089-P2-K1-A5
Method	BLASTN
NCBI GI	g3318612
BLAST score	162
E value	6.0e-86
Match length	223
% identity	92
NCBI Description	Zea mays mRNA for mitochondrial phosphate transporter, complete cds
Seq. No.	298121
Seq. ID	LIB3150-089-P2-K1-B5
Method	BLASTN
NCBI GI	g342631
BLAST score	56
E value	9.0e-23
Match length	175
% identity	84
NCBI Description	Maize mitochondrial F-1-ATPase subunit-2 mRNA, complete cds
Seq. No.	298122
Seq. ID	LIB3150-089-P2-K1-G11
Method	BLASTN
NCBI GI	g168581
BLAST score	79
E value	2.0e-36
Match length	221
% identity	85
NCBI Description	Z.mays pyruvate,orthophosphate dikinase (PPDK2) gene, 3' end
Seq. No.	298123
Seq. ID	LIB3150-090-P2-K1-C11
Method	BLASTN
NCBI GI	g602252
BLAST score	89
E value	1.0e-42
Match length	141
% identity	91
NCBI Description	Zea mays enolase (eno2) mRNA, complete cds
Seq. No.	298124
Seq. ID	LIB3150-090-P2-K1-C3
Method	BLASTN
NCBI GI	g2642323
BLAST score	205

DRAFT

E value	1.0e-111
Match length	297
% identity	93
NCBI Description	Zea mays profilin (PRO4) mRNA, complete cds
Seq. No.	298125
Seq. ID	LIB3150-090-P2-K1-D4
Method	BLASTX
NCBI GI	g4490708
BLAST score	166
E value	2.0e-11
Match length	56
% identity	57
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]
Seq. No.	298126
Seq. ID	LIB3150-091-P1-N1-A4
Method	BLASTX
NCBI GI	g22166
BLAST score	212
E value	4.0e-23
Match length	89
% identity	71
NCBI Description	(X15711) adenine nucleotide translocator [Zea mays]
Seq. No.	298127
Seq. ID	LIB3150-091-P1-N1-A8
Method	BLASTX
NCBI GI	g451193
BLAST score	204
E value	4.0e-16
Match length	52
% identity	81
NCBI Description	(L28008) wali7 [Triticum aestivum] >gi_1090845_prf_2019486B wali7 gene [Triticum aestivum]
Seq. No.	298128
Seq. ID	LIB3150-091-P1-N1-B10
Method	BLASTN
NCBI GI	g5091496
BLAST score	40
E value	3.0e-13
Match length	166
% identity	82
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence
Seq. No.	298129
Seq. ID	LIB3150-091-P1-N1-D8
Method	BLASTX
NCBI GI	g3355620
BLAST score	165
E value	2.0e-11
Match length	40
% identity	85
NCBI Description	(AJ000235) partial sequence, homology to phosphoribosylformylglycinamidine synthase [Hordeum

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vulgare]

Seq. No. 298130
Seq. ID LIB3150-091-P1-N1-F1
Method BLASTN
NCBI GI g2431768
BLAST score 64
E value 2.0e-27
Match length 160
% identity 85
NCBI Description Zea mays acidic ribosomal protein P1a (rppla) mRNA, complete cds

Seq. No. 298131
Seq. ID LIB3150-091-P1-N1-G4
Method BLASTX
NCBI GI g3236242
BLAST score 176
E value 8.0e-13
Match length 100
% identity 45
NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No. 298132
Seq. ID LIB3150-091-P1-N1-G7
Method BLASTX
NCBI GI g1174613
BLAST score 162
E value 1.0e-14
Match length 84
% identity 57
NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614 (D17788) rice homologue of Tat binding protein [Oryza sativa]

Seq. No. 298133
Seq. ID LIB3150-092-P1-N1-B1
Method BLASTX
NCBI GI g462243
BLAST score 208
E value 1.0e-16
Match length 85
% identity 61
NCBI Description HISTONE H4 >gi_421921_pir_S32769 histone H4 - tomato >gi_297150_emb_CAA48923 (X69179) histone H4 [Lycopersicon esculentum] >gi_297152_emb_CAA48924 (X69180) histone H4 [Lycopersicon esculentum] >gi_2746721 (AF038387) histone H4 [Capsicum annuum]

Seq. No. 298134
Seq. ID LIB3150-092-P1-N1-B4
Method BLASTX
NCBI GI g461498
BLAST score 227
E value 8.0e-19

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Match length	92
% identity	58
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir_S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]
Seq. No.	298135
Seq. ID	LIB3150-092-P1-N1-C3
Method	BLASTX
NCBI GI	g627584
BLAST score	168
E value	6.0e-12
Match length	114
% identity	34
NCBI Description	protein p84 - human >gi_550058 (L36529) protein p84 [Homo sapiens]
Seq. No.	298136
Seq. ID	LIB3150-092-P1-N1-D8
Method	BLASTX
NCBI GI	g1174867
BLAST score	151
E value	1.0e-11
Match length	71
% identity	58
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2 KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275) ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi_1094912_prf_2107179A cytochrome c oxidase:SUBUNIT=8.2kD [Solanum tuberosum]
Seq. No.	298137
Seq. ID	LIB3150-092-P2-K1-A4
Method	BLASTN
NCBI GI	g168492
BLAST score	35
E value	3.0e-10
Match length	39
% identity	97
NCBI Description	Corn histone H3 (H3C3) gene, complete cds
Seq. No.	298138
Seq. ID	LIB3150-092-P2-K1-D12
Method	BLASTN
NCBI GI	g1321660
BLAST score	47
E value	2.0e-17
Match length	71
% identity	92
NCBI Description	Rice mRNA for ascorbate peroxidase, complete cds
Seq. No.	298139
Seq. ID	LIB3150-092-P2-K1-E1
Method	BLASTN

NCBI GI g747916
 BLAST score 44
 E value 1.0e-15
 Match length 124
 % identity 85
 NCBI Description Z.mays CaM2 mRNA for calmodulin

Seq. No. 298140
 Seq. ID LIB3150-093-P1-N1-A3
 Method BLASTX
 NCBI GI g3163946
 BLAST score 179
 E value 2.0e-13
 Match length 50
 % identity 70
 NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No. 298141
 Seq. ID LIB3150-093-P1-N1-A7
 Method BLASTX
 NCBI GI g3024018
 BLAST score 166
 E value 1.0e-11
 Match length 89
 % identity 42
 NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
 >gi_1546919_emb_CAA69225_(Y07920) translation initiation
 factor 5A [Zea mays] >gi_2668738 (AF034943) translation
 initiation factor 5A [Zea mays]

Seq. No. 298142
 Seq. ID LIB3150-093-P1-N1-A8
 Method BLASTX
 NCBI GI g2224897
 BLAST score 211
 E value 3.0e-17
 Match length 68
 % identity 56
 NCBI Description (U67132) DNA-binding protein PcMYB1 [Petroselinum crispum]

Seq. No. 298143
 Seq. ID LIB3150-093-P1-N1-F1
 Method BLASTX
 NCBI GI g113622
 BLAST score 268
 E value 3.0e-41
 Match length 106
 % identity 92
 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
 >gi_68197_pir_ADRZY fructose-bisphosphate aldolase (EC
 4.1.2.13), cytosolic - rice >gi_20204_emb_CAA37290
 (X53130) fructose-diphosphate aldolase (AA 1-358) [Oryza
 sativa]

Seq. No. 298144
 Seq. ID LIB3150-093-P1-N1-G2
 Method BLASTN

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NCBI GI g4151124
BLAST score 58
E value 4.0e-24
Match length 78
% identity 94
NCBI Description Zea mays PDI-like protein mRNA, complete cds

Seq. No. 298145
Seq. ID LIB3150-093-P1-N1-H2
Method BLASTX
NCBI GI g1085973
BLAST score 191
E value 6.0e-15
Match length 62
% identity 65
NCBI Description isopentyl pyrophosphate isomerase - Clarkia breweri
(fragment) >gi_572635_emb_CAA57947_(X82627) isopentenyl
pyrophosphate isomerase [Clarkia breweri]

Seq. No. 298146
Seq. ID LIB3150-093-P1-N1-H4
Method BLASTN
NCBI GI g22144
BLAST score 180
E value 8.0e-97
Match length 205
% identity 96
NCBI Description Maize anaerobically regulated gene for fructose
bisphosphate aldolase (EC 4.1.2.13)

Seq. No. 298147
Seq. ID LIB3150-093-P1-N1-H5
Method BLASTX
NCBI GI g461498
BLAST score 297
E value 3.0e-27
Match length 78
% identity 79
NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
(ALAAT-2) >gi_320619_pir_S28429 alanine transaminase (EC
2.6.1.2) - proso millet >gi_296204_emb_CAA49199_(X69421)
alanine aminotransferase [Panicum miliaceum]

Seq. No. 298148
Seq. ID LIB3150-093-P2-K1-C10
Method BLASTN
NCBI GI g1154858
BLAST score 45
E value 4.0e-16
Match length 145
% identity 82
NCBI Description H.vulgare mRNA for L24 ribosomal protein

Seq. No. 298149
Seq. ID LIB3150-093-P2-K1-F2
Method BLASTX

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NCBI GI g3885884
BLAST score 211
E value 6.0e-17
Match length 45
% identity 89
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 298150
Seq. ID LIB3150-094-P1-N1-C5
Method BLASTN
NCBI GI g22272
BLAST score 41
E value 5.0e-14
Match length 65
% identity 91
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298151
Seq. ID LIB3150-094-P1-N1-C8
Method BLASTX
NCBI GI g1351014
BLAST score 205
E value 3.0e-16
Match length 91
% identity 54
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010)
ribosomal protein S8 [Oryza sativa]

Seq. No. 298152
Seq. ID LIB3150-094-P1-N1-D6
Method BLASTX
NCBI GI g4469020
BLAST score 180
E value 2.0e-13
Match length 66
% identity 48
NCBI Description (AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 298153
Seq. ID LIB3150-094-P1-N1-F2
Method BLASTX
NCBI GI g4115918
BLAST score 200
E value 1.0e-15
Match length 44
% identity 86
NCBI Description (AF118222) similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]

Seq. No. 298154
Seq. ID LIB3150-094-P1-N1-F8
Method BLASTX
NCBI GI g4539437
BLAST score 345
E value 1.0e-35
Match length 122

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% identity 64
NCBI Description (AL049523) putative protein [Arabidopsis thaliana]

Seq. No. 298155
Seq. ID LIB3150-094-P1-N1-G12
Method BLASTX
NCBI GI g1332579
BLAST score 492
E value 9.0e-50
Match length 132
% identity 8
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 298156
Seq. ID LIB3150-094-P1-N1-G7
Method BLASTN
NCBI GI g2282583
BLAST score 38
E value 4.0e-12
Match length 106
% identity 84
NCBI Description Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete cds

Seq. No. 298157
Seq. ID LIB3150-094-P2-K1-C12
Method BLASTX
NCBI GI g3128181
BLAST score 157
E value 2.0e-10
Match length 51
% identity 61
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 298158
Seq. ID LIB3150-094-P2-K1-C2
Method BLASTN
NCBI GI g22516
BLAST score 57
E value 1.0e-23
Match length 109
% identity 88
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298159
Seq. ID LIB3150-094-P2-K1-E11
Method BLASTN
NCBI GI g312180
BLAST score 73
E value 6.0e-33
Match length 125
% identity 90
NCBI Description Z.mays GapC4 gene

Seq. No. 298160
Seq. ID LIB3150-094-P2-K1-E12
Method BLASTX

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NCBI GI	g121296
BLAST score	362
E value	1.0e-34
Match length	109
% identity	60
NCBI Description	1,4-ALPHA-GLUCAN BRANCHING ENZYME (GLYCOGEN BRANCHING ENZYME) >gi_66573_pir_NQECA 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - Escherichia coli >gi_146142 (M13751) branching enzyme (EC 2.4.1.18) [Escherichia coli] >gi_1789839 (AE000419) 1,4-alpha-glucan branching enzyme [Escherichia coli]
Seq. No.	298161
Seq. ID	LIB3150-094-P2-K1-G8
Method	BLASTX
NCBI GI	g2583123
BLAST score	226
E value	1.0e-18
Match length	47
% identity	83
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]
Seq. No.	298162
Seq. ID	LIB3150-095-P1-N1-A1
Method	BLASTX
NCBI GI	g3738257
BLAST score	168
E value	2.0e-12
Match length	46
% identity	78
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]
Seq. No.	298163
Seq. ID	LIB3150-095-P1-N1-B5
Method	BLASTX
NCBI GI	g2851508
BLAST score	327
E value	2.0e-30
Match length	87
% identity	70
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597, gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]
Seq. No.	298164
Seq. ID	LIB3150-095-P1-N1-C2
Method	BLASTX
NCBI GI	g4432819
BLAST score	153
E value	1.0e-10
Match length	48
% identity	62
NCBI Description	(AC006593) putative kinesin light chain [Arabidopsis

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thaliana]

Seq. No. 298165
Seq. ID LIB3150-095-P1-N1-D1
Method BLASTX
NCBI GI g122085
BLAST score 455
E value 2.0e-45
Match length 109
% identity 85
NCBI Description HISTONE H3 >gi_81641_pir_S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir_S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir_S57626 histone H3 - maize >gi_20251_emb_CAA31969_(X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_(X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493_(M36658) histone H3 (H3C3) [Zea mays] >gi_168495_(M13378) histone H3 [Zea mays] >gi_168497_(M13379) histone H3 [Zea mays] >gi_168506_(M35388) histone H3 [Zea mays] >gi_169655_(M77493) histone H3 [Petroselinum crispum] >gi_169657_(M77494) histone H3 [Petroselinum crispum] >gi_169659_(M77495) histone H3 [Petroselinum crispum] >gi_387565_(M17130) histone H3 [Arabidopsis thaliana] >gi_387567_(M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_(X84377) histone 3 [Zea mays] >gi_1040764_(M35387) histone H3 [Arabidopsis thaliana] >gi_1314779_(U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_(X82414) Histone H3 [Asparagus officinalis] >gi_1667592_(U77296) histone 3 [Oryza sativa] >gi_3249101_(AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511, gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf_1303352A histone H3 [Helicoverpa zea] >gi_225839_prf_1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 298166
Seq. ID LIB3150-095-P1-N1-D3
Method BLASTN
NCBI GI g1421729
BLAST score 38
E value 6.0e-12
Match length 110
% identity 84
NCBI Description Zea mays T cytoplasm male sterility restorer factor 2 (rf2) mRNA, complete cds

Seq. No. 298167
Seq. ID LIB3150-095-P1-N1-E1
Method BLASTN
NCBI GI g1037129
BLAST score 296
E value 1.0e-166
Match length 400
% identity 94
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298168
Seq. ID LIB3150-095-P1-N1-E12
Method BLASTX
NCBI GI g419803
BLAST score 249
E value 1.0e-21
Match length 69
% identity 68
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298169
Seq. ID LIB3150-095-P2-K1-A7
Method BLASTN
NCBI GI g1154858
BLAST score 45
E value 2.0e-16
Match length 57
% identity 95
NCBI Description H.vulgare mRNA for L24 ribosomal protein

Seq. No. 298170
Seq. ID LIB3150-095-P2-K1-H12
Method BLASTN
NCBI GI g2341060
BLAST score 270
E value 1.0e-150
Match length 314
% identity 96
NCBI Description Zea mays translational initiation factor eIF-4A (tif-4A3) mRNA, complete cds

Seq. No. 298171
Seq. ID LIB3150-096-P1-N1-D10
Method BLASTX
NCBI GI g99771
BLAST score 335
E value 2.0e-31
Match length 109
% identity 66
NCBI Description ubiquitin 81-aa extension protein 1 - Arabidopsis thaliana >gi_166934 (J05539) ubiquitin extension protein (UBQ5) [Arabidopsis thaliana]

Seq. No. 298172
Seq. ID LIB3150-096-P1-N1-D2
Method BLASTX
NCBI GI g22168
BLAST score 231
E value 9.0e-20
Match length 62
% identity 76
NCBI Description (X15712) adenine nucleotide translocator [Zea mays]

Seq. No. 298173
Seq. ID LIB3150-096-P1-N1-D3
Method BLASTX

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NCBI GI g1136122
BLAST score 496
E value 2.0e-50
Match length 119
% identity 79
NCBI Description (X91807) alfa-tubulin [Oryza sativa]

Seq. No. 298174
Seq. ID LIB3150-096-P1-N1-E1
Method BLASTX
NCBI GI g3925363
BLAST score 157
E value 1.0e-10
Match length 94
% identity 46
NCBI Description (AF067961) homeodomain protein [Malus domestica]

Seq. No. 298175
Seq. ID LIB3150-096-P1-N1-E7
Method BLASTX
NCBI GI g1723669
BLAST score 153
E value 5.0e-10
Match length 78
% identity 41
NCBI Description HYPOTHETICAL 71.3 KD PROTEIN IN SCM4-MUP1 INTERGENIC REGION
>gi_2131657_pir_S64348 hypothetical protein YGR054w -
yeast (Saccharomyces cerevisiae) >gi_1323065_emb_CAA97054_
(Z72839) ORF YGR054w [Saccharomyces cerevisiae]

Seq. No. 298176
Seq. ID LIB3150-096-P1-N1-G4
Method BLASTX
NCBI GI g2505940
BLAST score 172
E value 2.0e-12
Match length 65
% identity 58
NCBI Description (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]

Seq. No. 298177
Seq. ID LIB3150-097-P1-N1-A8
Method BLASTX
NCBI GI g312179
BLAST score 386
E value 2.0e-37
Match length 86
% identity 87
NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase
(phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
>gi_1185554 (U45858) glyceraldehyde-3-phosphate
dehydrogenase [Zea mays]

Seq. No. 298178
Seq. ID LIB3150-097-P1-N1-E7
Method BLASTN

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NCBI GI	g22292
BLAST score	50
E value	4.0e-19
Match length	82
% identity	91
NCBI Description	Z.mays mRNA for glycine-rich protein
Seq. No.	298179
Seq. ID	LIB3150-097-P1-N1-E9
Method	BLASTX
NCBI GI	g2129946
BLAST score	346
E value	1.0e-32
Match length	87
% identity	80
NCBI Description	ADP-ribosylation factor homolog GTP-binding protein NTGB1 - common tobacco (fragment) >gi_1184987 (U46927) NTGB1 [Nicotiana tabacum]
Seq. No.	298180
Seq. ID	LIB3150-097-P1-N1-F7
Method	BLASTX
NCBI GI	g1703374
BLAST score	199
E value	2.0e-15
Match length	72
% identity	67
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_2129457_pir_S66337 ADP-ribosylation factor 1 - Chlamydomonas reinhardtii >gi_861205 (U27120) ADP-ribosylation factor [Chlamydomonas reinhardtii]
Seq. No.	298181
Seq. ID	LIB3150-097-P1-N1-F9
Method	BLASTX
NCBI GI	g1184774
BLAST score	232
E value	2.0e-26
Match length	103
% identity	69
NCBI Description	(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]
Seq. No.	298182
Seq. ID	LIB3150-097-P1-N1-G7
Method	BLASTX
NCBI GI	g1184774
BLAST score	204
E value	8.0e-25
Match length	95
% identity	72
NCBI Description	(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]
Seq. No.	298183
Seq. ID	LIB3150-097-P1-N1-H10
Method	BLASTN

NCBI GI g571474
BLAST score 33
E value 4.0e-09
Match length 65
% identity 88
NCBI Description Chlamydomonas reinhardtii histone H3 (ch3-III), histone H4 (ch4-III), histone H2B (ch2b-III) and histone H2A (ch2a-III) genes, complete cds

Seq. No. 298184
Seq. ID LIB3150-098-P1-N1-B1
Method BLASTX
NCBI GI g1658313
BLAST score 210
E value 6.0e-17
Match length 52
% identity 75
NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 298185
Seq. ID LIB3150-098-P1-N1-B9
Method BLASTX
NCBI GI g3176711
BLAST score 192
E value 1.0e-14
Match length 88
% identity 57
NCBI Description (AC002392) bZIP-like protein [Arabidopsis thaliana]

Seq. No. 298186
Seq. ID LIB3150-098-P1-N1-D3
Method BLASTX
NCBI GI g4469005
BLAST score 242
E value 2.0e-20
Match length 88
% identity 51
NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 298187
Seq. ID LIB3150-098-P1-N1-E5
Method BLASTX
NCBI GI g3015621
BLAST score 236
E value 3.0e-20
Match length 72
% identity 72
NCBI Description (AF035460) low molecular weight heat shock protein precursor [Zea mays]

Seq. No. 298188
Seq. ID LIB3150-098-P1-N1-H4
Method BLASTX
NCBI GI g2499932
BLAST score 172
E value 1.0e-12
Match length 52

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% identity 67
NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305
(U22442) adenine phosphoribosyltransferase form 1 [Triticum aestivum]

Seq. No. 298189
Seq. ID LIB3150-099-P1-N1-F12
Method BLASTX
NCBI GI g3687251
BLAST score 208
E value 8.0e-17
Match length 62
% identity 63
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]

Seq. No. 298190
Seq. ID LIB3150-099-P1-N1-H8
Method BLASTN
NCBI GI g22172
BLAST score 39
E value 1.0e-12
Match length 71
% identity 89
NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit

Seq. No. 298191
Seq. ID LIB3150-100-P1-N1-A7
Method BLASTN
NCBI GI g2811133
BLAST score 125
E value 4.0e-64
Match length 201
% identity 91
NCBI Description Zea mays starch synthase isoform zSTSII-1 (zSSIIa) mRNA, partial cds

Seq. No. 298192
Seq. ID LIB3150-100-P1-N1-E1
Method BLASTX
NCBI GI g4530611
BLAST score 401
E value 4.0e-39
Match length 81
% identity 91
NCBI Description (AF134552) serine/threonine protein phosphatase PP2A-2 catalytic subunit [Oryza sativa subsp. indica]

Seq. No. 298193
Seq. ID LIB3150-100-P1-N1-E12
Method BLASTX
NCBI GI g2244760
BLAST score 155
E value 9.0e-11
Match length 62
% identity 50
NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]

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Seq. No.	298194
Seq. ID	LIB3150-100-P1-N1-H3
Method	BLASTN
NCBI GI	g1037129
BLAST score	284
E value	1.0e-159
Match length	358
% identity	95
NCBI Description	(gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]
Seq. No.	298195
Seq. ID	LIB3150-100-P1-N1-H5
Method	BLASTX
NCBI GI	g1168609
BLAST score	188
E value	2.0e-14
Match length	71
% identity	51
NCBI Description	AUXIN-RESISTANCE PROTEIN AXR1 >gi_479664_pir_S35071 auxin-resistance protein AXR1 - Arabidopsis thaliana >gi_304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to Arabidopsis AXR1 (gb ATHAXR1122). [Arabidopsis thaliana] >gi_448755_prf_1917337A ubiquitin-activating enzyme E1 [Arabidopsis thaliana]
Seq. No.	298196
Seq. ID	LIB3150-100-P2-K1-C5
Method	BLASTX
NCBI GI	g445612
BLAST score	149
E value	2.0e-09
Match length	39
% identity	77
NCBI Description	ribosomal protein S19 [Solanum tuberosum]
Seq. No.	298197
Seq. ID	LIB3150-100-P2-K1-D1
Method	BLASTX
NCBI GI	g1351270
BLAST score	238
E value	5.0e-20
Match length	53
% identity	89
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_478410_pir_JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi_169821 (M87064) triosephosphate isomerase [Oryza sativa]
Seq. No.	298198
Seq. ID	LIB3150-100-P2-K1-D8
Method	BLASTN
NCBI GI	g22469
BLAST score	61
E value	9.0e-26
Match length	207

% identity 81
NCBI Description Maize mRNA for cytoplasmic ribosomal protein S11

Seq. No. 298199
Seq. ID LIB3150-100-P2-K1-E6
Method BLASTX
NCBI GI g3372518
BLAST score 635
E value 1.0e-66
Match length 123
% identity 97
NCBI Description (AF050631) invertase [Zea mays]

Seq. No. 298200
Seq. ID LIB3150-101-P1-N1-C3
Method BLASTX
NCBI GI g1711036
BLAST score 322
E value 5.0e-30
Match length 98
% identity 66
NCBI Description (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]

Seq. No. 298201
Seq. ID LIB3150-101-P1-N1-F11
Method BLASTX
NCBI GI g1184774
BLAST score 401
E value 3.0e-39
Match length 91
% identity 85
NCBI Description (U45856) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 298202
Seq. ID LIB3150-102-P2-K1-E7
Method BLASTN
NCBI GI g2340107
BLAST score 95
E value 4.0e-46
Match length 186
% identity 89
NCBI Description Zea mays starch branching enzyme IIa (Sbe2a) mRNA, partial cds

Seq. No. 298203
Seq. ID LIB3150-103-P2-K1-A11
Method BLASTX
NCBI GI g136063
BLAST score 157
E value 2.0e-10
Match length 35
% identity 91
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
>gi_68426_pir_ISZMT triose-phosphate isomerase (EC 5.3.1.1) - maize >gi_168647 (L00371) triosephosphate

isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)
triosephosphate isomerase [Zea mays]

Seq. No. 298204
Seq. ID LIB3150-103-P2-K1-B11
Method BLASTX
NCBI GI g1076531
BLAST score 166
E value 2.0e-11
Match length 38
% identity 82
NCBI Description hypothetical protein, pollen allergen homolog - garden pea
>gi_2129891_pir_S65056 pollen allergen homolog precursor
(clone PPA1) - garden pea >gi_732905_emb_CAA59470_ (X85187)
homology with pollen allergens [Pisum sativum]

Seq. No. 298205
Seq. ID LIB3150-103-P2-K1-D3
Method BLASTX
NCBI GI g4150963
BLAST score 164
E value 3.0e-11
Match length 57
% identity 60
NCBI Description (Y18620) DsPTP1 protein [Arabidopsis thaliana]

Seq. No. 298206
Seq. ID LIB3150-103-P2-K1-E8
Method BLASTN
NCBI GI g625147
BLAST score 144
E value 3.0e-75
Match length 270
% identity 97
NCBI Description Zea mays protein disulfide isomerase (pdi) mRNA, complete
cds

Seq. No. 298207
Seq. ID LIB3150-103-P2-K1-F7
Method BLASTX
NCBI GI g1076820
BLAST score 166
E value 1.0e-11
Match length 41
% identity 80
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize

Seq. No. 298208
Seq. ID LIB3150-103-P2-K1-G12
Method BLASTX
NCBI GI g731827
BLAST score 143
E value 9.0e-09
Match length 54
% identity 50
NCBI Description MITOCHONDRIAL ACIDIC PROTEIN MAM33 PRECURSOR
>gi_626327_pir_S48409 hypothetical protein YIL070c - yeast

(Saccharomyces cerevisiae) >gi_557799_emb_CAA86153_
(Z38060) orf, len: 266, CAI: 0.21 [Saccharomyces
cerevisiae]

Seq. No. 298209
Seq. ID LIB3150-104-P2-K1-A5
Method BLASTX
NCBI GI g1762945
BLAST score 150
E value 1.0e-09
Match length 45
% identity 69
NCBI Description (U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No. 298210
Seq. ID LIB3150-104-P2-K1-D5
Method BLASTX
NCBI GI g3790441
BLAST score 148
E value 2.0e-09
Match length 36
% identity 89
NCBI Description (AF030515) chaperonin 60 alpha subunit [Canavalia lineata]

Seq. No. 298211
Seq. ID LIB3150-104-P2-K1-D8
Method BLASTN
NCBI GI g2662309
BLAST score 41
E value 8.0e-14
Match length 61
% identity 92
NCBI Description Hordeum vulgare mRNA for bpw1, complete cds

Seq. No. 298212
Seq. ID LIB3150-104-P2-K1-F1
Method BLASTX
NCBI GI g3334323
BLAST score 374
E value 7.0e-36
Match length 87
% identity 83
NCBI Description GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1 (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi_2104550 (AF001535) AGAA.4 [Arabidopsis thaliana]

Seq. No. 298213
Seq. ID LIB3150-104-P2-K1-F2
Method BLASTN
NCBI GI g3925236
BLAST score 74
E value 2.0e-33
Match length 152
% identity 87

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NCBI Description Zea mays 6-phosphogluconate dehydrogenase gene, partial cds

Seq. No. 298214
Seq. ID LIB3150-104-P2-K1-H6
Method BLASTX
NCBI GI g3763917
BLAST score 209
E value 8.0e-17
Match length 44
% identity 84

NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]
>gi_4531438_gb_AAD22123.1_AC006224_5 (AC006224)
hypothetical protein [Arabidopsis thaliana]

Seq. No. 298215
Seq. ID LIB3150-105-P2-K1-A4
Method BLASTN
NCBI GI g902526
BLAST score 84
E value 1.0e-39
Match length 136
% identity 90

NCBI Description Zea mays clone MuBG7 ubiquitin fusion protein gene,
complete cds

Seq. No. 298216
Seq. ID LIB3150-105-P2-K1-B7
Method BLASTN
NCBI GI g2642323
BLAST score 246
E value 1.0e-136
Match length 279
% identity 97

NCBI Description Zea mays profilin (PRO4) mRNA, complete cds

Seq. No. 298217
Seq. ID LIB3150-105-P2-K1-E5
Method BLASTN
NCBI GI g217973
BLAST score 131
E value 1.0e-67
Match length 230
% identity 92

NCBI Description Zea mays gene for triosephosphate isomerase, complete cds

Seq. No. 298218
Seq. ID LIB3150-105-P2-K1-G1
Method BLASTN
NCBI GI g602252
BLAST score 42
E value 1.0e-14
Match length 211
% identity 78

NCBI Description Zea mays enolase (eno2) mRNA, complete cds

Seq. No. 298219
Seq. ID LIB3150-106-P2-K1-B5

Method BLASTX
NCBI GI g2230873
BLAST score 197
E value 4.0e-15
Match length 67
% identity 60
NCBI Description (X98494) M phase phosphoprotein 10 [Homo sapiens]

Seq. No. 298220
Seq. ID LIB3150-106-P2-K1-F12
Method BLASTN
NCBI GI g1335965
BLAST score 40
E value 3.0e-13
Match length 148
% identity 82
NCBI Description Zea mays acetyl CoA carboxylase mRNA, partial cds

Seq. No. 298221
Seq. ID LIB3150-106-P2-K1-F3
Method BLASTX
NCBI GI g1172977
BLAST score 359
E value 3.0e-34
Match length 77
% identity 86
NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 298222
Seq. ID LIB3150-106-P2-K1-H1
Method BLASTX
NCBI GI g1076800
BLAST score 215
E value 3.0e-17
Match length 57
% identity 77
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme - maize >gi_600116_emb_CAA84406 (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi_1096503_prf_2111423A ascorbate peroxidase [Zea mays]

Seq. No. 298223
Seq. ID LIB3150-106-P2-K1-H3
Method BLASTN
NCBI GI g22144
BLAST score 292
E value 1.0e-163
Match length 344
% identity 96
NCBI Description Maize anaerobically regulated gene for fructose bisphosphate aldolase (EC 4.1.2.13)

Seq. No. 298224
Seq. ID LIB3150-106-P2-K1-H8
Method BLASTX
NCBI GI g2996166

DOCUMENT NUMBER

BLAST score 255
E value 5.0e-22
Match length 55
% identity 82
NCBI Description (AF051757) putative 60S ribosomal protein L15 [Picea mariana] >gi_2996168 (AF051758) putative 60S ribosomal protein L15 [Picea mariana] >gi_2996170 (AF051759) putative 60S ribosomal protein L15 [Picea mariana]

Seq. No. 298225
Seq. ID LIB3150-107-P1-N1-E12
Method BLASTX
NCBI GI g3548818
BLAST score 206
E value 3.0e-16
Match length 113
% identity 43
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 298226
Seq. ID LIB3150-107-P1-N1-E4
Method BLASTN
NCBI GI g577818
BLAST score 62
E value 2.0e-26
Match length 125
% identity 89
NCBI Description Z.mays gene for H2B histone (gH2B4)

Seq. No. 298227
Seq. ID LIB3150-107-P1-N1-F4
Method BLASTX
NCBI GI g462195
BLAST score 242
E value 2.0e-20
Match length 71
% identity 66
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
>gi_100682_pir_S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No. 298228
Seq. ID LIB3150-107-P1-N1-H4
Method BLASTX
NCBI GI g4510423
BLAST score 175
E value 7.0e-13
Match length 87
% identity 45
NCBI Description (AC006929) unknown protein [Arabidopsis thaliana]

Seq. No. 298229
Seq. ID LIB3150-107-P2-K1-A10
Method BLASTN
NCBI GI g498774

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BLAST score	220
E value	1.0e-120
Match length	267
% identity	96
NCBI Description	Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein
Seq. No.	298230
Seq. ID	LIB3150-107-P2-K1-B10
Method	BLASTX
NCBI GI	g2492519
BLAST score	161
E value	6.0e-11
Match length	43
% identity	77
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase subunit [Spinacia oleracea]
Seq. No.	298231
Seq. ID	LIB3150-107-P2-K1-B5
Method	BLASTN
NCBI GI	g498772
BLAST score	143
E value	1.0e-74
Match length	252
% identity	89
NCBI Description	Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein
Seq. No.	298232
Seq. ID	LIB3150-107-P2-K1-F12
Method	BLASTN
NCBI GI	g2341060
BLAST score	181
E value	3.0e-97
Match length	285
% identity	91
NCBI Description	Zea mays translational initiation factor eIF-4A (tif-4A3) mRNA, complete cds
Seq. No.	298233
Seq. ID	LIB3150-107-P2-K1-H2
Method	BLASTN
NCBI GI	g22324
BLAST score	172
E value	6.0e-92
Match length	212
% identity	95
NCBI Description	Z.mays mRNA for H2B histone (clone cH2B221)
Seq. No.	298234
Seq. ID	LIB3150-108-P1-N1-A11
Method	BLASTX
NCBI GI	g1658313
BLAST score	148
E value	2.0e-09
Match length	102
% identity	39

NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 298235
Seq. ID LIB3150-108-P1-N1-C4
Method BLASTX
NCBI GI g419803
BLAST score 347
E value 1.0e-32
Match length 122
% identity 60
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298236
Seq. ID LIB3150-108-P1-N1-C5
Method BLASTX
NCBI GI g168664
BLAST score 317
E value 2.0e-29
Match length 65
% identity 88
NCBI Description (M13507) zein protein precursor [Zea mays]

Seq. No. 298237
Seq. ID LIB3150-108-P1-N1-E2
Method BLASTX
NCBI GI g3335372
BLAST score 172
E value 3.0e-12
Match length 122
% identity 38
NCBI Description (AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No. 298238
Seq. ID LIB3150-108-P1-N1-E5
Method BLASTX
NCBI GI g1658313
BLAST score 321
E value 8.0e-30
Match length 91
% identity 34
NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 298239
Seq. ID LIB3150-108-P1-N1-G2
Method BLASTX
NCBI GI g3746936
BLAST score 175
E value 3.0e-13
Match length 69
% identity 54
NCBI Description (AF091808) actin 1 [Anemia phyllitidis]

Seq. No. 298240
Seq. ID LIB3150-108-P1-N1-H7
Method BLASTX
NCBI GI g2282584

BLAST score 486
E value 4.0e-49
Match length 110
% identity 85
NCBI Description (U76259) elongation factor 1-alpha [Zea mays]

Seq. No. 298241
Seq. ID LIB3150-108-P2-K1-B9
Method BLASTN
NCBI GI g1575127
BLAST score 103
E value 1.0e-50
Match length 345
% identity 82
NCBI Description Zea mays luminal binding protein cBiPe2 mRNA, complete cds

Seq. No. 298242
Seq. ID LIB3150-108-P2-K1-E10
Method BLASTX
NCBI GI g445613
BLAST score 174
E value 2.0e-12
Match length 50
% identity 64
NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No. 298243
Seq. ID LIB3150-108-P2-K1-E5
Method BLASTN
NCBI GI g168512
BLAST score 147
E value 6.0e-77
Match length 365
% identity 88
NCBI Description Maize major protein (L3) mRNA from the surface of lipid bodies, 3' end

Seq. No. 298244
Seq. ID LIB3150-108-P2-K1-F7
Method BLASTX
NCBI GI g4512699
BLAST score 181
E value 3.0e-13
Match length 53
% identity 62
NCBI Description (AC006569) putative NADH-ubiquinone oxireductase [Arabidopsis thaliana]

Seq. No. 298245
Seq. ID LIB3150-108-P2-K1-H3
Method BLASTN
NCBI GI g1184773
BLAST score 154
E value 3.0e-81
Match length 182
% identity 97
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3

(gpc3) mRNA, complete cds

Seq. No. 298246
Seq. ID LIB3150-109-P2-K1-A4
Method BLASTX
NCBI GI g2827700
BLAST score 200
E value 2.0e-15
Match length 84
% identity 49
NCBI Description (AL021684) DEAD box ATP dependent helicase protein [Arabidopsis thaliana]

Seq. No. 298247
Seq. ID LIB3150-109-P2-K1-B5
Method BLASTX
NCBI GI g4309698
BLAST score 307
E value 4.0e-28
Match length 130
% identity 56
NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No. 298248
Seq. ID LIB3150-109-P2-K1-D12
Method BLASTN
NCBI GI g22272
BLAST score 98
E value 1.0e-47
Match length 287
% identity 86
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 298249
Seq. ID LIB3150-109-P2-K1-E6
Method BLASTN
NCBI GI g168505
BLAST score 41
E value 5.0e-14
Match length 45
% identity 98
NCBI Description Zea mays histone H3 gene, complete cds

Seq. No. 298250
Seq. ID LIB3150-109-P2-K1-F10
Method BLASTX
NCBI GI g1169533
BLAST score 335
E value 3.0e-31
Match length 81
% identity 85
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
>gi_515827_emb_CAA56645_(X80474) enolase [Neocallimastix frontalis]

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Seq. No.	298251
Seq. ID	LIB3150-109-P2-K1-G2
Method	BLASTX
NCBI GI	g136057
BLAST score	194
E value	9.0e-15
Match length	45
% identity	84
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_99499_pir_A32187 (S)-tetrahydroberberine oxidase - Coptis japonica >gi_556171 (J04121) triosephosphate isomerase [Coptis japonica]
Seq. No.	298252
Seq. ID	LIB3150-109-P2-K1-H10
Method	BLASTN
NCBI GI	g998429
BLAST score	144
E value	3.0e-75
Match length	333
% identity	85
NCBI Description	GRF1=general regulatory factor [Zea mays, XL80, Genomic, 5348 nt]
Seq. No.	298253
Seq. ID	LIB3150-110-P2-K1-C4
Method	BLASTN
NCBI GI	g22272
BLAST score	72
E value	3.0e-32
Match length	215
% identity	82
NCBI Description	Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
Seq. No.	298254
Seq. ID	LIB3150-110-P2-K1-D11
Method	BLASTN
NCBI GI	g1532072
BLAST score	72
E value	4.0e-32
Match length	247
% identity	81
NCBI Description	Z.mays mRNA for S-adenosylmethionine decarboxylase
Seq. No.	298255
Seq. ID	LIB3150-110-P2-K1-D12
Method	BLASTN
NCBI GI	g312178
BLAST score	89
E value	2.0e-42
Match length	143
% identity	58
NCBI Description	Z.mays GapC2 gene
Seq. No.	298256
Seq. ID	LIB3150-110-P2-K1-G2
Method	BLASTN

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NCBI GI	g531832
BLAST score	36
E value	3.0e-11
Match length	76
% identity	87
NCBI Description	Cloning vector pSport2, complete sequence
Seq. No.	298257
Seq. ID	LIB3150-110-P2-K1-G6
Method	BLASTN
NCBI GI	g902585
BLAST score	35
E value	4.0e-10
Match length	55
% identity	91
NCBI Description	Zea mays clone MubG9 ubiquitin gene, complete cds
Seq. No.	298258
Seq. ID	LIB3150-111-P2-K1-C5
Method	BLASTN
NCBI GI	g293886
BLAST score	38
E value	6.0e-12
Match length	74
% identity	88
NCBI Description	Zea mays glyceraldehyde-3-phosphate dehydrogenase mRNA, 3' end, (clone GAPC3)
Seq. No.	298259
Seq. ID	LIB3150-112-P2-K1-A3
Method	BLASTX
NCBI GI	g2695941
BLAST score	200
E value	1.0e-15
Match length	50
% identity	76
NCBI Description	(AJ222784) ribosomal like-protein [Hordeum vulgare]
Seq. No.	298260
Seq. ID	LIB3150-112-P2-K1-A5
Method	BLASTX
NCBI GI	g2498077
BLAST score	510
E value	8.0e-52
Match length	99
% identity	97
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase [Saccharum officinarum]
Seq. No.	298261
Seq. ID	LIB3150-112-P2-K1-A6
Method	BLASTN
NCBI GI	g2431766
BLAST score	173
E value	1.0e-92
Match length	217

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% identity 95
NCBI Description Zea mays acidic ribosomal protein P3a (rpp3a) mRNA,
complete cds

Seq. No. 298262
Seq. ID LIB3150-112-P2-K1-B7
Method BLASTX
NCBI GI g3860277
BLAST score 392
E value 5.0e-38
Match length 88
% identity 86
NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 298263
Seq. ID LIB3150-112-P2-K1-C2
Method BLASTX
NCBI GI g19614
BLAST score 171
E value 4.0e-12
Match length 45
% identity 78
NCBI Description (X13677) histone H3 (AA 1-58) [Medicago sativa]

Seq. No. 298264
Seq. ID LIB3150-112-P2-K1-F5
Method BLASTN
NCBI GI g1184773
BLAST score 44
E value 9.0e-16
Match length 116
% identity 86
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GACP3 (gpc3) mRNA, complete cds

Seq. No. 298265
Seq. ID LIB3150-112-P2-K1-G3
Method BLASTX
NCBI GI g1653293
BLAST score 160
E value 8.0e-11
Match length 58
% identity 57
NCBI Description (D90912) ornithine acetyltransferase [Synechocystis sp.]

Seq. No. 298266
Seq. ID LIB3150-112-P2-K1-H5
Method BLASTN
NCBI GI g2257755
BLAST score 202
E value 1.0e-110
Match length 311
% identity 91
NCBI Description Zea mays nucleolar histone deacetylase HD2-p39 mRNA,
complete cds

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Seq. No.	298267
Seq. ID	LIB3150-113-P2-K1-C5
Method	BLASTN
NCBI GI	g2345153
BLAST score	175
E value	8.0e-94
Match length	255
% identity	93
NCBI Description	Zea mays ribosomal protein S4 (rps4) mRNA, complete cds
Seq. No.	298268
Seq. ID	LIB3150-113-P2-K1-C6
Method	BLASTN
NCBI GI	g3294466
BLAST score	43
E value	4.0e-15
Match length	127
% identity	82
NCBI Description	Zea mays phosphoglucomutase 1 mRNA, complete cds
Seq. No.	298269
Seq. ID	LIB3150-113-P2-K1-G5
Method	BLASTN
NCBI GI	g22516
BLAST score	160
E value	6.0e-85
Match length	212
% identity	94
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.	298270
Seq. ID	LIB3150-113-P2-K1-H8
Method	BLASTX
NCBI GI	g4581156
BLAST score	290
E value	5.0e-26
Match length	63
% identity	90
NCBI Description	(AC006919) putative pyruvate kinase [Arabidopsis thaliana]
Seq. No.	298271
Seq. ID	LIB3150-114-P2-K1-C8
Method	BLASTX
NCBI GI	g1174536
BLAST score	144
E value	5.0e-09
Match length	37
% identity	70
NCBI Description	ASPARAGINYL-tRNA SYNTHETASE (ASPARAGINE--tRNA LIGASE) (ASNRS) >gi_1073865_pir_B64115 asparagine--tRNA ligase (EC 6.1.1.22) - Haemophilus influenzae (strain Rd KW20) >gi_1574761 (U32810) asparaginyl-tRNA synthetase (asnS) [Haemophilus influenzae Rd]
Seq. No.	298272
Seq. ID	LIB3150-114-P2-K1-H5

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Method	BLASTN
NCBI GI	g168694
BLAST score	59
E value	1.0e-24
Match length	125
% identity	94
NCBI Description	Maize gamma zein mRNA, partial cds
Seq. No.	298273
Seq. ID	LIB3150-116-P2-K1-B8
Method	BLASTX
NCBI GI	g1706323
BLAST score	217
E value	2.0e-17
Match length	114
% identity	45
NCBI Description	ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir_S64704 ornithine decarboxylase (EC 4.1.1.17) - jimsonweed >gi_871008_emb_CAA61121_ (X87847) ornithine decarboxylase [Datura stramonium]
Seq. No.	298274
Seq. ID	LIB3150-116-P2-K1-G5
Method	BLASTN
NCBI GI	g1895083
BLAST score	34
E value	1.0e-09
Match length	86
% identity	85
NCBI Description	Zea mays golgi associated protein se-wap41 mRNA, complete cds
Seq. No.	298275
Seq. ID	LIB3150-117-P2-K1-B7
Method	BLASTX
NCBI GI	g2642446
BLAST score	154
E value	3.0e-10
Match length	51
% identity	65
NCBI Description	(AC002391) similar to auxin-responsive GH3 protein [Arabidopsis thaliana]
Seq. No.	298276
Seq. ID	LIB3150-117-P2-K1-F8
Method	BLASTN
NCBI GI	g2104711
BLAST score	41
E value	6.0e-14
Match length	69
% identity	90
NCBI Description	Zea mays endosperm specific protein mRNA, complete cds
Seq. No.	298277
Seq. ID	LIB3150-117-P2-K1-G4
Method	BLASTN
NCBI GI	g998429

SEQUENCES FOUND

BLAST score	211
E value	1.0e-115
Match length	319
% identity	91
NCBI Description	GRF1=general regulatory factor [Zea mays, XL80, Genomic, 5348 nt]
Seq. No.	298278
Seq. ID	LIB3150-117-P2-K1-H6
Method	BLASTX
NCBI GI	g4506635
BLAST score	186
E value	5.0e-14
Match length	61
% identity	62
NCBI Description	ribosomal protein L32 >gi_132886_sp_P02433_RL32_HUMAN 60S RIBOSOMAL PROTEIN L32 >gi_71335_pir_R5HU32 ribosomal protein L32 - human >gi_71336_pir_R5MS32 ribosomal protein L32 - mouse >gi_71337_pir_R5RT32 ribosomal protein L32 - rat >gi_36132_emb_CAA27048 (X03342) rpL32 (aa 1-135) [Homo sapiens] >gi_57117_emb_CAA29777 (X06483) ribosomal protein L32 [Rattus norvegicus] >gi_200781 (K02060) ribosomal protein L32-3A [Mus musculus] >gi_226004_prf_1405339A ribosomal protein L32 [Rattus norvegicus]
Seq. No.	298279
Seq. ID	LIB3150-118-P2-K1-G9
Method	BLASTN
NCBI GI	g2431770
BLAST score	60
E value	5.0e-25
Match length	228
% identity	82
NCBI Description	Zea mays acidic ribosomal protein P2b (rpp2b) mRNA, complete cds
Seq. No.	298280
Seq. ID	LIB3151-001-P1-K1-A11
Method	BLASTX
NCBI GI	g22216
BLAST score	246
E value	4.0e-21
Match length	64
% identity	80
NCBI Description	(X55722) 22kD zein [Zea mays]
Seq. No.	298281
Seq. ID	LIB3151-001-P1-K1-A4
Method	BLASTX
NCBI GI	g121472
BLAST score	144
E value	3.0e-12
Match length	88
% identity	50
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -

maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298282
Seq. ID LIB3151-001-P1-K1-A8
Method BLASTX
NCBI GI g141597
BLAST score 346
E value 1.0e-32
Match length 129
% identity 63
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 298283
Seq. ID LIB3151-001-P1-K1-B6
Method BLASTX
NCBI GI g168701
BLAST score 520
E value 8.0e-55
Match length 140
% identity 79
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298284
Seq. ID LIB3151-001-P1-K1-B7
Method BLASTN
NCBI GI g22549
BLAST score 227
E value 1.0e-125
Match length 311
% identity 93
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298285
Seq. ID LIB3151-001-P1-K1-C12
Method BLASTX
NCBI GI g141608
BLAST score 160
E value 2.0e-11
Match length 64
% identity 62
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 298286
Seq. ID LIB3151-001-P1-K1-C5
Method BLASTX
NCBI GI g141597
BLAST score 311
E value 2.0e-28
Match length 116
% identity 60

DRAFT Sequence

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 298287
Seq. ID LIB3151-001-P1-K1-D10
Method BLASTX
NCBI GI g141617
BLAST score 243
E value 2.0e-21
Match length 101
% identity 54
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298288
Seq. ID LIB3151-001-P1-K1-D12
Method BLASTN
NCBI GI g168484
BLAST score 279
E value 1.0e-156
Match length 355
% identity 95
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298289
Seq. ID LIB3151-001-P1-K1-D7
Method BLASTX
NCBI GI g224513
BLAST score 172
E value 7.0e-13
Match length 51
% identity 75
NCBI Description zein M6 [Zea mays]

Seq. No. 298290
Seq. ID LIB3151-001-P1-K1-D8
Method BLASTX
NCBI GI g135060
BLAST score 405
E value 1.0e-39
Match length 90
% identity 87
NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
(SHRUNKEN-1) >gi_66570_pir_YUZMS sucrose synthase (EC
2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose
synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382)
sucrose synthase [Zea mays]

Seq. No. 298291
Seq. ID LIB3151-001-P1-K1-E12
Method BLASTN
NCBI GI g4185305

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BLAST score	193
E value	1.0e-104
Match length	289
% identity	92
NCBI Description	Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes
Seq. No.	298292
Seq. ID	LIB3151-001-P1-K1-E4
Method	BLASTX
NCBI GI	g1172977
BLAST score	217
E value	1.0e-17
Match length	92
% identity	50
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.	298293
Seq. ID	LIB3151-001-P1-K1-E7
Method	BLASTX
NCBI GI	g2832243
BLAST score	180
E value	2.0e-13
Match length	74
% identity	55
NCBI Description	(AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.	298294
Seq. ID	LIB3151-001-P1-K1-F2
Method	BLASTN
NCBI GI	g22549
BLAST score	238
E value	1.0e-131
Match length	278
% identity	97
NCBI Description	Maize gene for a 27kDa storage protein, zein
Seq. No.	298295
Seq. ID	LIB3151-001-P1-K1-F4
Method	BLASTX
NCBI GI	g168695
BLAST score	157
E value	2.0e-10
Match length	89
% identity	46
NCBI Description	(M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A zein gamma [Zea mays]
Seq. No.	298296
Seq. ID	LIB3151-001-P1-K1-F7
Method	BLASTN
NCBI GI	g168681
BLAST score	102
E value	4.0e-50

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Match length 245
% identity 86
NCBI Description Maize 19 kDa zein mRNA, clone cz19D1, complete cds.
>gi_270686_gb_I03333 Sequence 8 from Patent US

Seq. No. 298297
Seq. ID LIB3151-001-P1-K1-G10
Method BLASTN
NCBI GI g22549
BLAST score 33
E value 3.0e-09
Match length 61
% identity 89
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298298
Seq. ID LIB3151-001-P1-K1-G11
Method BLASTX
NCBI GI g22122
BLAST score 222
E value 2.0e-18
Match length 53
% identity 87
NCBI Description (X04050) alcohol dehydrogenase 1 [Zea mays] >gi_3420021
(AF050457) alcohol dehydrogenase 1 [Zea mays]

Seq. No. 298299
Seq. ID LIB3151-001-P1-K1-H11
Method BLASTN
NCBI GI g22549
BLAST score 113
E value 6.0e-57
Match length 197
% identity 89
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298300
Seq. ID LIB3151-001-P1-K1-H8
Method BLASTN
NCBI GI g168665
BLAST score 208
E value 1.0e-113
Match length 252
% identity 96
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298301
Seq. ID LIB3151-002-P1-K1-A3
Method BLASTX
NCBI GI g121472
BLAST score 142
E value 7.0e-09
Match length 70
% identity 44
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -

maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298302
Seq. ID LIB3151-002-P1-K1-A7
Method BLASTX
NCBI GI g82660
BLAST score 162
E value 3.0e-11
Match length 62
% identity 56
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 298303
Seq. ID LIB3151-002-P1-K1-C2
Method BLASTX
NCBI GI g121472
BLAST score 149
E value 7.0e-22
Match length 106
% identity 54
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298304
Seq. ID LIB3151-002-P1-K1-C3
Method BLASTX
NCBI GI g135417
BLAST score 209
E value 7.0e-17
Match length 49
% identity 78
NCBI Description TUBULIN ALPHA-3 CHAIN >gi_100946_pir_JN0105 tubulin
alpha-3 chain - maize >gi_22150_emb_CAA44861 (X63176)
Alpha-tubulin #3 [Zea mays] >gi_485377 (M60171) alpha-3
tubulin [Zea mays]

Seq. No. 298305
Seq. ID LIB3151-002-P1-K1-C5
Method BLASTX
NCBI GI g550542
BLAST score 183
E value 3.0e-26
Match length 133
% identity 51
NCBI Description (X81831) cytochrome P450 [Zea mays]
>gi_1850903_emb_CAA72196_ (Y11368) cytochrome p450 [Zea
mays]

Seq. No. 298306
Seq. ID LIB3151-002-P1-K1-C6

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Method BLASTX
NCBI GI g121472
BLAST score 257
E value 3.0e-22
Match length 110
% identity 45
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea
mays] >gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 298307
Seq. ID LIB3151-002-P1-K1-D1
Method BLASTN
NCBI GI g168679
BLAST score 40
E value 4.0e-13
Match length 56
% identity 93
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
>gi_270687_gb_I03334_Sequence 9 from Patent US

Seq. No. 298308
Seq. ID LIB3151-002-P1-K1-E2
Method BLASTX
NCBI GI g2832246
BLAST score 367
E value 4.0e-35
Match length 124
% identity 66
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 298309
Seq. ID LIB3151-002-P1-K1-E3
Method BLASTX
NCBI GI g121472
BLAST score 184
E value 1.0e-13
Match length 80
% identity 49
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea
mays] >gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 298310
Seq. ID LIB3151-002-P1-K1-E5
Method BLASTX
NCBI GI g16073
BLAST score 369
E value 2.0e-35
Match length 109
% identity 70

NCBI Description (X59526) zein protein [Acetabularia mediterranea]
Seq. No. 298311
Seq. ID LIB3151-002-P1-K1-G1
Method BLASTN
NCBI GI g22215
BLAST score 70
E value 4.0e-31
Match length 312
% identity 84
NCBI Description Z.mays ZSF4C1 gene for zein

Seq. No. 298312
Seq. ID LIB3151-002-P1-K1-G5
Method BLASTX
NCBI GI g2146739
BLAST score 227
E value 1.0e-18
Match length 69
% identity 65
NCBI Description hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
(U28214) hexokinase 1 [Arabidopsis thaliana]

Seq. No. 298313
Seq. ID LIB3151-002-P1-K1-G6
Method BLASTX
NCBI GI g168699
BLAST score 236
E value 7.0e-20
Match length 68
% identity 74
NCBI Description (M60836) zein [Zea mays]

Seq. No. 298314
Seq. ID LIB3151-002-P1-K1-H2
Method BLASTX
NCBI GI g168701
BLAST score 276
E value 1.0e-24
Match length 96
% identity 65
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298315
Seq. ID LIB3151-002-P1-K1-H7
Method BLASTN
NCBI GI g168425
BLAST score 180
E value 9.0e-97
Match length 252
% identity 93
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 298316
Seq. ID LIB3151-003-Q1-K1-A10
Method BLASTX
NCBI GI g2832247

DRAFT Sequence Database

BLAST score . 261
E value 9.0e-23
Match length 99
% identity 58
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 298317
Seq. ID LIB3151-003-Q1-K1-A11
Method BLASTN
NCBI GI g22514
BLAST score 33
E value 4.0e-09
Match length 168
% identity 80
NCBI Description Maize Zcl gene for Zein Zcl (14 kD zein-2)

Seq. No. 298318
Seq. ID LIB3151-003-Q1-K1-A4
Method BLASTX
NCBI GI g141615
BLAST score 162
E value 2.0e-14
Match length 73
% identity 73
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
>gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 298319
Seq. ID LIB3151-003-Q1-K1-A5
Method BLASTX
NCBI GI g2440160
BLAST score 215
E value 1.0e-17
Match length 67
% identity 63
NCBI Description (Y14836) beta-galactosidase [Phagemid cloning vector pTZ19U]

Seq. No. 298320
Seq. ID LIB3151-003-Q1-K1-A9
Method BLASTX
NCBI GI g121472
BLAST score 205
E value 4.0e-16
Match length 98
% identity 45
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize
>gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays]
>gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays]
>gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298321
Seq. ID LIB3151-003-Q1-K1-B12
Method BLASTX
NCBI GI g548852

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BLAST score 353
E value 2.0e-33
Match length 82
% identity 78
NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi_481227_pir_S38357 ribosomal protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S subunit ribosomal protein [Oryza sativa]

Seq. No. 298322
Seq. ID LIB3151-003-Q1-K1-C1
Method BLASTN
NCBI GI g168484
BLAST score 45
E value 2.0e-16
Match length 53
% identity 96
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298323
Seq. ID LIB3151-003-Q1-K1-C12
Method BLASTX
NCBI GI g4249662
BLAST score 168
E value 7.0e-12
Match length 87
% identity 45
NCBI Description (AF089810) Altered Response to Gravity [Arabidopsis thaliana]

Seq. No. 298324
Seq. ID LIB3151-003-Q1-K1-C4
Method BLASTX
NCBI GI g141597
BLAST score 214
E value 2.0e-17
Match length 108
% identity 44
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 298325
Seq. ID LIB3151-003-Q1-K1-C6
Method BLASTX
NCBI GI g168699
BLAST score 402
E value 3.0e-39
Match length 96
% identity 83
NCBI Description (M60836) zein [Zea mays]

Seq. No. 298326
Seq. ID LIB3151-003-Q1-K1-D1
Method BLASTX
NCBI GI g100925
BLAST score 219

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E value 6.0e-18
Match length 84
% identity 49
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_(X58197) 27kDa storage protein, zein [Zea mays]

Seq. No. 298327
Seq. ID LIB3151-003-Q1-K1-D10
Method BLASTX
NCBI GI g2982322
BLAST score 246
E value 2.0e-21
Match length 66
% identity 74
NCBI Description (AF051246) probable proteasome subunit [Picea mariana]

Seq. No. 298328
Seq. ID LIB3151-003-Q1-K1-D12
Method BLASTX
NCBI GI g133867
BLAST score 464
E value 2.0e-46
Match length 111
% identity 77
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No. 298329
Seq. ID LIB3151-003-Q1-K1-E1
Method BLASTX
NCBI GI g224508
BLAST score 264
E value 5.0e-23
Match length 82
% identity 68
NCBI Description zein A20 [Zea mays]

Seq. No. 298330
Seq. ID LIB3151-003-Q1-K1-E10
Method BLASTX
NCBI GI g133867
BLAST score 494
E value 5.0e-50
Match length 114
% identity 83
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No. 298331
Seq. ID LIB3151-003-Q1-K1-E11
Method BLASTX
NCBI GI g729737
BLAST score 195
E value 3.0e-15
Match length 83

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% identity 55
NCBI Description HMG1/2-LIKE PROTEIN >gi_541981_pir_S39556 HMG protein -
fava bean

Seq. No. 298332
Seq. ID LIB3151-003-Q1-K1-E6
Method BLASTX
NCBI GI g141605
BLAST score 364
E value 6.0e-35
Match length 93
% identity 83
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298333
Seq. ID LIB3151-003-Q1-K1-F12
Method BLASTX
NCBI GI g4586031
BLAST score 280
E value 6.0e-25
Match length 64
% identity 83
NCBI Description (AC007109) unknown protein [Arabidopsis thaliana]

Seq. No. 298334
Seq. ID LIB3151-003-Q1-K1-F5
Method BLASTN
NCBI GI g168484
BLAST score 285
E value 1.0e-159
Match length 373
% identity 95
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298335
Seq. ID LIB3151-003-Q1-K1-G4
Method BLASTN
NCBI GI g22326
BLAST score 35
E value 3.0e-10
Match length 82
% identity 87
NCBI Description Z.mays gene for Hageman factor inhibitor

Seq. No. 298336
Seq. ID LIB3151-003-Q1-K1-G7
Method BLASTX
NCBI GI g168699
BLAST score 169
E value 3.0e-12
Match length 82
% identity 51
NCBI Description (M60836) zein [Zea mays]

Seq. No. 298337

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Seq. ID	LIB3151-003-Q1-K1-G9
Method	BLASTX
NCBI GI	g3757519
BLAST score	383
E value	6.0e-37
Match length	143
% identity	53
NCBI Description	(AC005167) hypothetical protein [Arabidopsis thaliana]
Seq. No.	298338
Seq. ID	LIB3151-003-Q1-K1-H11
Method	BLASTX
NCBI GI	g3292831
BLAST score	348
E value	4.0e-33
Match length	104
% identity	62
NCBI Description	(AL031018) putative serine/threonine kinase [Arabidopsis thaliana]
Seq. No.	298339
Seq. ID	LIB3151-003-Q1-K1-H5
Method	BLASTN
NCBI GI	g22528
BLAST score	125
E value	6.0e-64
Match length	347
% identity	85
NCBI Description	Zea mays mRNA encoding a zein (clone A20)
Seq. No.	298340
Seq. ID	LIB3151-004-Q1-K1-A11
Method	BLASTN
NCBI GI	g4140643
BLAST score	46
E value	8.0e-17
Match length	57
% identity	95
NCBI Description	Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	298341
Seq. ID	LIB3151-004-Q1-K1-A5
Method	BLASTX
NCBI GI	g100925
BLAST score	178
E value	4.0e-13
Match length	54
% identity	61
NCBI Description	zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_(X58197) 27kDa storage protein, zein [Zea mays]
Seq. No.	298342
Seq. ID	LIB3151-004-Q1-K1-B12
Method	BLASTX
NCBI GI	g121472
BLAST score	222

D E S C R I P T I O N

E value 4.0e-18
Match length 97
% identity 47
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea
mays] >gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 298343
Seq. ID LIB3151-004-Q1-K1-C11
Method BLASTX
NCBI GI g141605
BLAST score 445
E value 2.0e-44
Match length 100
% identity 92
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
maize >gi_168680_(M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298344
Seq. ID LIB3151-004-Q1-K1-C5
Method BLASTX
NCBI GI g2340108
BLAST score 327
E value 2.0e-30
Match length 109
% identity 60
NCBI Description (U65948) starch branching enzyme IIa [Zea mays]

Seq. No. 298345
Seq. ID LIB3151-004-Q1-K1-C8
Method BLASTX
NCBI GI g3157932
BLAST score 161
E value 2.0e-11
Match length 78
% identity 45
NCBI Description (AC002131) Similar to hypothetical protein HYP1 gb_Z97338
from A. thaliana. [Arabidopsis thaliana]

Seq. No. 298346
Seq. ID LIB3151-004-Q1-K1-D9
Method BLASTX
NCBI GI g141617
BLAST score 259
E value 2.0e-22
Match length 64
% identity 77
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
>gi_168666_(M16460) 16-kDa zein protein [Zea mays]

D E S C R I P T I O N

Seq. No. 298347
Seq. ID LIB3151-004-Q1-K1-E11
Method BLASTN
NCBI GI g22445
BLAST score 69
E value 2.0e-30
Match length 137
% identity 89
NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. No. 298348
Seq. ID LIB3151-004-Q1-K1-E12
Method BLASTN
NCBI GI g1037129
BLAST score 98
E value 1.0e-47
Match length 341
% identity 83
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298349
Seq. ID LIB3151-004-Q1-K1-E3
Method BLASTN
NCBI GI g535019
BLAST score 119
E value 3.0e-60
Match length 257
% identity 45
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)

Seq. No. 298350
Seq. ID LIB3151-004-Q1-K1-E4
Method BLASTN
NCBI GI g22524
BLAST score 107
E value 4.0e-53
Match length 163
% identity 91
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)

Seq. No. 298351
Seq. ID LIB3151-004-Q1-K1-E6
Method BLASTN
NCBI GI g168484
BLAST score 84
E value 2.0e-39
Match length 128
% identity 91
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298352
Seq. ID LIB3151-004-Q1-K1-F10
Method BLASTX
NCBI GI g168691
BLAST score 271
E value 6.0e-24

Match length 99
% identity 61
NCBI Description (M29628) zein [Zea mays]

Seq. No. 298353
Seq. ID LIB3151-004-Q1-K1-F11
Method BLASTX
NCBI GI g141598
BLAST score 170
E value 4.0e-12
Match length 44
% identity 75
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
>gi_72313_pir_ZIZM99_19K zein precursor (clone ZG99) - maize
>gi_22519_emb_CAA24717_(V01470) zein [Zea mays]
>gi_22534_emb_CAA24726_(V01479) zein [Zea mays]

Seq. No. 298354
Seq. ID LIB3151-004-Q1-K1-F3
Method BLASTN
NCBI GI g168484
BLAST score 161
E value 2.0e-85
Match length 348
% identity 87
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298355
Seq. ID LIB3151-004-Q1-K1-F9
Method BLASTX
NCBI GI g141603
BLAST score 550
E value 1.0e-56
Match length 135
% identity 87
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2_19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_(V01476) zein [Zea mays]

Seq. No. 298356
Seq. ID LIB3151-004-Q1-K1-G6
Method BLASTN
NCBI GI g4336204
BLAST score 38
E value 5.0e-12
Match length 46
% identity 96
NCBI Description Zea mays cytochrome b5 reductase (NFR) mRNA, complete cds

Seq. No. 298357
Seq. ID LIB3151-004-Q1-K1-H2
Method BLASTX
NCBI GI g1345838
BLAST score 236
E value 7.0e-20
Match length 58
% identity 76

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NCBI Description PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE)
>gi_2130143_pir_S65060 phytoene desaturase precursor -
maize >gi_1051180 (U37285) phytoene desaturase [Zea mays]

Seq. No. 298358
Seq. ID LIB3151-004-Q1-K1-H6
Method BLASTX
NCBI GI g141600
BLAST score 167
E value 3.0e-16
Match length 98
% identity 54
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) -
maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 298359
Seq. ID LIB3151-004-Q1-K1-H9
Method BLASTX
NCBI GI g119748
BLAST score 219
E value 5.0e-18
Match length 48
% identity 83
NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC
(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
>gi_67241_pir_PASPY fructose-bisphosphatase (EC 3.1.3.11),
cytosolic - spinach >gi_21245_emb_CAA43860 (X61690)
fructose-bisphosphatase [Spinacia oleracea]

Seq. No. 298360
Seq. ID LIB3151-005-Q1-K1-A4
Method BLASTN
NCBI GI g168484
BLAST score 280
E value 1.0e-156
Match length 328
% identity 96
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298361
Seq. ID LIB3151-005-Q1-K1-B1
Method BLASTX
NCBI GI g419803
BLAST score 218
E value 1.0e-17
Match length 83
% identity 52
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298362
Seq. ID LIB3151-005-Q1-K1-C7
Method BLASTX
NCBI GI g629861
BLAST score 267
E value 2.0e-23

Match length 125
% identity 51
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298363
Seq. ID LIB3151-005-Q1-K1-E12
Method BLASTX
NCBI GI g266398
BLAST score 349
E value 4.0e-33
Match length 96
% identity 68
NCBI Description TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
INHIBITOR) (CHFI) >gi_68849_pir_TIZM1 trypsin/factor XIIa
inhibitor precursor - maize >gi_22327_emb_CAA37998_
(X54064) corn Hageman factor inhibitor [Zea mays]

Seq. No. 298364
Seq. ID LIB3151-005-Q1-K1-E5
Method BLASTX
NCBI GI g141608
BLAST score 316
E value 3.0e-29
Match length 118
% identity 60
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 298365
Seq. ID LIB3151-005-Q1-K1-E8
Method BLASTX
NCBI GI g168701
BLAST score 169
E value 5.0e-12
Match length 53
% identity 58
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298366
Seq. ID LIB3151-005-Q1-K1-E9
Method BLASTX
NCBI GI g719291
BLAST score 197
E value 2.0e-15
Match length 83
% identity 46
NCBI Description (U19134) unknown [Arabidopsis thaliana]
>gi_1095007_prf_2107236A SABRE gene [Arabidopsis thaliana]

Seq. No. 298367
Seq. ID LIB3151-005-Q1-K1-F1
Method BLASTN
NCBI GI g1037129
BLAST score 349
E value 0.0e+00

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Match length 445
% identity 95
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298368
Seq. ID LIB3151-005-Q1-K1-F10
Method BLASTX
NCBI GI g168699
BLAST score 337
E value 1.0e-31
Match length 108
% identity 67
NCBI Description (M60836) zein [Zea mays]

Seq. No. 298369
Seq. ID LIB3151-005-Q1-K1-F7
Method BLASTX
NCBI GI g121472
BLAST score 228
E value 5.0e-19
Match length 88
% identity 49
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298370
Seq. ID LIB3151-005-Q1-K1-G11
Method BLASTN
NCBI GI g168665
BLAST score 46
E value 5.0e-17
Match length 217
% identity 81
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298371
Seq. ID LIB3151-005-Q1-K1-G4
Method BLASTX
NCBI GI g584706
BLAST score 384
E value 2.0e-37
Match length 97
% identity 77
NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
>gi_2130066_pir_JC5124 aspartate transaminase (EC
2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_
(D14673) aspartate aminotransferase [Oryza sativa]

Seq. No. 298372
Seq. ID LIB3151-005-Q1-K1-G5
Method BLASTX
NCBI GI g72307

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BLAST score 351
E value 2.0e-33
Match length 112
% identity 67
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686 (J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 298373
Seq. ID LIB3151-005-Q1-K1-H11
Method BLASTX
NCBI GI g141597
BLAST score 221
E value 1.0e-32
Match length 130
% identity 62
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 298374
Seq. ID LIB3151-006-Q1-K1-B2
Method BLASTX
NCBI GI g141610
BLAST score 184
E value 1.0e-13
Match length 51
% identity 75
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)

Seq. No. 298375
Seq. ID LIB3151-006-Q1-K1-C3
Method BLASTX
NCBI GI g168664
BLAST score 282
E value 2.0e-25
Match length 94
% identity 60
NCBI Description (M13507) zein protein precursor [Zea mays]

Seq. No. 298376
Seq. ID LIB3151-006-Q1-K1-C6
Method BLASTX
NCBI GI g141617
BLAST score 271
E value 8.0e-24
Match length 66
% identity 77
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666 (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298377
Seq. ID LIB3151-006-Q1-K1-C9
Method BLASTX

NCBI GI g2623248
BLAST score 471
E value 3.0e-47
Match length 145
% identity 67
NCBI Description (AF030882) SUL isoamylase [Zea mays]

Seq. No. 298378
Seq. ID LIB3151-006-Q1-K1-D11
Method BLASTX
NCBI GI g4185308
BLAST score 175
E value 9.0e-13
Match length 93
% identity 46
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]

Seq. No. 298379
Seq. ID LIB3151-006-Q1-K1-D5
Method BLASTX
NCBI GI g629861
BLAST score 233
E value 2.0e-19
Match length 110
% identity 50
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298380
Seq. ID LIB3151-006-Q1-K1-E8
Method BLASTN
NCBI GI g168425
BLAST score 40
E value 2.0e-13
Match length 192
% identity 81
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 298381
Seq. ID LIB3151-006-Q1-K1-F1
Method BLASTN
NCBI GI g22514
BLAST score 156
E value 2.0e-82
Match length 312
% identity 88
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 298382
Seq. ID LIB3151-006-Q1-K1-F4
Method BLASTX
NCBI GI g2345154
BLAST score 279
E value 6.0e-31
Match length 94
% identity 81
NCBI Description (AF015522) ribosomal protein S4 [Zea mays]

Seq. No. 298383
Seq. ID LIB3151-006-Q1-K1-G9
Method BLASTX
NCBI GI g168701
BLAST score 197
E value 2.0e-15
Match length 73
% identity 60
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298384
Seq. ID LIB3151-006-Q1-K1-H12
Method BLASTX
NCBI GI g22220
BLAST score 165
E value 2.0e-11
Match length 76
% identity 49
NCBI Description (X55723) 22 kD zein [Zea mays]

Seq. No. 298385
Seq. ID LIB3151-006-Q1-K1-H2
Method BLASTX
NCBI GI g141608
BLAST score 294
E value 2.0e-30
Match length 113
% identity 68
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays].

Seq. No. 298386
Seq. ID LIB3151-006-Q1-K1-H8
Method BLASTX
NCBI GI g141615
BLAST score 273
E value 2.0e-25
Match length 89
% identity 78
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
>gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 298387
Seq. ID LIB3151-007-Q1-K1-A12
Method BLASTN
NCBI GI g1037129
BLAST score 314
E value 1.0e-176
Match length 376
% identity 96
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298388
Seq. ID LIB3151-007-Q1-K1-A2

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Method	BLASTX
NCBI GI	g168699
BLAST score	566
E value	2.0e-58
Match length	142
% identity	57
NCBI Description	(M60836) zein [Zea mays]
Seq. No.	298389
Seq. ID	LIB3151-007-Q1-K1-A3
Method	BLASTX
NCBI GI	g121472
BLAST score	384
E value	5.0e-37
Match length	142
% identity	54
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea mays] >gi_168485_(M16066) glutelin-2 [Zea mays]
Seq. No.	298390
Seq. ID	LIB3151-007-Q1-K1-A4
Method	BLASTX
NCBI GI	g141599
BLAST score	367
E value	4.0e-35
Match length	101
% identity	75
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2) >gi_72316_pir_ZIZMA2 19K zein precursor (clone cZ19A2) - maize (fragment) >gi_168670_(M12142) 19 kDa zein protein [Zea mays]
Seq. No.	298391
Seq. ID	LIB3151-007-Q1-K1-B9
Method	BLASTX
NCBI GI	g141603
BLAST score	420
E value	2.0e-41
Match length	104
% identity	87
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20) >gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize >gi_22529_emb_CAA24723_(V01476) zein [Zea mays]
Seq. No.	298392
Seq. ID	LIB3151-007-Q1-K1-C10
Method	BLASTX
NCBI GI	g3549665
BLAST score	140
E value	9.0e-09
Match length	74
% identity	50
NCBI Description	(AL031394) hypothetical protein [Arabidopsis thaliana]

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Seq. No.	298393
Seq. ID	LIB3151-007-Q1-K1-C11
Method	BLASTX
NCBI GI	g141605
BLAST score	177
E value	4.0e-13
Match length	71
% identity	54
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) >gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.	298394
Seq. ID	LIB3151-007-Q1-K1-C12
Method	BLASTN
NCBI GI	g22516
BLAST score	160
E value	8.0e-85
Match length	312
% identity	88
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.	298395
Seq. ID	LIB3151-007-Q1-K1-C2
Method	BLASTX
NCBI GI	g141597
BLAST score	230
E value	2.0e-27
Match length	119
% identity	60
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2] [Zea mays]
Seq. No.	298396
Seq. ID	LIB3151-007-Q1-K1-C5
Method	BLASTX
NCBI GI	g419803
BLAST score	162
E value	6.0e-16
Match length	109
% identity	46
NCBI Description	zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
Seq. No.	298397
Seq. ID	LIB3151-007-Q1-K1-D11
Method	BLASTN
NCBI GI	g22514
BLAST score	69
E value	6.0e-31
Match length	125
% identity	89
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

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Seq. No. 298398
Seq. ID LIB3151-007-Q1-K1-D3
Method BLASTX
NCBI GI g141616
BLAST score 290
E value 4.0e-26
Match length 118
% identity 52
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 298399
Seq. ID LIB3151-007-Q1-K1-E5
Method BLASTX
NCBI GI g141605
BLAST score 186
E value 3.0e-14
Match length 62
% identity 68
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize
>gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298400
Seq. ID LIB3151-007-Q1-K1-E6
Method BLASTX
NCBI GI g2832243
BLAST score 358
E value 5.0e-34
Match length 126
% identity 61
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298401
Seq. ID LIB3151-007-Q1-K1-F9
Method BLASTN
NCBI GI g22516
BLAST score 133
E value 1.0e-68
Match length 241
% identity 89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298402
Seq. ID LIB3151-007-Q1-K1-G10
Method BLASTX
NCBI GI g141617
BLAST score 353
E value 2.0e-33
Match length 82
% identity 80
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666 (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298403
Seq. ID LIB3151-007-Q1-K1-G11
Method BLASTN
NCBI GI g168673
BLAST score 46
E value 7.0e-17
Match length 66
% identity 92
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 298404
Seq. ID LIB3151-007-Q1-K1-G7
Method BLASTX
NCBI GI g141597
BLAST score 313
E value 1.0e-28
Match length 140
% identity 57
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 298405
Seq. ID LIB3151-007-Q1-K1-H3
Method BLASTX
NCBI GI g141597
BLAST score 286
E value 9.0e-26
Match length 102
% identity 66
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 298406
Seq. ID LIB3151-008-Q1-K1-A11
Method BLASTX
NCBI GI g82660
BLAST score 156
E value 8.0e-11
Match length 64
% identity 55
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 298407
Seq. ID LIB3151-008-Q1-K1-A12
Method BLASTX
NCBI GI g168701
BLAST score 407
E value 9.0e-40
Match length 120
% identity 73
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298408
Seq. ID LIB3151-008-Q1-K1-A3
Method BLASTX
NCBI GI g82660
BLAST score 331
E value 6.0e-31
Match length 94
% identity 72
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 298409
Seq. ID LIB3151-008-Q1-K1-C10
Method BLASTX
NCBI GI g168701
BLAST score 288
E value 7.0e-26
Match length 89
% identity 62
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298410
Seq. ID LIB3151-008-Q1-K1-D10
Method BLASTX
NCBI GI g141616
BLAST score 210
E value 6.0e-17
Match length 85
% identity 52
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 298411
Seq. ID LIB3151-008-Q1-K1-F10
Method BLASTX
NCBI GI g508545
BLAST score 359
E value 3.0e-34
Match length 123
% identity 64
NCBI Description (L34340) zein [Zea mays]

Seq. No. 298412
Seq. ID LIB3151-008-Q1-K1-F11
Method BLASTX
NCBI GI g629861
BLAST score 394
E value 3.0e-38
Match length 138
% identity 61
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298413
Seq. ID LIB3151-008-Q1-K1-F12
Method BLASTN
NCBI GI g22514

QCBN04070000

BLAST score 90
E value 3.0e-43
Match length 226
% identity 85
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 298414
Seq. ID LIB3151-008-Q1-K1-G12
Method BLASTX
NCBI GI g141617
BLAST score 293
E value 2.0e-26
Match length 98
% identity 57
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595 (X53515) zein Zc1 [Zea mays]
>gi_168666 (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298415
Seq. ID LIB3151-009-Q1-K1-A8
Method BLASTX
NCBI GI g141605
BLAST score 201
E value 8.0e-16
Match length 84
% identity 55
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize
>gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298416
Seq. ID LIB3151-009-Q1-K1-C10
Method BLASTN
NCBI GI g168665
BLAST score 41
E value 4.0e-14
Match length 153
% identity 82
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298417
Seq. ID LIB3151-009-Q1-K1-C6
Method BLASTX
NCBI GI g168695
BLAST score 249
E value 1.0e-21
Match length 79
% identity 62
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
zein gamma [Zea mays]

Seq. No. 298418
Seq. ID LIB3151-009-Q1-K1-C8
Method BLASTN
NCBI GI g168704

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BLAST score	34
E value	1.0e-09
Match length	42
% identity	95
NCBI Description	Zea mays zein protein gene, complete cds
Seq. No.	298419
Seq. ID	LIB3151-009-Q1-K1-C9
Method	BLASTN
NCBI GI	g22544
BLAST score	124
E value	3.0e-63
Match length	144
% identity	97
NCBI Description	Maize mRNA (clone A30) for zein (a plant storage protein)
Seq. No.	298420
Seq. ID	LIB3151-009-Q1-K1-D2
Method	BLASTN
NCBI GI	g508544
BLAST score	118
E value	9.0e-60
Match length	238
% identity	88
NCBI Description	Zea mays 24-kD alpha-zein gene (floury2), complete cds
Seq. No.	298421
Seq. ID	LIB3151-009-Q1-K1-D8
Method	BLASTX
NCBI GI	g2832243
BLAST score	336
E value	1.0e-31
Match length	100
% identity	72
NCBI Description	(AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.	298422
Seq. ID	LIB3151-009-Q1-K1-E2
Method	BLASTX
NCBI GI	g3122673
BLAST score	236
E value	4.0e-20
Match length	62
% identity	74
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_(Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.	298423
Seq. ID	LIB3151-009-Q1-K1-E6
Method	BLASTN
NCBI GI	g168704
BLAST score	45
E value	2.0e-16
Match length	117
% identity	85
NCBI Description	Zea mays zein protein gene, complete cds

Seq. No. 298424
Seq. ID LIB3151-009-Q1-K1-G10
Method BLASTX
NCBI GI g141612
BLAST score 251
E value 5.0e-30
Match length 108
% identity 36
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)
>gi_72306_pir_ZIZMC2 22K zein precursor (clone cZ22C2) -
maize (fragment) >gi_168688 (M12141) 22 kDa zein protein
[Zea mays]

Seq. No. 298425
Seq. ID LIB3151-009-Q1-K1-G6
Method BLASTN
NCBI GI g1037129
BLAST score 241
E value 1.0e-133
Match length 325
% identity 94
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298426
Seq. ID LIB3151-009-Q1-K1-H2
Method BLASTX
NCBI GI g224508
BLAST score 386
E value 6.0e-39
Match length 119
% identity 75
NCBI Description zein A20 [Zea mays]

Seq. No. 298427
Seq. ID LIB3151-009-Q1-K1-H9
Method BLASTN
NCBI GI g22516
BLAST score 50
E value 2.0e-19
Match length 82
% identity 90
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298428
Seq. ID LIB3151-010-Q1-K1-B10
Method BLASTX
NCBI GI g419803
BLAST score 380
E value 1.0e-36
Match length 112
% identity 66
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
mays]

Seq. No. 298429
Seq. ID LIB3151-010-Q1-K1-B5

Method BLASTN
NCBI GI g168685
BLAST score 60
E value 3.0e-25
Match length 248
% identity 82
NCBI Description Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA

Seq. No. 298430
Seq. ID LIB3151-010-Q1-K1-C8
Method BLASTN
NCBI GI g22288
BLAST score 54
E value 1.0e-21
Match length 174
% identity 83
NCBI Description Maize mRNA fragment for endosperm glutelin-2

Seq. No. 298431
Seq. ID LIB3151-010-Q1-K1-D10
Method BLASTX
NCBI GI g168697
BLAST score 301
E value 2.0e-27
Match length 86
% identity 77
NCBI Description (M60835) zein [Zea mays]

Seq. No. 298432
Seq. ID LIB3151-010-Q1-K1-D6
Method BLASTX
NCBI GI g168695
BLAST score 224
E value 2.0e-18
Match length 106
% identity 50
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
zein gamma [Zea mays]

Seq. No. 298433
Seq. ID LIB3151-010-Q1-K1-D7
Method BLASTN
NCBI GI g22445
BLAST score 38
E value 4.0e-12
Match length 98
% identity 85
NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. No. 298434
Seq. ID LIB3151-010-Q1-K1-E9
Method BLASTN
NCBI GI g22172
BLAST score 72
E value 2.0e-32
Match length 124
% identity 90

NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit

Seq. No. 298435
Seq. ID LIB3151-010-Q1-K1-F2
Method BLASTN
NCBI GI g168665
BLAST score 208
E value 1.0e-113
Match length 236
% identity 97
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298436
Seq. ID LIB3151-010-Q1-K1-F9
Method BLASTX
NCBI GI g419803
BLAST score 285
E value 1.0e-25
Match length 110
% identity 53
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298437
Seq. ID LIB3151-010-Q1-K1-G1
Method BLASTX
NCBI GI g100938
BLAST score 200
E value 8.0e-16
Match length 84
% identity 56
NCBI Description zein precursor - maize >gi_22442_emb_CAA32513_ (X14335)
zein precursor (AA -21 to 90) [Zea mays]

Seq. No. 298438
Seq. ID LIB3151-010-Q1-K1-G10
Method BLASTX
NCBI GI g16073
BLAST score 182
E value 2.0e-13
Match length 101
% identity 46
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298439
Seq. ID LIB3151-010-Q1-K1-H7
Method BLASTN
NCBI GI g22516
BLAST score 287
E value 1.0e-160
Match length 329
% identity 97
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298440
Seq. ID LIB3151-011-Q1-K1-A11
Method BLASTN

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NCBI GI	g168665
BLAST score	163
E value	1.0e-86
Match length	230
% identity	94
NCBI Description	Maize 16-kDa zein-2 mRNA, complete cds
Seq. No.	298441
Seq. ID	LIB3151-011-Q1-K1-B12
Method	BLASTX
NCBI GI	g121472
BLAST score	158
E value	3.0e-11
Match length	41
% identity	73
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb CAA37594 (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]
Seq. No.	298442
Seq. ID	LIB3151-011-Q1-K1-B4
Method	BLASTX
NCBI GI	g224508
BLAST score	270
E value	6.0e-24
Match length	79
% identity	78
NCBI Description	zein A20 [Zea mays]
Seq. No.	298443
Seq. ID	LIB3151-011-Q1-K1-C1
Method	BLASTX
NCBI GI	g168691
BLAST score	189
E value	1.0e-14
Match length	73
% identity	55
NCBI Description	(M29628) zein [Zea mays]
Seq. No.	298444
Seq. ID	LIB3151-011-Q1-K1-C7
Method	BLASTX
NCBI GI	g419803
BLAST score	264
E value	3.0e-23
Match length	92
% identity	59
NCBI Description	zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
Seq. No.	298445
Seq. ID	LIB3151-011-Q1-K1-C8
Method	BLASTN
NCBI GI	g1037129

BLAST score 234
E value 1.0e-129
Match length 362
% identity 91
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298446
Seq. ID LIB3151-011-Q1-K1-E11
Method BLASTN
NCBI GI g22549
BLAST score 52
E value 1.0e-20
Match length 148
% identity 84
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298447
Seq. ID LIB3151-011-Q1-K1-E6
Method BLASTN
NCBI GI g22544
BLAST score 109
E value 2.0e-54
Match length 133
% identity 96
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 298448
Seq. ID LIB3151-011-Q1-K1-F12
Method BLASTX
NCBI GI g629861
BLAST score 236
E value 9.0e-28
Match length 98
% identity 66
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298449
Seq. ID LIB3151-011-Q1-K1-F3
Method BLASTX
NCBI GI g2832243
BLAST score 141
E value 2.0e-15
Match length 102
% identity 56
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298450
Seq. ID LIB3151-011-Q1-K1-G9
Method BLASTX
NCBI GI g168701
BLAST score 548
E value 3.0e-56
Match length 138
% identity 82
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298451
Seq. ID LIB3151-011-Q1-K1-H11
Method BLASTN
NCBI GI g168698
BLAST score 46
E value 7.0e-17
Match length 157
% identity 83
NCBI Description Z.mays zein mRNA, complete cds

Seq. No. 298452
Seq. ID LIB3151-012-Q1-K1-A11
Method BLASTN
NCBI GI g535019
BLAST score 64
E value 2.0e-27
Match length 136
% identity 44
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)

Seq. No. 298453
Seq. ID LIB3151-012-Q1-K1-A3
Method BLASTX
NCBI GI g141610
BLAST score 172
E value 3.0e-12
Match length 64
% identity 56
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)

Seq. No. 298454
Seq. ID LIB3151-012-Q1-K1-A8
Method BLASTX
NCBI GI g419803
BLAST score 247
E value 3.0e-21
Match length 84
% identity 58
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298455
Seq. ID LIB3151-012-Q1-K1-B7
Method BLASTX
NCBI GI g82660
BLAST score 450
E value 9.0e-45
Match length 147
% identity 65
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment) >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 298456
Seq. ID LIB3151-012-Q1-K1-C10
Method BLASTN
NCBI GI g168704

Seq. No. 298457
 Seq. ID LIB3151-012-Q1-K1-C12
 Method BLASTX
 NCBI GI g141604
 BLAST score 415
 E value 1.0e-40
 Match length 132
 % identity 71
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
 >gi_72310_pir_ZIZM91 19K zein precursor (clone cZ19C1) - maize
 >gi_168678 (M12146) 19 kDa zein protein [Zea mays]

Seq. No. 298458
 Seq. ID LIB3151-012-Q1-K1-C6
 Method BLASTX
 NCBI GI g224507
 BLAST score 173
 E value 1.0e-19
 Match length 93
 % identity 61
 NCBI Description zein A1 [Zea mays]

Seq. No. 298459
 Seq. ID LIB3151-012-Q1-K1-D12
 Method BLASTN
 NCBI GI g168677
 BLAST score 34
 E value 6.0e-10
 Match length 50
 % identity 94
 NCBI Description Maize 19 kDa zein mRNA, clone cZ19C1, complete cds

Seq. No. 298460
 Seq. ID LIB3151-012-Q1-K1-D3
 Method BLASTX
 NCBI GI g141617
 BLAST score 229
 E value 5.0e-19
 Match length 100
 % identity 51
 NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
 >gi_100941_pir_S12140 zein Zc1 - maize
 >gi_100945_pir_B29017 zein 2 - maize
 >gi_22515_emb_CAA37595 (X53515) zein Zc1 [Zea mays]
 >gi_168666 (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298461
 Seq. ID LIB3151-012-Q1-K1-D6
 Method BLASTN
 NCBI GI g168484
 BLAST score 192

E value 1.0e-104
 Match length 386
 % identity 94
 NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298462
 Seq. ID LIB3151-012-Q1-K1-E12
 Method BLASTX
 NCBI GI g224507
 BLAST score 178
 E value 4.0e-13
 Match length 63
 % identity 60
 NCBI Description zein A1 [Zea mays]

Seq. No. 298463
 Seq. ID LIB3151-012-Q1-K1-E3
 Method BLASTX
 NCBI GI g100940
 BLAST score 265
 E value 3.0e-23
 Match length 91
 % identity 60
 NCBI Description zein zA1 - maize

Seq. No. 298464
 Seq. ID LIB3151-012-Q1-K1-E6
 Method BLASTN
 NCBI GI g168675
 BLAST score 70
 E value 2.0e-31
 Match length 114
 % identity 91
 NCBI Description Maize mutant zein (zE19) gene, complete cds

Seq. No. 298465
 Seq. ID LIB3151-012-Q1-K1-F11
 Method BLASTN
 NCBI GI g22516
 BLAST score 363
 E value 0.0e+00
 Match length 423
 % identity 96
 NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298466
 Seq. ID LIB3151-012-Q1-K1-F5
 Method BLASTN
 NCBI GI g168692
 BLAST score 62
 E value 2.0e-26
 Match length 216
 % identity 88
 NCBI Description Maize zein mRNA, complete cds, clone ZG7

Seq. No. 298467
 Seq. ID LIB3151-012-Q1-K1-G5

Method BLASTX
 NCBI GI g1332579
 BLAST score 642
 E value 2.0e-67
 Match length 151
 % identity 9
 NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

 Seq. No. 298468
 Seq. ID LIB3151-012-Q1-K1-G7
 Method BLASTX
 NCBI GI g168695
 BLAST score 143
 E value 9.0e-09
 Match length 28
 % identity 93
 NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
 zein gamma [Zea mays]

 Seq. No. 298469
 Seq. ID LIB3151-012-Q1-K1-H11
 Method BLASTX
 NCBI GI g121472
 BLAST score 254
 E value 9.0e-23
 Match length 118
 % identity 50
 NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
 (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
 >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
 maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
 [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea
 mays] >gi_168485_(M16066) glutelin-2 [Zea mays]

 Seq. No. 298470
 Seq. ID LIB3151-012-Q1-K1-H7
 Method BLASTN
 NCBI GI g22514
 BLAST score 89
 E value 2.0e-42
 Match length 222
 % identity 90
 NCBI Description Maize Zc1 gene for Zein Zc1 (14 kd zein-2)

 Seq. No. 298471
 Seq. ID LIB3151-012-Q1-K1-H8
 Method BLASTX
 NCBI GI g82660
 BLAST score 203
 E value 5.0e-16
 Match length 59
 % identity 69
 NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
 >gi_809117_emb_CAA24720_(V01473) zein [Zea mays]

 Seq. No. 298472
 Seq. ID LIB3151-013-Q1-K1-B11

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Method BLASTX
NCBI GI g951449
BLAST score 498
E value 2.0e-50
Match length 149
% identity 65
NCBI Description (L46681) aspartic protease precursor [Lycopersicon esculentum]

Seq. No. 298473
Seq. ID LIB3151-013-Q1-K1-B3
Method BLASTX
NCBI GI g2995405
BLAST score 281
E value 6.0e-25
Match length 86
% identity 59
NCBI Description (Y12432) polyprotein [Ananas comosus]

Seq. No. 298474
Seq. ID LIB3151-013-Q1-K1-B5
Method BLASTX
NCBI GI g3094012
BLAST score 204
E value 5.0e-16
Match length 79
% identity 59
NCBI Description (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]

Seq. No. 298475
Seq. ID LIB3151-013-Q1-K1-B9
Method BLASTX
NCBI GI g3885334
BLAST score 153
E value 6.0e-10
Match length 73
% identity 51
NCBI Description (AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No. 298476
Seq. ID LIB3151-013-Q1-K1-C2
Method BLASTX
NCBI GI g3540180
BLAST score 171
E value 4.0e-12
Match length 84
% identity 50
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 298477
Seq. ID LIB3151-013-Q1-K1-C8
Method BLASTX
NCBI GI g100484
BLAST score 512
E value 5.0e-52
Match length 147

% identity 60
NCBI Description hypothetical protein - garden snapdragon

Seq. No. 298478
Seq. ID LIB3151-013-Q1-K1-C9
Method BLASTN
NCBI GI g3108252
BLAST score 123
E value 1.0e-62
Match length 300
% identity 86
NCBI Description Gossypium barbadense clone pXP039 repetitive DNA sequence

Seq. No. 298479
Seq. ID LIB3151-013-Q1-K1-E11
Method BLASTX
NCBI GI g2995405
BLAST score 474
E value 1.0e-47
Match length 148
% identity 61
NCBI Description (Y12432) polyprotein [Ananas comosus]

Seq. No. 298480
Seq. ID LIB3151-013-Q1-K1-F7
Method BLASTX
NCBI GI g2995405
BLAST score 425
E value 7.0e-42
Match length 136
% identity 59
NCBI Description (Y12432) polyprotein [Ananas comosus]

Seq. No. 298481
Seq. ID LIB3151-013-Q1-K1-G1
Method BLASTX
NCBI GI g2995405
BLAST score 491
E value 1.0e-49
Match length 119
% identity 76
NCBI Description (Y12432) polyprotein [Ananas comosus]

Seq. No. 298482
Seq. ID LIB3151-013-Q1-K1-G9
Method BLASTX
NCBI GI g3024122
BLAST score 233
E value 1.0e-19
Match length 51
% identity 86
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No. 298483
Seq. ID LIB3151-013-Q1-K1-H4

Method BLASTX
NCBI GI g2995405
BLAST score 380
E value 1.0e-36
Match length 140
% identity 54
NCBI Description (Y12432) polyprotein [Ananas comosus]

Seq. No. 298484
Seq. ID LIB3151-013-Q1-K1-H9
Method BLASTX
NCBI GI g1418990
BLAST score 465
E value 2.0e-46
Match length 99
% identity 86
NCBI Description (Z75524) unknown [Lycopersicon esculentum]

Seq. No. 298485
Seq. ID LIB3151-014-Q1-K1-A1
Method BLASTX
NCBI GI g4539359
BLAST score 222
E value 3.0e-18
Match length 53
% identity 74
NCBI Description (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 298486
Seq. ID LIB3151-014-Q1-K1-A11
Method BLASTX
NCBI GI g141599
BLAST score 237
E value 5.0e-20
Match length 88
% identity 59
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)
>gi_72316_pir_ZIZMA2 19K zein precursor (clone cZ19A2) -
maize (fragment) >gi_168670 (M12142) 19 kDa zein protein
[Zea mays]

Seq. No. 298487
Seq. ID LIB3151-014-Q1-K1-A6
Method BLASTX
NCBI GI g1332579
BLAST score 509
E value 9.0e-52
Match length 109
% identity 10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 298488
Seq. ID LIB3151-014-Q1-K1-A7
Method BLASTX
NCBI GI g419803
BLAST score 190
E value 8.0e-15

Match length 117
% identity 49
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298489
Seq. ID LIB3151-014-Q1-K1-B3
Method BLASTX
NCBI GI g224508
BLAST score 429
E value 2.0e-42
Match length 118
% identity 79
NCBI Description zein A20 [Zea mays]

Seq. No. 298490
Seq. ID LIB3151-014-Q1-K1-C10
Method BLASTN
NCBI GI g22288
BLAST score 111
E value 9.0e-56
Match length 211
% identity 88
NCBI Description Maize mRNA fragment for endosperm glutelin-2

Seq. No. 298491
Seq. ID LIB3151-014-Q1-K1-C12
Method BLASTN
NCBI GI g4185305
BLAST score 38
E value 4.0e-12
Match length 70
% identity 89
NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

Seq. No. 298492
Seq. ID LIB3151-014-Q1-K1-E1
Method BLASTX
NCBI GI g100925
BLAST score 194
E value 2.0e-15
Match length 55
% identity 65
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_(X58197) 27kDa storage protein, zein [Zea mays]

Seq. No. 298493
Seq. ID LIB3151-014-Q1-K1-E10
Method BLASTX
NCBI GI g116333
BLAST score 256
E value 3.0e-27
Match length 105
% identity 54

NCBI Description ENDOCHITINASE B PRECURSOR (SEED CHITINASE B) >gi_168443
(M84165) chitinase B [Zea mays]

Seq. No. 298494
Seq. ID LIB3151-014-Q1-K1-E4
Method BLASTX
NCBI GI g168695
BLAST score 303
E value 9.0e-28
Match length 111
% identity 54
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
zein gamma [Zea mays]

Seq. No. 298495
Seq. ID LIB3151-014-Q1-K1-F12
Method BLASTN
NCBI GI g22447
BLAST score 40
E value 3.0e-13
Match length 88
% identity 86
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein

Seq. No. 298496
Seq. ID LIB3151-014-Q1-K1-G2
Method BLASTX
NCBI GI g433970
BLAST score 161
E value 9.0e-15
Match length 81
% identity 18
NCBI Description (Z28649) polyubiquitin [Acetabularia cliftonii]

Seq. No. 298497
Seq. ID LIB3151-014-Q1-K1-G3
Method BLASTN
NCBI GI g168665
BLAST score 217
E value 1.0e-119
Match length 272
% identity 97
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298498
Seq. ID LIB3151-014-Q1-K1-G5
Method BLASTX
NCBI GI g141603
BLAST score 353
E value 2.0e-33
Match length 126
% identity 63
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 298499

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Seq. ID	LIB3151-014-Q1-K1-G6
Method	BLASTX
NCBI GI	g22216
BLAST score	207
E value	2.0e-16
Match length	82
% identity	54
NCBI Description	(X55722) 22kD zein [Zea mays]
Seq. No.	298500
Seq. ID	LIB3151-014-Q1-K1-G9
Method	BLASTX
NCBI GI	g141597
BLAST score	268
E value	2.0e-23
Match length	142
% identity	46
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728_(V01481) reading frame zein [2] [Zea mays]
Seq. No.	298501
Seq. ID	LIB3151-014-Q1-K1-H9
Method	BLASTX
NCBI GI	g508545
BLAST score	264
E value	6.0e-23
Match length	65
% identity	85
NCBI Description	(L34340) zein [Zea mays]
Seq. No.	298502
Seq. ID	LIB3151-015-Q1-K1-A7
Method	BLASTN
NCBI GI	g168704
BLAST score	93
E value	6.0e-45
Match length	171
% identity	95
NCBI Description	Zea mays zein protein gene, complete cds
Seq. No.	298503
Seq. ID	LIB3151-015-Q1-K1-A8
Method	BLASTN
NCBI GI	g531828
BLAST score	33
E value	2.0e-09
Match length	73
% identity	86
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	298504
Seq. ID	LIB3151-015-Q1-K1-B6
Method	BLASTX
NCBI GI	g72307
BLAST score	153

E value 5.0e-10
Match length 53
% identity 66
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
(J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 298505
Seq. ID LIB3151-015-Q1-K1-B7
Method BLASTX
NCBI GI g1167955
BLAST score 156
E value 2.0e-10
Match length 104
% identity 39
NCBI Description (U43497) putative 32.7 kDa jasmonate-induced protein
[Hordeum vulgare] >gi_2465428 (AF021257) 32 kDa protein
[Hordeum vulgare]

Seq. No. 298506
Seq. ID LIB3151-015-Q1-K1-C1
Method BLASTX
NCBI GI g100938
BLAST score 170
E value 2.0e-12
Match length 64
% identity 61
NCBI Description zein precursor - maize >gi_22442_emb_CAA32513_ (X14335)
zein precursor (AA -21 to 90) [Zea mays]

Seq. No. 298507
Seq. ID LIB3151-015-Q1-K1-D4
Method BLASTX
NCBI GI g168695
BLAST score 230
E value 5.0e-19
Match length 86
% identity 58
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
zein gamma [Zea mays]

Seq. No. 298508
Seq. ID LIB3151-015-Q1-K1-E4
Method BLASTN
NCBI GI g168694
BLAST score 38
E value 6.0e-12
Match length 74
% identity 88
NCBI Description Maize gamma zein mRNA, partial cds

Seq. No. 298509
Seq. ID LIB3151-015-Q1-K1-F10
Method BLASTX
NCBI GI g22216
BLAST score 298
E value 3.0e-27
Match length 107

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% identity	62
NCBI Description	(X55722) 22kD zein [Zea mays]
Seq. No.	298510
Seq. ID	LIB3151-015-Q1-K1-F7
Method	BLASTN
NCBI GI	g22537
BLAST score	73
E value	7.0e-33
Match length	105
% identity	58
NCBI Description	Maize mRNA for zein polypeptide (clone M6)
Seq. No.	298511
Seq. ID	LIB3151-015-Q1-K1-G5
Method	BLASTN
NCBI GI	g22516
BLAST score	106
E value	1.0e-52
Match length	254
% identity	86
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.	298512
Seq. ID	LIB3151-015-Q1-K1-G8
Method	BLASTN
NCBI GI	g22531
BLAST score	165
E value	9.0e-88
Match length	376
% identity	86
NCBI Description	Zea mays mRNA encoding a zein (clone pZ22.1) >gi_270688_gb_I03336 Sequence 10 from Patent US 4885357 >gi_270741_gb_I03273 Sequence 2 from Patent US
Seq. No.	298513
Seq. ID	LIB3151-015-Q1-K1-H4
Method	BLASTN
NCBI GI	g22516
BLAST score	258
E value	1.0e-143
Match length	374
% identity	92
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.	298514
Seq. ID	LIB3151-016-Q1-K1-A10
Method	BLASTX
NCBI GI	g141617
BLAST score	337
E value	1.0e-31
Match length	109
% identity	61
NCBI Description	ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) >gi_100941_pir_S12140 zein Zc1 - maize >gi_100945_pir_B29017 zein 2 - maize >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]

>gi_168666 (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298515
Seq. ID LIB3151-016-Q1-K1-A12
Method BLASTX
NCBI GI g136063
BLAST score 152
E value 2.0e-10
Match length 50
% identity 62
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
>gi_68426_pir_ISZMT triose-phosphate isomerase (EC
5.3.1.1) - maize >gi_168647 (L00371) triosephosphate
isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)
triosephosphate isomerase [Zea mays]

Seq. No. 298516
Seq. ID LIB3151-016-Q1-K1-A2
Method BLASTX
NCBI GI g141614
BLAST score 148
E value 6.0e-11
Match length 80
% identity 54
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
>gi_82662_pir_B22831 22K zein precursor (clone M1) - maize
>gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea
mays] >gi_224510_prf_1107201D zein M1 [Zea mays]

Seq. No. 298517
Seq. ID LIB3151-016-Q1-K1-A3
Method BLASTX
NCBI GI g224508
BLAST score 312
E value 7.0e-29
Match length 92
% identity 73
NCBI Description zein A20 [Zea mays]

Seq. No. 298518
Seq. ID LIB3151-016-Q1-K1-B10
Method BLASTN
NCBI GI g22516
BLAST score 276
E value 1.0e-154
Match length 384
% identity 93
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298519
Seq. ID LIB3151-016-Q1-K1-B12
Method BLASTX
NCBI GI g224507
BLAST score 185
E value 9.0e-14
Match length 111
% identity 41

NCBI Description zein A1 [Zea mays]

Seq. No. 298520
Seq. ID LIB3151-016-Q1-K1-B3
Method BLASTX
NCBI GI g141608
BLAST score 191
E value 2.0e-27
Match length 109
% identity 62
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 298521
Seq. ID LIB3151-016-Q1-K1-C7
Method BLASTX
NCBI GI g72307
BLAST score 367
E value 4.0e-35
Match length 101
% identity 78
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
(J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 298522
Seq. ID LIB3151-016-Q1-K1-D10
Method BLASTN
NCBI GI g4185305
BLAST score 147
E value 5.0e-77
Match length 295
% identity 88
NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
(sz22-21) gene, complete cds; retrotransposon Opie-2 gag
protein, polyprotein, and copia protein genes, complete
cds; and unknown genes

Seq. No. 298523
Seq. ID LIB3151-016-Q1-K1-D11
Method BLASTN
NCBI GI g22549
BLAST score 164
E value 3.0e-87
Match length 252
% identity 91
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298524
Seq. ID LIB3151-016-Q1-K1-D2
Method BLASTX
NCBI GI g4325282
BLAST score 163
E value 2.0e-11
Match length 52
% identity 56
NCBI Description (AF123310) NAC domain protein NAM [Arabidopsis thaliana]

>gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
[Arabidopsis thaliana]

Seq. No. 298525
Seq. ID LIB3151-016-Q1-K1-D7
Method BLASTX
NCBI GI g419803
BLAST score 388
E value 8.0e-38
Match length 92
% identity 77
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298526
Seq. ID LIB3151-016-Q1-K1-E4
Method BLASTX
NCBI GI g121472
BLAST score 275
E value 2.0e-24
Match length 64
% identity 75
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays]
>gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298527
Seq. ID LIB3151-016-Q1-K1-G10
Method BLASTX
NCBI GI g508545
BLAST score 340
E value 6.0e-32
Match length 119
% identity 61
NCBI Description (L34340) zein [Zea mays]

Seq. No. 298528
Seq. ID LIB3151-016-Q1-K1-G5
Method BLASTX
NCBI GI g141616
BLAST score 216
E value 1.0e-17
Match length 88
% identity 50
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 298529
Seq. ID LIB3151-016-Q1-K1-H3
Method BLASTN
NCBI GI g168484
BLAST score 80
E value 3.0e-37
Match length 120

% identity 92
NCBI Description Maize endosperm glutelin-2 gene; complete cds

Seq. No. 298530
Seq. ID LIB3151-016-Q1-K1-H7
Method BLASTX
NCBI GI g2832246
BLAST score 255
E value 3.0e-22
Match length 95
% identity 58
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 298531
Seq. ID LIB3151-016-Q1-K1-H9
Method BLASTN
NCBI GI g168681
BLAST score 69
E value 1.0e-30
Match length 234
% identity 82
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 298532
Seq. ID LIB3151-017-Q1-K1-A12
Method BLASTN
NCBI GI g1037129
BLAST score 183
E value 2.0e-98
Match length 294
% identity 90
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298533
Seq. ID LIB3151-017-Q1-K1-A8
Method BLASTN
NCBI GI g2832242
BLAST score 121
E value 1.0e-61
Match length 219
% identity 13
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 298534
Seq. ID LIB3151-017-Q1-K1-B5
Method BLASTX
NCBI GI g16073
BLAST score 331
E value 6.0e-31
Match length 119
% identity 61
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298535
Seq. ID LIB3151-017-Q1-K1-B8

Method BLASTN
NCBI GI g22514
BLAST score 99
E value 2.0e-48
Match length 183
% identity 89
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 298536
Seq. ID LIB3151-017-Q1-K1-C3
Method BLASTN
NCBI GI g22549
BLAST score 100
E value 7.0e-49
Match length 124
% identity 98
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298537
Seq. ID LIB3151-017-Q1-K1-C7
Method BLASTX
NCBI GI g121472
BLAST score 199
E value 1.0e-15
Match length 77
% identity 52
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298538
Seq. ID LIB3151-017-Q1-K1-C9
Method BLASTX
NCBI GI g419803
BLAST score 224
E value 2.0e-26
Match length 81
% identity 75
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
mays]

Seq. No. 298539
Seq. ID LIB3151-017-Q1-K1-D1
Method BLASTX
NCBI GI g135398
BLAST score 282
E value 1.0e-25
Match length 57
% identity 89
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir_S15773 tubulin alpha-1
chain - maize >gi_22147_emb_CAA33734 (X15704)
alpha1-tubulin [Zea mays]

Seq. No. 298540

Seq. ID LIB3151-017-Q1-K1-E10
Method BLASTX
NCBI GI g141597
BLAST score 308
E value 2.0e-28
Match length 92
% identity 68
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3_19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 298541
Seq. ID LIB3151-017-Q1-K1-F11
Method BLASTN
NCBI GI g168663
BLAST score 41
E value 8.0e-14
Match length 101
% identity 87
NCBI Description Maize sulfur-rich zein protein of Mr 15,000, complete cds

Seq. No. 298542
Seq. ID LIB3151-017-Q1-K1-F5
Method BLASTN
NCBI GI g168661
BLAST score 46
E value 4.0e-17
Match length 113
% identity 87
NCBI Description Maize 15 kDa zein mRNA, clone cz15A3, complete cds

Seq. No. 298543
Seq. ID LIB3151-017-Q1-K1-F6
Method BLASTN
NCBI GI g22514
BLAST score 175
E value 6.0e-94
Match length 247
% identity 93
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 298544
Seq. ID LIB3151-017-Q1-K1-G10
Method BLASTN
NCBI GI g168665
BLAST score 142
E value 3.0e-74
Match length 206
% identity 92
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298545
Seq. ID LIB3151-017-Q1-K1-G6
Method BLASTX
NCBI GI g1076678
BLAST score 261

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E value 6.0e-23
Match length 80
% identity 71
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No. 298546
Seq. ID LIB3151-017-Q1-K1-G7
Method BLASTN
NCBI GI g22326
BLAST score 65
E value 3.0e-28
Match length 149
% identity 86
NCBI Description Z.mays gene for Hageman factor inhibitor

Seq. No. 298547
Seq. ID LIB3151-017-Q1-K1-H5
Method BLASTN
NCBI GI g22542
BLAST score 156
E value 1.0e-82
Match length 200
% identity 94
NCBI Description Maize gene for Mr 19000 alpha zein and 5'-flanking region

Seq. No. 298548
Seq. ID LIB3151-017-Q1-K1-H7
Method BLASTX
NCBI GI g121472
BLAST score 163
E value 6.0e-33
Match length 97
% identity 79
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298549
Seq. ID LIB3151-018-Q1-K1-B3
Method BLASTX
NCBI GI g141605
BLAST score 530
E value 3.0e-54
Match length 121
% identity 90
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298550
Seq. ID LIB3151-018-Q1-K1-B9
Method BLASTN
NCBI GI g22516
BLAST score 137

DRAFT Sequence Database

E value	4.0e-71
Match length	269
% identity	88
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.	298551
Seq. ID	LIB3151-018-Q1-K1-C12
Method	BLASTX
NCBI GI	g168701
BLAST score	403
E value	2.0e-39
Match length	120
% identity	72
NCBI Description	(M60837) zein [Zea mays]
Seq. No.	298552
Seq. ID	LIB3151-018-Q1-K1-C3
Method	BLASTX
NCBI GI	g4096786
BLAST score	223
E value	3.0e-18
Match length	58
% identity	74
NCBI Description	(U39958) NADP-malic enzyme [Zea mays]
Seq. No.	298553
Seq. ID	LIB3151-018-Q1-K1-C5
Method	BLASTX
NCBI GI	g141617
BLAST score	318
E value	9.0e-33
Match length	105
% identity	70
NCBI Description	ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) >gi_100941_pir_S12140 zein Zc1 - maize >gi_100945_pir_B29017 zein 2 - maize >gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays] >gi_168666_(M16460) 16-kDa zein protein [Zea mays]
Seq. No.	298554
Seq. ID	LIB3151-018-Q1-K1-D5
Method	BLASTN
NCBI GI	g1037129
BLAST score	49
E value	1.0e-18
Match length	109
% identity	87
NCBI Description	(gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]
Seq. No.	298555
Seq. ID	LIB3151-018-Q1-K1-F4
Method	BLASTN
NCBI GI	g1037129
BLAST score	279
E value	1.0e-155
Match length	418

% identity	91
NCBI Description	(gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]
Seq. No.	298556
Seq. ID	LIB3151-018-Q1-K1-F9
Method	BLASTX
NCBI GI	g4559384
BLAST score	176
E value	1.0e-12
Match length	79
% identity	44
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]
Seq. No.	298557
Seq. ID	LIB3151-018-Q1-K1-H1
Method	BLASTX
NCBI GI	g4097690
BLAST score	205
E value	2.0e-16
Match length	75
% identity	60
NCBI Description	(U66592) prohibitin 2 [Arabidopsis thaliana] >gi_4099801 (U89791) prohibitin-like protein [Arabidopsis thaliana] >gi_4204301 (AC003027) prohibitin 2 [Arabidopsis thaliana]
Seq. No.	298558
Seq. ID	LIB3151-018-Q1-K1-H2
Method	BLASTX
NCBI GI	g2832247
BLAST score	223
E value	3.0e-18
Match length	92
% identity	53
NCBI Description	(AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.	298559
Seq. ID	LIB3151-018-Q1-K1-H7
Method	BLASTX
NCBI GI	g136757
BLAST score	395
E value	2.0e-38
Match length	75
% identity	97
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_100881_pir_S07314 UDPglucose--starch glucosyltransferase (EC 2.4.1.11) precursor - maize >gi_168653 (M24258) amyloplast-specific transit protein [Zea mays] >gi_1644339_emb_CAA27574_ (X03935) glucosyl transferase [Zea mays]
Seq. No.	298560
Seq. ID	LIB3151-019-Q1-K1-A6
Method	BLASTX
NCBI GI	g168701
BLAST score	224
E value	5.0e-31

Match length 103
% identity 69
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298561
Seq. ID LIB3151-019-Q1-K1-A8
Method BLASTX
NCBI GI g168701
BLAST score 197
E value 2.0e-15
Match length 78
% identity 63
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298562
Seq. ID LIB3151-019-Q1-K1-A9
Method BLASTX
NCBI GI g4185308
BLAST score 220
E value 4.0e-18
Match length 83
% identity 61
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]

Seq. No. 298563
Seq. ID LIB3151-019-Q1-K1-B8
Method BLASTN
NCBI GI g168484
BLAST score 304
E value 1.0e-170
Match length 375
% identity 95
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298564
Seq. ID LIB3151-019-Q1-K1-C6
Method BLASTN
NCBI GI g168681
BLAST score 226
E value 1.0e-124
Match length 298
% identity 58
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 298565
Seq. ID LIB3151-019-Q1-K1-C8
Method BLASTX
NCBI GI g4206306
BLAST score 650
E value 2.0e-68
Match length 130
% identity 100
NCBI Description (AF049110) prpol [Zea mays]

Seq. No. 298566
Seq. ID LIB3151-019-Q1-K1-D10

Method BLASTX
 NCBI GI g82660
 BLAST score 235
 E value 1.0e-19
 Match length 119
 % identity 46
 NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
 >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 298567
 Seq. ID LIB3151-019-Q1-K1-D11
 Method BLASTX
 NCBI GI g2832243
 BLAST score 167
 E value 7.0e-12
 Match length 65
 % identity 62
 NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298568
 Seq. ID LIB3151-019-Q1-K1-D2
 Method BLASTX
 NCBI GI g1707924
 BLAST score 201
 E value 2.0e-21
 Match length 81
 % identity 69
 NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 1
 PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
 PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE
 ADENYL TRANSFERASE) (SHRUNKEN-2) >gi_1947182 (M81603)
 shrunken-2 [Zea mays] >gi_444329_prf_1906378A ADP glucose
 pyrophosphorylase [Zea mays]

Seq. No. 298569
 Seq. ID LIB3151-019-Q1-K1-D4
 Method BLASTX
 NCBI GI g141605
 BLAST score 145
 E value 3.0e-19
 Match length 94
 % identity 66
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
 >gi_72312_pir_ZIZM92 19K zein precursor (clone cz19C2) -
 maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298570
 Seq. ID LIB3151-019-Q1-K1-E11
 Method BLASTX
 NCBI GI g2832243
 BLAST score 253
 E value 8.0e-22
 Match length 109
 % identity 56
 NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298571

Seq. ID LIB3151-019-Q1-K1-E2
Method BLASTX
NCBI GI g224513
BLAST score 189
E value 1.0e-15
Match length 98
% identity 48
NCBI Description zein M6 [Zea mays]

Seq. No. 298572
Seq. ID LIB3151-019-Q1-K1-F12
Method BLASTX
NCBI GI g168695
BLAST score 178
E value 3.0e-13
Match length 67
% identity 58
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
zein gamma [Zea mays]

Seq. No. 298573
Seq. ID LIB3151-019-Q1-K1-F5
Method BLASTN
NCBI GI g22516
BLAST score 65
E value 3.0e-28
Match length 137
% identity 87
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298574
Seq. ID LIB3151-019-Q1-K1-G6
Method BLASTN
NCBI GI g168484
BLAST score 96
E value 8.0e-47
Match length 156
% identity 90
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298575
Seq. ID LIB3151-019-Q1-K1-H3
Method BLASTN
NCBI GI g22549
BLAST score 281
E value 1.0e-157
Match length 357
% identity 95
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298576
Seq. ID LIB3151-019-Q1-K1-H4
Method BLASTX
NCBI GI g170354
BLAST score 506
E value 2.0e-51
Match length 109

% identity 20
NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]

Seq. No. 298577
Seq. ID LIB3151-019-Q1-K1-H6
Method BLASTN
NCBI GI g168675
BLAST score 61
E value 1.0e-25
Match length 182
% identity 91
NCBI Description Maize mutant zein (zE19) gene, complete cds

Seq. No. 298578
Seq. ID LIB3151-019-Q1-K1-H7
Method BLASTX
NCBI GI g2832247
BLAST score 181
E value 2.0e-13
Match length 91
% identity 49
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 298579
Seq. ID LIB3151-019-Q1-K1-H8
Method BLASTN
NCBI GI g168425
BLAST score 62
E value 1.0e-26
Match length 154
% identity 85
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 298580
Seq. ID LIB3151-020-Q1-K1-D10
Method BLASTX
NCBI GI g168691
BLAST score 245
E value 8.0e-21
Match length 92
% identity 60
NCBI Description (M29628) zein [Zea mays]

Seq. No. 298581
Seq. ID LIB3151-020-Q1-K1-D4
Method BLASTX
NCBI GI g141603
BLAST score 177
E value 6.0e-13
Match length 99
% identity 45
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2_19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 298582
Seq. ID LIB3151-020-Q1-K1-D8

Method BLASTX
NCBI GI g629862
BLAST score 162
E value 2.0e-11
Match length 75
% identity 48
NCBI Description zein Zd1, 19K - maize >gi_535021_emb_CAA47640_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298583
Seq. ID LIB3151-020-Q1-K1-D9
Method BLASTX
NCBI GI g508545
BLAST score 235
E value 1.0e-19
Match length 98
% identity 54
NCBI Description (L34340) zein [Zea mays]

Seq. No. 298584
Seq. ID LIB3151-020-Q1-K1-E10
Method BLASTX
NCBI GI g141613
BLAST score 155
E value 2.0e-10
Match length 81
% identity 44
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
>gi_72305_pir_ZIZM21_22K zein precursor (clone pZ22.1) -
maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]

Seq. No. 298585
Seq. ID LIB3151-020-Q1-K1-E12
Method BLASTN
NCBI GI g1037129
BLAST score 296
E value 1.0e-166
Match length 392
% identity 94
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298586
Seq. ID LIB3151-020-Q1-K1-F1
Method BLASTX
NCBI GI g2832247
BLAST score 153
E value 3.0e-10
Match length 77
% identity 45
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 298587
Seq. ID LIB3151-020-Q1-K1-F5
Method BLASTN
NCBI GI g4140643
BLAST score 42

E value 2.0e-14
Match length 82
% identity 88
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 298588
Seq. ID LIB3151-020-Q1-K1-H7
Method BLASTN
NCBI GI g22549
BLAST score 45
E value 3.0e-16
Match length 49
% identity 98
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298589
Seq. ID LIB3151-021-Q1-K1-A11
Method BLASTX
NCBI GI g141607
BLAST score 297
E value 5.0e-27
Match length 66
% identity 94
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
>gi_22521_emb_CAA24718_(V01471) zein [Zea mays] >gi_168672
(J01244) zein 19 kd protein (partial) [Zea mays]

Seq. No. 298590
Seq. ID LIB3151-021-Q1-K1-B1
Method BLASTX
NCBI GI g168691
BLAST score 323
E value 4.0e-30
Match length 95
% identity 69
NCBI Description (M29628) zein [Zea mays]

Seq. No. 298591
Seq. ID LIB3151-021-Q1-K1-B3
Method BLASTX
NCBI GI g629861
BLAST score 352
E value 2.0e-33
Match length 105
% identity 70
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_(X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298592
Seq. ID LIB3151-021-Q1-K1-C1
Method BLASTX
NCBI GI g4140644
BLAST score 306
E value 5.0e-41
Match length 133
% identity 70

NCBI Description (AF090447) 22-kDa zein protein 12 [Zea mays]
Seq. No. 298593
Seq. ID LIB3151-021-Q1-K1-C6
Method BLASTN
NCBI GI g22528
BLAST score 47
E value 1.0e-17
Match length 79
% identity 91
NCBI Description Zea mays mRNA encoding a zein (clone A20)
Seq. No. 298594
Seq. ID LIB3151-021-Q1-K1-D9
Method BLASTX
NCBI GI g168701
BLAST score 505
E value 3.0e-51
Match length 126
% identity 84
NCBI Description (M60837) zein [Zea mays]
Seq. No. 298595
Seq. ID LIB3151-021-Q1-K1-E6
Method BLASTX
NCBI GI g508545
BLAST score 302
E value 1.0e-27
Match length 85
% identity 71
NCBI Description (L34340) zein [Zea mays]
Seq. No. 298596
Seq. ID LIB3151-021-Q1-K1-G2
Method BLASTN
NCBI GI g22516
BLAST score 183
E value 2.0e-98
Match length 386
% identity 88
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No. 298597
Seq. ID LIB3151-021-Q1-K1-G3
Method BLASTX
NCBI GI g141608
BLAST score 269
E value 9.0e-24
Match length 101
% identity 61
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]
Seq. No. 298598
Seq. ID LIB3151-021-Q1-K1-H3
Method BLASTX

NCBI GI g100925
BLAST score 144
E value 3.0e-09
Match length 38
% identity 68
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_(X58197) 27kDa storage protein, zein [Zea mays]

Seq. No. 298599
Seq. ID LIB3151-021-Q1-K1-H4
Method BLASTX
NCBI GI g141600
BLAST score 144
E value 1.0e-09
Match length 56
% identity 55
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) - maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 298600
Seq. ID LIB3151-021-Q1-K1-H7
Method BLASTN
NCBI GI g168685
BLAST score 43
E value 3.0e-15
Match length 59
% identity 93
NCBI Description Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA

Seq. No. 298601
Seq. ID LIB3151-022-Q1-K1-A3
Method BLASTX
NCBI GI g72307
BLAST score 198
E value 2.0e-15
Match length 100
% identity 49
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686 (J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 298602
Seq. ID LIB3151-022-Q1-K1-A5
Method BLASTX
NCBI GI g4519539
BLAST score 158
E value 2.0e-12
Match length 83
% identity 44
NCBI Description (AB016256) NAD-dependent sorbitol dehydrogenase [Malus domestica]

Seq. No. 298603
Seq. ID LIB3151-022-Q1-K1-A6
Method BLASTN
NCBI GI g168665
BLAST score 41

E value 1.0e-13
Match length 101
% identity 85
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298604
Seq. ID LIB3151-022-Q1-K1-C8
Method BLASTN
NCBI GI g1037129
BLAST score 285
E value 1.0e-159
Match length 425
% identity 92
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298605
Seq. ID LIB3151-022-Q1-K1-D3
Method BLASTX
NCBI GI g136757
BLAST score 242
E value 1.0e-20
Match length 80
% identity 68
NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
>gi_100881_pir_S07314 UDPglucose--starch
glucosyltransferase (EC 2.4.1.11) precursor - maize
>gi_168653 (M24258) amyloplast-specific transit protein
[Zea mays] >gi_1644339_emb_CAA27574_ (X03935) glucosyl
transferase [Zea mays]

Seq. No. 298606
Seq. ID LIB3151-022-Q1-K1-E8
Method BLASTN
NCBI GI g1037129
BLAST score 350
E value 0.0e+00
Match length 426
% identity 96
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298607
Seq. ID LIB3151-022-Q1-K1-F10
Method BLASTX
NCBI GI g168695
BLAST score 239
E value 4.0e-20
Match length 103
% identity 50
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
zein gamma [Zea mays]

Seq. No. 298608
Seq. ID LIB3151-022-Q1-K1-G1
Method BLASTX
NCBI GI g224509

BLAST score 188
E value 4.0e-14
Match length 82
% identity 54
NCBI Description zein E19 [Zea mays]

Seq. No. 298609
Seq. ID LIB3151-022-Q1-K1-H10
Method BLASTX
NCBI GI g82660
BLAST score 252
E value 1.0e-21
Match length 77
% identity 68
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_(V01473) zein [Zea mays]

Seq. No. 298610
Seq. ID LIB3151-022-Q1-K1-H5
Method BLASTX
NCBI GI g16073
BLAST score 353
E value 1.0e-33
Match length 99
% identity 77
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298611
Seq. ID LIB3151-022-Q1-K1-H7
Method BLASTX
NCBI GI g224514
BLAST score 281
E value 5.0e-25
Match length 66
% identity 89
NCBI Description zein M8 [Zea mays]

Seq. No. 298612
Seq. ID LIB3151-022-Q1-K1-H9
Method BLASTX
NCBI GI g224508
BLAST score 284
E value 2.0e-25
Match length 113
% identity 60
NCBI Description zein A20 [Zea mays]

Seq. No. 298613
Seq. ID LIB3151-023-Q1-K1-A11
Method BLASTX
NCBI GI g508545
BLAST score 208
E value 1.0e-16
Match length 94
% identity 49
NCBI Description (L34340) zein [Zea mays]

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Seq. No. 298614
Seq. ID LIB3151-023-Q1-K1-A3
Method BLASTX
NCBI GI g224508
BLAST score 151
E value 8.0e-15
Match length 81
% identity 63
NCBI Description zein A20 [Zea mays]

Seq. No. 298615
Seq. ID LIB3151-023-Q1-K1-A4
Method BLASTX
NCBI GI g224513
BLAST score 219
E value 2.0e-18
Match length 73
% identity 64
NCBI Description zein M6 [Zea mays]

Seq. No. 298616
Seq. ID LIB3151-023-Q1-K1-A7
Method BLASTN
NCBI GI g168681
BLAST score 92
E value 2.0e-44
Match length 148
% identity 92
NCBI Description Maize 19 kDa zein mRNA, clone cz19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 298617
Seq. ID LIB3151-023-Q1-K1-A9
Method BLASTX
NCBI GI g141597
BLAST score 400
E value 6.0e-39
Match length 102
% identity 79
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3_19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 298618
Seq. ID LIB3151-023-Q1-K1-B10
Method BLASTX
NCBI GI g508545
BLAST score 393
E value 4.0e-38
Match length 128
% identity 66
NCBI Description (L34340) zein [Zea mays]

Seq. No. 298619
Seq. ID LIB3151-023-Q1-K1-B11
Method BLASTX

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NCBI GI	g224514
BLAST score	201
E value	8.0e-16
Match length	60
% identity	72
NCBI Description	zein M8 [Zea mays]
Seq. No.	298620
Seq. ID	LIB3151-023-Q1-K1-B12
Method	BLASTN
NCBI GI	g168484
BLAST score	129
E value	2.0e-66
Match length	217
% identity	92
NCBI Description	Maize endosperm glutelin-2 gene, complete cds
Seq. No.	298621
Seq. ID	LIB3151-023-Q1-K1-B5
Method	BLASTX
NCBI GI	g419803
BLAST score	258
E value	1.0e-22
Match length	80
% identity	65
NCBI Description	zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
Seq. No.	298622
Seq. ID	LIB3151-023-Q1-K1-B7
Method	BLASTX
NCBI GI	g100940
BLAST score	226
E value	1.0e-18
Match length	100
% identity	52
NCBI Description	zein zA1 - maize
Seq. No.	298623
Seq. ID	LIB3151-023-Q1-K1-C6
Method	BLASTX
NCBI GI	g141603
BLAST score	281
E value	5.0e-25
Match length	121
% identity	53
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20) >gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
Seq. No.	298624
Seq. ID	LIB3151-023-Q1-K1-C8
Method	BLASTX
NCBI GI	g121472
BLAST score	155
E value	2.0e-18
Match length	89

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% identity 55
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119). -
maize >gi_22289_emb CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298625
Seq. ID LIB3151-023-Q1-K1-D10
Method BLASTN
NCBI GI g2832242
BLAST score 123
E value 6.0e-63
Match length 143
% identity 11
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 298626
Seq. ID LIB3151-023-Q1-K1-D3
Method BLASTN
NCBI GI g535019
BLAST score 55
E value 4.0e-22
Match length 131
% identity 43
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)

Seq. No. 298627
Seq. ID LIB3151-023-Q1-K1-D5
Method BLASTX
NCBI GI g2832246
BLAST score 341
E value 3.0e-32
Match length 98
% identity 76
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 298628
Seq. ID LIB3151-023-Q1-K1-E4
Method BLASTX
NCBI GI g508545
BLAST score 322
E value 8.0e-30
Match length 126
% identity 56
NCBI Description (L34340) zein [Zea mays]

Seq. No. 298629
Seq. ID LIB3151-023-Q1-K1-E6
Method BLASTN
NCBI GI g535019
BLAST score 63
E value 6.0e-27
Match length 139
% identity 44
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)

Seq. No. 298630
Seq. ID LIB3151-023-Q1-K1-F10
Method BLASTX
NCBI GI g168664
BLAST score 217
E value 5.0e-18
Match length 51
% identity 86
NCBI Description (M13507) zein protein precursor [Zea mays]

Seq. No. 298631
Seq. ID LIB3151-023-Q1-K1-G8
Method BLASTX
NCBI GI g16073
BLAST score 451
E value 6.0e-45
Match length 121
% identity 79
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298632
Seq. ID LIB3151-023-Q1-K1-H11
Method BLASTX
NCBI GI g1710521
BLAST score 223
E value 2.0e-18
Match length 67
% identity 75
NCBI Description 60S RIBOSOMAL PROTEIN L24 >gi_1154859_emb_CAA63960_(X94296) L24 ribosomal protein [Hordeum vulgare]

Seq. No. 298633
Seq. ID LIB3151-023-Q1-K1-H3
Method BLASTX
NCBI GI g132584
BLAST score 231
E value 2.0e-19
Match length 77
% identity 58
NCBI Description RIBOSOME-INACTIVATING PROTEIN 3 (RNA N-GLYCOSIDASE) (B-32 PROTEIN) >gi_168451 (M83926) ribosome-inactivating protein [Zea mays]

Seq. No. 298634
Seq. ID LIB3151-023-Q1-K1-H7
Method BLASTX
NCBI GI g141616
BLAST score 179
E value 1.0e-13
Match length 41
% identity 78
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 298635
Seq. ID LIB3151-023-Q1-K1-H9

DRAFT

Method BLASTX
NCBI GI g141616
BLAST score 157
E value 1.0e-10
Match length 98
% identity 43
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 298636
Seq. ID LIB3151-024-Q1-K1-A9
Method BLASTN
NCBI GI g168484
BLAST score 192
E value 1.0e-104
Match length 316
% identity 95
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298637
Seq. ID LIB3151-024-Q1-K1-B2
Method BLASTX
NCBI GI g3970823
BLAST score 293
E value 2.0e-26
Match length 98
% identity 63
NCBI Description (X17555) pyruvate decarboxylase [Zea mays]

Seq. No. 298638
Seq. ID LIB3151-024-Q1-K1-B4
Method BLASTX
NCBI GI g168691
BLAST score 290
E value 3.0e-26
Match length 103
% identity 59
NCBI Description (M29628) zein [Zea mays]

Seq. No. 298639
Seq. ID LIB3151-024-Q1-K1-B7
Method BLASTX
NCBI GI g629862
BLAST score 216
E value 1.0e-17
Match length 79
% identity 58
NCBI Description zein Zd1, 19K - maize >gi_535021_emb_CAA47640_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298640
Seq. ID LIB3151-024-Q1-K1-C7
Method BLASTN
NCBI GI g22516
BLAST score 160
E value 7.0e-85
Match length 311

% identity 88
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298641
Seq. ID LIB3151-024-Q1-K1-C8
Method BLASTN
NCBI GI g22516
BLAST score 110
E value 3.0e-55
Match length 182
% identity 90
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298642
Seq. ID LIB3151-024-Q1-K1-C9
Method BLASTN
NCBI GI g22516
BLAST score 71
E value 7.0e-32
Match length 119
% identity 91
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298643
Seq. ID LIB3151-024-Q1-K1-D1
Method BLASTN
NCBI GI g168661
BLAST score 120
E value 8.0e-61
Match length 184
% identity 96
NCBI Description Maize 15 kDa zein mRNA, clone cz15A3, complete cds

Seq. No. 298644
Seq. ID LIB3151-024-Q1-K1-D12
Method BLASTX
NCBI GI g141600
BLAST score 167
E value 5.0e-12
Match length 64
% identity 58
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cz19B1) -
maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 298645
Seq. ID LIB3151-024-Q1-K1-D2
Method BLASTX
NCBI GI g1076708
BLAST score 704
E value 1.0e-74
Match length 148
% identity 27
NCBI Description seed tetraubiquitin - common sunflower
>gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max]
>gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max]
>gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin

C O D E
D O C U M E N T

[Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092)
Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044)
putative polyubiquitin [Arabidopsis thaliana]
>gi_1096513_prf_2111434A tetraubiquitin [Helianthus
annuus]

Seq. No. 298646
Seq. ID LIB3151-024-Q1-K1-D8
Method BLASTX
NCBI GI g2832247
BLAST score 167
E value 7.0e-12
Match length 88
% identity 51
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 298647
Seq. ID LIB3151-024-Q1-K1-E4
Method BLASTX
NCBI GI g2832243
BLAST score 185
E value 2.0e-15
Match length 97
% identity 57
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298648
Seq. ID LIB3151-024-Q1-K1-E8
Method BLASTX
NCBI GI g4185308
BLAST score 156
E value 2.0e-10
Match length 86
% identity 45
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]

Seq. No. 298649
Seq. ID LIB3151-024-Q1-K1-F6
Method BLASTN
NCBI GI g168694
BLAST score 48
E value 5.0e-18
Match length 140
% identity 84
NCBI Description Maize gamma zein mRNA, partial cds

Seq. No. 298650
Seq. ID LIB3151-024-Q1-K1-G11
Method BLASTN
NCBI GI g22288
BLAST score 219
E value 1.0e-120
Match length 323
% identity 92
NCBI Description Maize mRNA fragment for endosperm glutelin-2

Seq. No. 298651

Seq. ID LIB3151-024-Q1-K1-G8
 Method BLASTN
 NCBI GI g16072
 BLAST score 68
 E value 4.0e-30
 Match length 140
 % identity 87
 NCBI Description Acetabularia mediterranea zein gene

Seq. No. 298652
 Seq. ID LIB3151-024-Q1-K1-H11
 Method BLASTN
 NCBI GI g168669
 BLAST score 43
 E value 6.0e-15
 Match length 107
 % identity 85
 NCBI Description Maize 19 kDa zein mRNA, clone cz19A2, partial cds

Seq. No. 298653
 Seq. ID LIB3151-024-Q1-K1-H12
 Method BLASTX
 NCBI GI g121472
 BLAST score 226
 E value 1.0e-18
 Match length 110
 % identity 40
 NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
 (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
 >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
 maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
 [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea
 mays] >gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 298654
 Seq. ID LIB3151-024-Q1-K1-H2
 Method BLASTX
 NCBI GI g462195
 BLAST score 145
 E value 3.0e-09
 Match length 39
 % identity 74
 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
 >gi_100682_pir_S21636 GOS2 protein - rice
 >gi_20238_emb_CAA36190_(X51910) GOS2 [Oryza sativa]
 >gi_3789950_(AF094774) translation initiation factor [Oryza
 sativa]

Seq. No. 298655
 Seq. ID LIB3151-024-Q1-K1-H6
 Method BLASTX
 NCBI GI g462195
 BLAST score 361
 E value 2.0e-34
 Match length 98
 % identity 74
 NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

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>gi_100682_pir_S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No. 298656
Seq. ID LIB3151-025-Q1-K1-A10
Method BLASTX
NCBI GI g629861
BLAST score 478
E value 4.0e-48
Match length 133
% identity 75
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298657
Seq. ID LIB3151-025-Q1-K1-B9
Method BLASTX
NCBI GI g22216
BLAST score 222
E value 4.0e-18
Match length 88
% identity 60
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 298658
Seq. ID LIB3151-025-Q1-K1-C11
Method BLASTX
NCBI GI g141615
BLAST score 164
E value 3.0e-13
Match length 85
% identity 58
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
>gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 298659
Seq. ID LIB3151-025-Q1-K1-C12
Method BLASTN
NCBI GI g168652
BLAST score 87
E value 3.0e-41
Match length 267
% identity 88
NCBI Description Maize amyloplast-specific transit protein (waxy; wx+ locus), complete cds

Seq. No. 298660
Seq. ID LIB3151-025-Q1-K1-D11
Method BLASTX
NCBI GI g419803
BLAST score 146
E value 2.0e-16
Match length 102
% identity 51
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea

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Seq. No. 298661
Seq. ID LIB3151-025-Q1-K1-E11
Method BLASTX
NCBI GI g629861
BLAST score 379
E value 2.0e-36
Match length 138
% identity 59
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298662
Seq. ID LIB3151-025-Q1-K1-F11
Method BLASTX
NCBI GI g595775
BLAST score 156
E value 2.0e-10
Match length 85
% identity 48
NCBI Description (U13869) lacZ alpha peptide [Cloning vector]

Seq. No. 298663
Seq. ID LIB3151-025-Q1-K1-G10
Method BLASTX
NCBI GI g168703
BLAST score 157
E value 6.0e-11
Match length 58
% identity 57
NCBI Description (M86591) 22 kDa zein protein [Zea mays]

Seq. No. 298664
Seq. ID LIB3151-026-Q1-K1-A6
Method BLASTN
NCBI GI g168681
BLAST score 111
E value 1.0e-55
Match length 319
% identity 84
NCBI Description Maize 19 kDa zein mRNA, clone cz19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 298665
Seq. ID LIB3151-026-Q1-K1-B10
Method BLASTX
NCBI GI g100925
BLAST score 142
E value 4.0e-09
Match length 57
% identity 49
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_
(X58197) 27kDa storage protein, zein [Zea mays]

Seq. No. 298666
Seq. ID LIB3151-026-Q1-K1-C5

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Method BLASTX
NCBI GI g121472
BLAST score 416
E value 7.0e-41
Match length 124
% identity 60
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298667
Seq. ID LIB3151-026-Q1-K1-D2
Method BLASTX
NCBI GI g2832243
BLAST score 278
E value 7.0e-25
Match length 84
% identity 76
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298668
Seq. ID LIB3151-026-Q1-K1-E9
Method BLASTX
NCBI GI g141612
BLAST score 420
E value 3.0e-41
Match length 120
% identity 74
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)
>gi_72306_pir_ZIZMC2 22K zein precursor (clone cZ22C2) -
maize (fragment) >gi_168688 (M12141) 22 kDa zein protein
[Zea mays]

Seq. No. 298669
Seq. ID LIB3151-027-Q1-K1-B3
Method BLASTX
NCBI GI g141609
BLAST score 173
E value 2.0e-12
Match length 114
% identity 38
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi_100944_pir_S15656
zein, 19K - maize >gi_22448_emb_CAA41543_(X58700) 19 kDa
zein [Zea mays]

Seq. No. 298670
Seq. ID LIB3151-027-Q1-K1-B8
Method BLASTN
NCBI GI g168681
BLAST score 126
E value 2.0e-64
Match length 282
% identity 86
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.

>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 298671
Seq. ID LIB3151-027-Q1-K1-C8
Method BLASTN
NCBI GI g1037129
BLAST score 201
E value 1.0e-109
Match length 377
% identity 88
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298672
Seq. ID LIB3151-027-Q1-K1-D6
Method BLASTX
NCBI GI g4490333
BLAST score 154
E value 3.0e-10
Match length 95
% identity 40
NCBI Description (AL035656) EF-Hand containing protein-like [Arabidopsis thaliana]

Seq. No. 298673
Seq. ID LIB3151-027-Q1-K1-D8
Method BLASTX
NCBI GI g4314378
BLAST score 247
E value 5.0e-21
Match length 134
% identity 34
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 298674
Seq. ID LIB3151-027-Q1-K1-E1
Method BLASTX
NCBI GI g2832247
BLAST score 394
E value 3.0e-38
Match length 105
% identity 79
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 298675
Seq. ID LIB3151-027-Q1-K1-E7
Method BLASTN
NCBI GI g1037129
BLAST score 110
E value 4.0e-55
Match length 233
% identity 88
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298676
Seq. ID LIB3151-027-Q1-K1-F3

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Method	BLASTN
NCBI GI	g22549
BLAST score	56
E value	1.0e-22
Match length	262
% identity	84
NCBI Description	Maize gene for a 27kDa storage protein, zein
Seq. No.	298677
Seq. ID	LIB3151-027-Q1-K1-F6
Method	BLASTX
NCBI GI	g629861
BLAST score	178
E value	3.0e-20
Match length	99
% identity	64
NCBI Description	zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203) zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.	298678
Seq. ID	LIB3151-027-Q1-K1-F9
Method	BLASTX
NCBI GI	g629861
BLAST score	257
E value	2.0e-22
Match length	87
% identity	63
NCBI Description	zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203) zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.	298679
Seq. ID	LIB3151-027-Q1-K1-G4
Method	BLASTX
NCBI GI	g141617
BLAST score	295
E value	1.0e-26
Match length	74
% identity	77
NCBI Description	ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) >gi_100941_pir_S12140 zein Zc1 - maize >gi_100945_pir_B29017 zein 2 - maize >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays] >gi_168666_(M16460) 16-kDa zein protein [Zea mays]
Seq. No.	298680
Seq. ID	LIB3151-027-Q1-K1-G6
Method	BLASTX
NCBI GI	g141598
BLAST score	150
E value	2.0e-13
Match length	123
% identity	39
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99) >gi_72313_pir_ZIZM99 19K zein precursor (clone ZG99) - maize >gi_22519_emb_CAA24717_ (V01470) zein [Zea mays] >gi_22534_emb_CAA24726_ (V01479) zein [Zea mays]

Seq. No. 298681
Seq. ID LIB3151-027-Q1-K1-H1
Method BLASTX
NCBI GI g141617
BLAST score 318
E value 2.0e-29
Match length 65
% identity 91
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298682
Seq. ID LIB3151-028-Q1-K1-C12
Method BLASTX
NCBI GI g1663724
BLAST score 271
E value 6.0e-24
Match length 103
% identity 53
NCBI Description (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No. 298683
Seq. ID LIB3151-028-Q1-K1-F9
Method BLASTX
NCBI GI g508545
BLAST score 239
E value 4.0e-20
Match length 91
% identity 58
NCBI Description (L34340) zein [Zea mays]

Seq. No. 298684
Seq. ID LIB3151-028-Q1-K1-G10
Method BLASTX
NCBI GI g141597
BLAST score 187
E value 2.0e-14
Match length 69
% identity 57
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 298685
Seq. ID LIB3151-029-Q1-K1-A7
Method BLASTX
NCBI GI g121472
BLAST score 218
E value 4.0e-18
Match length 52
% identity 81
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298686
Seq. ID LIB3151-029-Q1-K1-A8
Method BLASTX
NCBI GI g168695
BLAST score 169
E value 2.0e-12
Match length 67
% identity 58
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
zein gamma [Zea mays]

Seq. No. 298687
Seq. ID LIB3151-029-Q1-K1-B11
Method BLASTX
NCBI GI g1184774
BLAST score 407
E value 6.0e-40
Match length 96
% identity 81
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC3 [Zea mays]

Seq. No. 298688
Seq. ID LIB3151-029-Q1-K1-B3
Method BLASTX
NCBI GI g168701
BLAST score 348
E value 5.0e-33
Match length 94
% identity 79
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298689
Seq. ID LIB3151-029-Q1-K1-B6
Method BLASTX
NCBI GI g224513
BLAST score 317
E value 3.0e-29
Match length 101
% identity 67
NCBI Description zein M6 [Zea mays]

Seq. No. 298690
Seq. ID LIB3151-029-Q1-K1-B7
Method BLASTN
NCBI GI g22537
BLAST score 114
E value 3.0e-57
Match length 313
% identity 85
NCBI Description Maize mRNA for zein polypeptide (clone M6)

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Seq. No. 298691
Seq. ID LIB3151-029-Q1-K1-B8
Method BLASTX
NCBI GI g2832247
BLAST score 165
E value 2.0e-20
Match length 116
% identity 54
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 298692
Seq. ID LIB3151-029-Q1-K1-C11
Method BLASTN
NCBI GI g22149
BLAST score 56
E value 9.0e-23
Match length 96
% identity 90
NCBI Description Z.mays mRNA for alpha-tubulin

Seq. No. 298693
Seq. ID LIB3151-029-Q1-K1-C6
Method BLASTX
NCBI GI g141608
BLAST score 176
E value 6.0e-24
Match length 80
% identity 75
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 298694
Seq. ID LIB3151-029-Q1-K1-D10
Method BLASTX
NCBI GI g224513
BLAST score 305
E value 8.0e-28
Match length 111
% identity 65
NCBI Description zein M6 [Zea mays]

Seq. No. 298695
Seq. ID LIB3151-029-Q1-K1-D11
Method BLASTN
NCBI GI g1037129
BLAST score 251
E value 1.0e-139
Match length 371
% identity 92
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298696
Seq. ID LIB3151-029-Q1-K1-D12
Method BLASTX
NCBI GI g100925

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BLAST score	227
E value	6.0e-19
Match length	86
% identity	47
NCBI Description	zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_(X58197) 27kDa storage protein, zein [Zea mays]
Seq. No.	298697
Seq. ID	LIB3151-029-Q1-K1-D3
Method	BLASTX
NCBI GI	g419803
BLAST score	415
E value	1.0e-40
Match length	144
% identity	60
NCBI Description	zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
Seq. No.	298698
Seq. ID	LIB3151-029-Q1-K1-D8
Method	BLASTX
NCBI GI	g121472
BLAST score	324
E value	5.0e-30
Match length	101
% identity	59
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea mays] >gi_168485_(M16066) glutelin-2 [Zea mays]
Seq. No.	298699
Seq. ID	LIB3151-029-Q1-K1-E10
Method	BLASTX
NCBI GI	g22220
BLAST score	149
E value	1.0e-09
Match length	63
% identity	54
NCBI Description	(X55723) 22 kd zein [Zea mays]
Seq. No.	298700
Seq. ID	LIB3151-029-Q1-K1-E11
Method	BLASTX
NCBI GI	g168691
BLAST score	202
E value	5.0e-16
Match length	61
% identity	69
NCBI Description	(M29628) zein [Zea mays]
Seq. No.	298701
Seq. ID	LIB3151-029-Q1-K1-E3
Method	BLASTX
NCBI GI	g16073

BLAST score 158
E value 7.0e-11
Match length 54
% identity 72
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298702
Seq. ID LIB3151-029-Q1-K1-F1
Method BLASTX
NCBI GI g168701
BLAST score 217
E value 1.0e-17
Match length 79
% identity 62
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298703
Seq. ID LIB3151-029-Q1-K1-F6
Method BLASTX
NCBI GI g468515
BLAST score 152
E value 1.0e-11
Match length 58
% identity 72
NCBI Description (X55726) zein [Zea mays]

Seq. No. 298704
Seq. ID LIB3151-029-Q1-K1-F8
Method BLASTX
NCBI GI g121472
BLAST score 174
E value 7.0e-15
Match length 77
% identity 56
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298705
Seq. ID LIB3151-029-Q1-K1-G1
Method BLASTX
NCBI GI g121472
BLAST score 329
E value 1.0e-30
Match length 127
% identity 53
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298706

CODES FOR CLONE

Seq. ID	LIB3151-029-Q1-K1-G9
Method	BLASTX
NCBI GI	g141608
BLAST score	289
E value	4.0e-26
Match length	81
% identity	74
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa zein [Zea mays]
Seq. No.	298707
Seq. ID	LIB3151-029-Q1-K1-H8
Method	BLASTN
NCBI GI	g168484
BLAST score	86
E value	1.0e-40
Match length	238
% identity	84
NCBI Description	Maize endosperm glutelin-2 gene, complete cds
Seq. No.	298708
Seq. ID	LIB3151-030-Q1-K1-A11
Method	BLASTX
NCBI GI	g141603
BLAST score	336
E value	1.0e-31
Match length	98
% identity	79
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20) >gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
Seq. No.	298709
Seq. ID	LIB3151-030-Q1-K1-B11
Method	BLASTX
NCBI GI	g141605
BLAST score	282
E value	2.0e-25
Match length	85
% identity	73
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) >gi_72312_pir_ZIZM92 19K zein precursor (clone CZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.	298710
Seq. ID	LIB3151-030-Q1-K1-C12
Method	BLASTX
NCBI GI	g100938
BLAST score	261
E value	1.0e-22
Match length	104
% identity	54
NCBI Description	zein precursor - maize >gi_22442_emb_CAA32513_ (X14335) zein precursor (AA -21 to 90) [Zea mays]
Seq. No.	298711

D E C E P T I O N S - H A R D C O D E

Seq. ID	LIB3151-030-Q1-K1-D11
Method	BLASTX
NCBI GI	g629861
BLAST score	273
E value	3.0e-24
Match length	72
% identity	74
NCBI Description	zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203) zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.	298712
Seq. ID	LIB3151-030-Q1-K1-D12
Method	BLASTX
NCBI GI	g16073
BLAST score	371
E value	1.0e-35
Match length	112
% identity	66
NCBI Description	(X59526) zein protein [Acetabularia mediterranea]
Seq. No.	298713
Seq. ID	LIB3151-030-Q1-K1-E10
Method	BLASTX
NCBI GI	g16073
BLAST score	205
E value	3.0e-16
Match length	104
% identity	51
NCBI Description	(X59526) zein protein [Acetabularia mediterranea]
Seq. No.	298714
Seq. ID	LIB3151-030-Q1-K1-E12
Method	BLASTX
NCBI GI	g141608
BLAST score	147
E value	4.0e-21
Match length	99
% identity	57
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa zein [Zea mays]
Seq. No.	298715
Seq. ID	LIB3151-030-Q1-K1-E9
Method	BLASTX
NCBI GI	g168691
BLAST score	402
E value	3.0e-39
Match length	123
% identity	68
NCBI Description	(M29628) zein [Zea mays]
Seq. No.	298716
Seq. ID	LIB3151-030-Q1-K1-F10
Method	BLASTN
NCBI GI	g168690
BLAST score	74

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E value	1.0e-33
Match length	242
% identity	83
NCBI Description	Maize zein mRNA, complete cds, clone ZG124
Seq. No.	298717
Seq. ID	LIB3151-030-Q1-K1-H11
Method	BLASTN
NCBI GI	g1037129
BLAST score	95
E value	3.0e-46
Match length	200
% identity	92
NCBI Description	(gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]
Seq. No.	298718
Seq. ID	LIB3151-031-Q1-K1-B7
Method	BLASTN
NCBI GI	g168685
BLAST score	191
E value	1.0e-103
Match length	327
% identity	91
NCBI Description	Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA
Seq. No.	298719
Seq. ID	LIB3151-031-Q1-K1-D1
Method	BLASTX
NCBI GI	g141605
BLAST score	554
E value	5.0e-57
Match length	135
% identity	85
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) >gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.	298720
Seq. ID	LIB3151-031-Q1-K1-D4
Method	BLASTX
NCBI GI	g121472
BLAST score	232
E value	2.0e-19
Match length	71
% identity	61
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]
Seq. No.	298721
Seq. ID	LIB3151-031-Q1-K1-D5
Method	BLASTX
NCBI GI	g2832243

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BLAST score	252
E value	1.0e-21
Match length	95
% identity	59
NCBI Description	(AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.	298722
Seq. ID	LIB3151-031-Q1-K1-E5
Method	BLASTX
NCBI GI	g141600
BLAST score	226
E value	2.0e-38
Match length	138
% identity	67
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1) >gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) - maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]
Seq. No.	298723
Seq. ID	LIB3151-031-Q1-K1-F7
Method	BLASTX
NCBI GI	g168699
BLAST score	158
E value	1.0e-10
Match length	55
% identity	67
NCBI Description	(M60836) zein [Zea mays]
Seq. No.	298724
Seq. ID	LIB3151-031-Q1-K1-F9
Method	BLASTN
NCBI GI	g22549
BLAST score	257
E value	1.0e-142
Match length	257
% identity	53
NCBI Description	Maize gene for a 27kDa storage protein, zein
Seq. No.	298725
Seq. ID	LIB3151-031-Q1-K1-H11
Method	BLASTN
NCBI GI	g22549
BLAST score	150
E value	5.0e-79
Match length	174
% identity	97
NCBI Description	Maize gene for a 27kDa storage protein, zein
Seq. No.	298726
Seq. ID	LIB3151-033-Q1-K1-A2
Method	BLASTX
NCBI GI	g141605
BLAST score	202
E value	6.0e-16
Match length	97
% identity	59
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)

>gi_72312_pir_ZIZM92 19K zein precursor (clone cz19C2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298727
Seq. ID LIB3151-033-Q1-K1-A3
Method BLASTN
NCBI GI g4582786
BLAST score 94
E value 1.0e-45
Match length 178
% identity 88
NCBI Description Zea mays mRNA for adenosine kinase, putative

Seq. No. 298728
Seq. ID LIB3151-033-Q1-K1-A4
Method BLASTN
NCBI GI g2832242
BLAST score 268
E value 1.0e-149
Match length 460
% identity 14
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 298729
Seq. ID LIB3151-033-Q1-K1-B1
Method BLASTX
NCBI GI g22216
BLAST score 322
E value 8.0e-30
Match length 101
% identity 67
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 298730
Seq. ID LIB3151-033-Q1-K1-B2
Method BLASTX
NCBI GI g2832243
BLAST score 344
E value 2.0e-32
Match length 102
% identity 73
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298731
Seq. ID LIB3151-033-Q1-K1-B3
Method BLASTX
NCBI GI g2832243
BLAST score 237
E value 2.0e-23
Match length 78
% identity 77
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298732
Seq. ID LIB3151-033-Q1-K1-B7
Method BLASTX
NCBI GI g141614

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BLAST score	160
E value	3.0e-11
Match length	61
% identity	61
NCBI Description	ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1) >gi_82662_pir_B22831 22K zein precursor (clone M1) - maize >gi_22527_emb_CAA24722 (V01475) reading frame zein [Zea mays] >gi_224510_prf_I107201D zein M1 [Zea mays]
Seq. No.	298733
Seq. ID	LIB3151-033-Q1-K1-C2
Method	BLASTN
NCBI GI	g2832242
BLAST score	95
E value	2.0e-46
Match length	163
% identity	19
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	298734
Seq. ID	LIB3151-033-Q1-K1-C5
Method	BLASTX
NCBI GI	g141605
BLAST score	386
E value	2.0e-37
Match length	94
% identity	83
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) >gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.	298735
Seq. ID	LIB3151-033-Q1-K1-E1
Method	BLASTX
NCBI GI	g168697
BLAST score	150
E value	8.0e-10
Match length	44
% identity	77
NCBI Description	(M60835) zein [Zea mays]
Seq. No.	298736
Seq. ID	LIB3151-033-Q1-K1-F5
Method	BLASTN
NCBI GI	g22549
BLAST score	70
E value	2.0e-31
Match length	130
% identity	88
NCBI Description	Maize gene for a 27kDa storage protein, zein
Seq. No.	298737
Seq. ID	LIB3151-034-Q1-K1-C12
Method	BLASTX
NCBI GI	g141617
BLAST score	287
E value	4.0e-26

Match length 85
% identity 66
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
>gi_168666_(M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298738
Seq. ID LIB3151-035-Q1-K1-B12
Method BLASTX
NCBI GI g100940
BLAST score 211
E value 5.0e-17
Match length 79
% identity 62
NCBI Description zein zA1 - maize

Seq. No. 298739
Seq. ID LIB3151-035-Q1-K1-B5
Method BLASTX
NCBI GI g168664
BLAST score 144
E value 2.0e-14
Match length 101
% identity 50
NCBI Description (M13507) zein protein precursor [Zea mays]

Seq. No. 298740
Seq. ID LIB3151-035-Q1-K1-C10
Method BLASTX
NCBI GI g100925
BLAST score 175
E value 1.0e-12
Match length 65
% identity 52
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_(X58197) 27kDa storage protein, zein [Zea mays]

Seq. No. 298741
Seq. ID LIB3151-035-Q1-K1-C7
Method BLASTX
NCBI GI g121472
BLAST score 217
E value 2.0e-17
Match length 127
% identity 41
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize
>gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor [Zea mays]
>gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea mays]
>gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 298742
Seq. ID LIB3151-035-Q1-K1-E9
Method BLASTX

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NCBI GI	g141615
BLAST score	368
E value	2.0e-35
Match length	110
% identity	72
NCBI Description	ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3) >gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]
Seq. No.	298743
Seq. ID	LIB3151-035-Q1-K1-F12
Method	BLASTX
NCBI GI	g141605
BLAST score	277
E value	6.0e-25
Match length	69
% identity	83
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) >gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.	298744
Seq. ID	LIB3151-035-Q1-K1-F3
Method	BLASTX
NCBI GI	g3023275
BLAST score	393
E value	1.0e-46
Match length	135
% identity	67
NCBI Description	ALPHA-GLUCOSIDASE PRECURSOR (MALTASE) >gi_2130027_pir_S65057 alpha-glucosidase (EC 3.2.1.20) - barley >gi_944901 (U22450) alpha-glucosidase [Hordeum vulgare]
Seq. No.	298745
Seq. ID	LIB3151-035-Q1-K1-G4
Method	BLASTN
NCBI GI	g22447
BLAST score	62
E value	1.0e-26
Match length	169
% identity	85
NCBI Description	Zea mays ZMPMS2 gene for 19 kDa zein protein
Seq. No.	298746
Seq. ID	LIB3151-035-Q1-K1-G6
Method	BLASTX
NCBI GI	g141615
BLAST score	221
E value	3.0e-18
Match length	71
% identity	72
NCBI Description	ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3) >gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]
Seq. No.	298747
Seq. ID	LIB3151-035-Q1-K1-H1
Method	BLASTN

NCBI GI g22100
BLAST score 54
E value 1.0e-21
Match length 82
% identity 91
NCBI Description Z.mays 27kDa zein locus DNA

Seq. No. 298748
Seq. ID LIB3151-035-Q1-K1-H9
Method BLASTX
NCBI GI g224513
BLAST score 155
E value 1.0e-10
Match length 63
% identity 57
NCBI Description zein M6 [Zea mays]

Seq. No. 298749
Seq. ID LIB3151-037-Q1-K1-A11
Method BLASTX
NCBI GI g2832243
BLAST score 233
E value 2.0e-19
Match length 84
% identity 62
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298750
Seq. ID LIB3151-037-Q1-K1-A3
Method BLASTX
NCBI GI g419803
BLAST score 182
E value 5.0e-14
Match length 45
% identity 78
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298751
Seq. ID LIB3151-037-Q1-K1-A8
Method BLASTN
NCBI GI g22537
BLAST score 37
E value 1.0e-11
Match length 61
% identity 90
NCBI Description Maize mRNA for zein polypeptide (clone M6)

Seq. No. 298752
Seq. ID LIB3151-037-Q1-K1-B5
Method BLASTX
NCBI GI g141603
BLAST score 485
E value 6.0e-49
Match length 129
% identity 83
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)

NCBI-BLAST

>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 298753
Seq. ID LIB3151-037-Q1-K1-B8
Method BLASTX
NCBI GI g16073
BLAST score 340
E value 4.0e-32
Match length 101
% identity 74
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298754
Seq. ID LIB3151-037-Q1-K1-C6
Method BLASTX
NCBI GI g629861
BLAST score 296
E value 6.0e-37
Match length 130
% identity 65
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298755
Seq. ID LIB3151-037-Q1-K1-E6
Method BLASTX
NCBI GI g419803
BLAST score 160
E value 6.0e-11
Match length 87
% identity 37
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298756
Seq. ID LIB3151-037-Q1-K1-F4
Method BLASTX
NCBI GI g121472
BLAST score 176
E value 7.0e-13
Match length 86
% identity 44
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize
>gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays]
>gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays]
>gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298757
Seq. ID LIB3151-037-Q1-K1-F8
Method BLASTX
NCBI GI g482985
BLAST score 164
E value 9.0e-12
Match length 57

% identity 60
NCBI Description chitinase (EC 3.2.1.14) precursor - maize (fragment)

Seq. No. 298758
Seq. ID LIB3151-037-Q1-K1-G1
Method BLASTX
NCBI GI g141608
BLAST score 301
E value 4.0e-31
Match length 137
% identity 56
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 298759
Seq. ID LIB3151-037-Q1-K1-G12
Method BLASTX
NCBI GI g168701
BLAST score 269
E value 1.0e-23
Match length 76
% identity 76
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298760
Seq. ID LIB3151-037-Q1-K1-H8
Method BLASTX
NCBI GI g419803
BLAST score 273
E value 1.0e-24
Match length 64
% identity 84
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
mays]

Seq. No. 298761
Seq. ID LIB3151-038-Q1-K1-A4
Method BLASTX
NCBI GI g72307
BLAST score 334
E value 3.0e-31
Match length 109
% identity 67
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
(J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 298762
Seq. ID LIB3151-038-Q1-K1-B5
Method BLASTN
NCBI GI g1037129
BLAST score 114
E value 2.0e-57
Match length 326
% identity 84
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]

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Seq. No.	298763
Seq. ID	LIB3151-038-Q1-K1-E7
Method	BLASTN
NCBI GI	g168681
BLAST score	71
E value	1.0e-31
Match length	231
% identity	83
NCBI Description	Maize 19 kDa zein mRNA, clone cZ19D1, complete cds. >gi_270686_gb_I03333_Sequence 8 from Patent US
Seq. No.	298764
Seq. ID	LIB3151-038-Q1-K1-F1
Method	BLASTX
NCBI GI	g4510430
BLAST score	254
E value	8.0e-22
Match length	70
% identity	67
NCBI Description	(AC006929) unknown protein, 3' partial [Arabidopsis thaliana]
Seq. No.	298765
Seq. ID	LIB3151-038-Q1-K1-G2
Method	BLASTX
NCBI GI	g508545
BLAST score	413
E value	2.0e-40
Match length	99
% identity	81
NCBI Description	(L34340) zein [Zea mays]
Seq. No.	298766
Seq. ID	LIB3151-038-Q1-K1-G3
Method	BLASTN
NCBI GI	g168484
BLAST score	203
E value	1.0e-110
Match length	367
% identity	89
NCBI Description	Maize endosperm glutelin-2 gene, complete cds
Seq. No.	298767
Seq. ID	LIB3151-038-Q1-K1-H2
Method	BLASTX
NCBI GI	g2832243
BLAST score	431
E value	2.0e-42
Match length	128
% identity	73
NCBI Description	(AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.	298768
Seq. ID	LIB3151-039-Q1-K1-B8
Method	BLASTN
NCBI GI	g18053

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BLAST score 46
E value 7.0e-17
Match length 66
% identity 92
NCBI Description C.lacryma-jobi L. mRNA for gamma-coixin (22KDa)

Seq. No. 298769
Seq. ID LIB3151-039-Q1-K1-C3
Method BLASTN
NCBI GI g1037129
BLAST score 309
E value 1.0e-173
Match length 375
% identity 95
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298770
Seq. ID LIB3151-039-Q1-K1-D9
Method BLASTN
NCBI GI g168484
BLAST score 174
E value 3.0e-93
Match length 294
% identity 90
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298771
Seq. ID LIB3151-039-Q1-K1-E12
Method BLASTX
NCBI GI g584706
BLAST score 191
E value 7.0e-15
Match length 38
% identity 100
NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
>gi_2130066_pir_JC5124 aspartate transaminase (EC
2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_
(D14673) aspartate aminotransferase [Oryza sátilva]

Seq. No. 298772
Seq. ID LIB3151-039-Q1-K1-E7
Method BLASTX
NCBI GI g141614
BLAST score 220
E value 5.0e-18
Match length 96
% identity 52
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
>gi_82662_pir_B22831 22K zein precursor (clone M1) - maize
>gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea mays] >gi_224510_prf_1107201D zein M1 [Zea mays]

Seq. No. 298773
Seq. ID LIB3151-039-Q1-K1-F6
Method BLASTX
NCBI GI g141597

BLAST score 249
E value 2.0e-24
Match length 103
% identity 66
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 298774
Seq. ID LIB3151-039-Q1-K1-F9
Method BLASTX
NCBI GI g141600
BLAST score 161
E value 3.0e-11
Match length 51
% identity 69
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) - maize
>gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 298775
Seq. ID LIB3151-039-Q1-K1-G2
Method BLASTX
NCBI GI g2827712
BLAST score 206
E value 3.0e-16
Match length 82
% identity 51
NCBI Description (AL021684) endoxylglucan tranferase-like protein
[Arabidopsis thaliana]

Seq. No. 298776
Seq. ID LIB3151-039-Q1-K1-G9
Method BLASTX
NCBI GI g141603
BLAST score 200
E value 1.0e-20
Match length 103
% identity 56
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 298777
Seq. ID LIB3151-039-Q1-K1-H4
Method BLASTN
NCBI GI g168679
BLAST score 57
E value 1.0e-23
Match length 120
% identity 88
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
>gi_270687_gb_I03334_ Sequence 9 from Patent US

Seq. No. 298778
Seq. ID LIB3151-039-Q1-K1-H7

Method BLASTN
NCBI GI g3057119
BLAST score 111
E value 9.0e-56
Match length 175
% identity 91
NCBI Description Zea mays starch synthase DULL1 (dull1) mRNA, complete cds

Seq. No. 298779
Seq. ID LIB3151-039-Q1-K1-H9
Method BLASTN
NCBI GI g22549
BLAST score 241
E value 1.0e-133
Match length 279
% identity 97
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298780
Seq. ID LIB3151-040-Q1-K1-B4
Method BLASTN
NCBI GI g168685
BLAST score 63
E value 6.0e-27
Match length 119
% identity 88
NCBI Description Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA

Seq. No. 298781
Seq. ID LIB3151-040-Q1-K1-D2
Method BLASTX
NCBI GI g419803
BLAST score 151
E value 2.0e-10
Match length 51
% identity 67
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298782
Seq. ID LIB3151-040-Q1-K1-E6
Method BLASTX
NCBI GI g2832243
BLAST score 209
E value 3.0e-17
Match length 58
% identity 78
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298783
Seq. ID LIB3151-040-Q1-K1-F7
Method BLASTX
NCBI GI g419803
BLAST score 362
E value 1.0e-34
Match length 115
% identity 66

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NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 298784
Seq. ID LIB3151-040-Q1-K1-G7
Method BLASTN
NCBI GI g168484
BLAST score 38
E value 6.0e-12
Match length 86
% identity 86
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298785
Seq. ID LIB3151-040-Q1-K1-H3
Method BLASTN
NCBI GI g2832242
BLAST score 57
E value 2.0e-23
Match length 127
% identity 10
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 298786
Seq. ID LIB3151-040-Q1-K1-H9
Method BLASTX
NCBI GI g121472
BLAST score 168
E value 7.0e-12
Match length 97
% identity 41
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298787
Seq. ID LIB3151-041-Q1-K1-A3
Method BLASTX
NCBI GI g2655029
BLAST score 636
E value 8.0e-67
Match length 113
% identity 100
NCBI Description (AF019296) starch synthase isoform zSTSII-1 [Zea mays]

Seq. No. 298788
Seq. ID LIB3151-041-Q1-K1-A8
Method BLASTN
NCBI GI g22215
BLAST score 46
E value 8.0e-17
Match length 54
% identity 96
NCBI Description Z.mays ZSF4C1 gene for zein

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Seq. No.	298789
Seq. ID	LIB3151-041-Q1-K1-C3
Method	BLASTX
NCBI GI	g508545
BLAST score	175
E value	9.0e-13
Match length	66
% identity	55
NCBI Description	(L34340) zein [Zea mays]
Seq. No.	298790
Seq. ID	LIB3151-041-Q1-K1-D5
Method	BLASTX
NCBI GI	g100925
BLAST score	168
E value	7.0e-12
Match length	42
% identity	64
NCBI Description	zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_(X58197) 27kDa storage protein, zein [Zea mays]
Seq. No.	298791
Seq. ID	LIB3151-041-Q1-K1-E1
Method	BLASTN
NCBI GI	g625147
BLAST score	97
E value	3.0e-47
Match length	345
% identity	83
NCBI Description	Zea mays protein disulfide isomerase (pdi) mRNA, complete cds
Seq. No.	298792
Seq. ID	LIB3151-041-Q1-K1-E3
Method	BLASTX
NCBI GI	g121472
BLAST score	151
E value	2.0e-10
Match length	55
% identity	53
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea mays] >gi_168485_(M16066) glutelin-2 [Zea mays]
Seq. No.	298793
Seq. ID	LIB3151-041-Q1-K1-F12
Method	BLASTN
NCBI GI	g168484
BLAST score	273
E value	1.0e-152
Match length	377
% identity	94
NCBI Description	Maize endosperm glutelin-2 gene, complete cds

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Seq. No. 298794
Seq. ID LIB3151-041-Q1-K1-F9
Method BLASTX
NCBI GI g141615
BLAST score 173
E value 1.0e-12
Match length 83
% identity 49
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
>gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 298795
Seq. ID LIB3151-041-Q1-K1-G5
Method BLASTX
NCBI GI g141603
BLAST score 436
E value 3.0e-43
Match length 119
% identity 77
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2_19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 298796
Seq. ID LIB3151-041-Q1-K1-H6
Method BLASTX
NCBI GI g508545
BLAST score 205
E value 3.0e-16
Match length 87
% identity 52
NCBI Description (L34340) zein [Zea mays]

Seq. No. 298797
Seq. ID LIB3151-042-Q1-K1-C9
Method BLASTX
NCBI GI g3426039
BLAST score 513
E value 3.0e-52
Match length 126
% identity 71
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 298798
Seq. ID LIB3151-042-Q1-K1-E7
Method BLASTX
NCBI GI g141608
BLAST score 170
E value 4.0e-12
Match length 47
% identity 72
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 298799

Seq. ID LIB3151-042-Q1-K1-G11
Method BLASTN
NCBI GI g168665
BLAST score 88
E value 4.0e-42
Match length 95
% identity 98
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298800
Seq. ID LIB3151-043-Q1-K1-B11
Method BLASTX
NCBI GI g100925
BLAST score 168
E value 4.0e-12
Match length 51
% identity 63
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb CAA41175_ (X58197) 27kDa storage protein, zein [Zea mays]

Seq. No. 298801
Seq. ID LIB3151-043-Q1-K1-B4
Method BLASTN
NCBI GI g168679
BLAST score 59
E value 1.0e-24
Match length 186
% identity 85
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C2, complete cds. >gi_270687_gb_I03334_Sequence 9 from Patent US

Seq. No. 298802
Seq. ID LIB3151-043-Q1-K1-B8
Method BLASTX
NCBI GI g1707924
BLAST score 141
E value 3.0e-09
Match length 55
% identity 56
NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 1 PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) (SHRUNKEN-2) >gi_1947182 (M81603) shrunken-2 [Zea mays] >gi_444329_prf_1906378A ADP glucose pyrophosphorylase [Zea mays]

Seq. No. 298803
Seq. ID LIB3151-043-Q1-K1-D2
Method BLASTX
NCBI GI g419803
BLAST score 216
E value 1.0e-17
Match length 89
% identity 52
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

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Seq. No. 298804
Seq. ID LIB3151-043-Q1-K1-D4
Method BLASTX
NCBI GI g584706
BLAST score 222
E value 3.0e-18
Match length 87
% identity 54
NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
>gi_2130066_pir_JC5124 aspartate transaminase (EC
2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_
(D14673) aspartate aminotransferase [Oryza sativa]

Seq. No. 298805
Seq. ID LIB3151-043-Q1-K1-E1
Method BLASTX
NCBI GI g141617
BLAST score 393
E value 3.0e-38
Match length 109
% identity 66
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298806
Seq. ID LIB3151-043-Q1-K1-E4
Method BLASTN
NCBI GI g168484
BLAST score 34
E value 6.0e-10
Match length 90
% identity 84
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298807
Seq. ID LIB3151-043-Q1-K1-E6
Method BLASTN
NCBI GI g22516
BLAST score 109
E value 2.0e-54
Match length 164
% identity 93
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298808
Seq. ID LIB3151-043-Q1-K1-E8
Method BLASTX
NCBI GI g141597
BLAST score 245
E value 6.0e-21
Match length 66
% identity 76
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize

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>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No.	298809
Seq. ID	LIB3151-044-Q1-K1-A4
Method	BLASTX
NCBI GI	g141610
BLAST score	217
E value	4.0e-18
Match length	55
% identity	82
NCBI Description	ZEIN-ALPHA PRECURSOR (CLONE Z4)
Seq. No.	298810
Seq. ID	LIB3151-044-Q1-K1-A5
Method	BLASTN
NCBI GI	g1037129
BLAST score	40
E value	1.0e-13
Match length	117
% identity	82
NCBI Description	(gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]
Seq. No.	298811
Seq. ID	LIB3151-044-Q1-K1-B3
Method	BLASTN
NCBI GI	g829147
BLAST score	111
E value	1.0e-55
Match length	167
% identity	92
NCBI Description	Z.mays gene for cyclophilin
Seq. No.	298812
Seq. ID	LIB3151-044-Q1-K1-B6
Method	BLASTX
NCBI GI	g141597
BLAST score	275
E value	9.0e-25
Match length	81
% identity	70
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2] [Zea mays]
Seq. No.	298813
Seq. ID	LIB3151-044-Q1-K1-C2
Method	BLASTN
NCBI GI	g168681
BLAST score	139
E value	2.0e-72
Match length	249
% identity	90
NCBI Description	Maize 19 kDa zein mRNA, clone cz19D1, complete cds. >gi_270686_gb_I03333_ Sequence 8 from Patent US

Seq. No. 298814
Seq. ID LIB3151-044-Q1-K1-C3
Method BLASTX
NCBI GI g100939
BLAST score 215
E value 2.0e-17
Match length 67
% identity 69
NCBI Description zein precursor - maize

Seq. No. 298815
Seq. ID LIB3151-044-Q1-K1-C9
Method BLASTX
NCBI GI g141608
BLAST score 179
E value 2.0e-22
Match length 131
% identity 55
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 298816
Seq. ID LIB3151-044-Q1-K1-D3
Method BLASTX
NCBI GI g419803
BLAST score 301
E value 2.0e-27
Match length 110
% identity 63
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
mays]

Seq. No. 298817
Seq. ID LIB3151-044-Q1-K1-F2
Method BLASTX
NCBI GI g141608
BLAST score 306
E value 4.0e-28
Match length 102
% identity 66
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 298818
Seq. ID LIB3151-044-Q1-K1-G2
Method BLASTX
NCBI GI g141600
BLAST score 181
E value 1.0e-13
Match length 49
% identity 82
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) -
maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

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Seq. No.	298819
Seq. ID	LIB3151-044-Q1-K1-G4
Method	BLASTX
NCBI GI	g22216
BLAST score	163
E value	8.0e-12
Match length	46
% identity	78
NCBI Description	(X55722) 22kD zein [Zea mays]
Seq. No.	298820
Seq. ID	LIB3151-045-Q1-K1-A8
Method	BLASTX
NCBI GI	g141607
BLAST score	290
E value	4.0e-26
Match length	114
% identity	58
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1) >gi_22521_emb_CAA24718_(V01471) zein [Zea mays] >gi_168672 (J01244) zein 19 kd protein (partial) [Zea mays]
Seq. No.	298821
Seq. ID	LIB3151-045-Q1-K1-B2
Method	BLASTN
NCBI GI	g168704
BLAST score	76
E value	1.0e-34
Match length	208
% identity	92
NCBI Description	Zea mays zein protein gene, complete cds
Seq. No.	298822
Seq. ID	LIB3151-045-Q1-K1-C11
Method	BLASTX
NCBI GI	g2642163
BLAST score	345
E value	1.0e-32
Match length	93
% identity	67
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No.	298823
Seq. ID	LIB3151-045-Q1-K1-C3
Method	BLASTX
NCBI GI	g168699
BLAST score	244
E value	8.0e-21
Match length	72
% identity	71
NCBI Description	(M60836) zein [Zea mays]
Seq. No.	298824
Seq. ID	LIB3151-045-Q1-K1-C4
Method	BLASTX
NCBI GI	g82660

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BLAST score 216
E value 1.0e-17
Match length 100
% identity 53
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 298825
Seq. ID LIB3151-045-Q1-K1-C5
Method BLASTX
NCBI GI g72307
BLAST score 163
E value 3.0e-11
Match length 75
% identity 52
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
(J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 298826
Seq. ID LIB3151-045-Q1-K1-D8
Method BLASTX
NCBI GI g114974
BLAST score 165
E value 2.0e-11
Match length 52
% identity 60
NCBI Description NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR
>gi_67491_pir_GLJY31 beta-glucosidase (EC 3.2.1.21)
precursor (clone TRE361) - white clover
>gi_21955_emb_CAA40058.1_ (X56734) beta-glucosidase
[Trifolium repens]

Seq. No. 298827
Seq. ID LIB3151-045-Q1-K1-F2
Method BLASTX
NCBI GI g224508
BLAST score 214
E value 1.0e-17
Match length 57
% identity 87
NCBI Description zein A20 [Zea mays]

Seq. No. 298828
Seq. ID LIB3151-045-Q1-K1-G6
Method BLASTX
NCBI GI g1705678
BLAST score 321
E value 8.0e-30
Match length 78
% identity 83
NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
valosin-containing protein [Glycine max]

Seq. No. 298829
Seq. ID LIB3151-045-Q1-K1-H6
Method BLASTX

NCBI GI g2058311
BLAST score 231
E value 2.0e-19
Match length 62
% identity 73
NCBI Description (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii]

Seq. No. 298830
Seq. ID LIB3151-046-Q1-K1-C4
Method BLASTX
NCBI GI g3786009
BLAST score 438
E value 2.0e-43
Match length 132
% identity 69
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 298831
Seq. ID LIB3151-046-Q1-K1-D5
Method BLASTX
NCBI GI g1182065
BLAST score 165
E value 5.0e-21
Match length 87
% identity 72
NCBI Description (X55661) 22 kD zein [Zea mays]

Seq. No. 298832
Seq. ID LIB3151-046-Q1-K1-F1
Method BLASTX
NCBI GI g2668744
BLAST score 478
E value 3.0e-48
Match length 92
% identity 97
NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No. 298833
Seq. ID LIB3151-046-Q1-K1-F4
Method BLASTN
NCBI GI g168681
BLAST score 73
E value 3.0e-33
Match length 160
% identity 86
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 298834
Seq. ID LIB3151-046-Q1-K1-G1
Method BLASTX
NCBI GI g141617
BLAST score 337
E value 1.0e-31
Match length 100
% identity 67
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)

>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298835
Seq. ID LIB3151-046-Q1-K1-G11
Method BLASTX
NCBI GI g224514
BLAST score 310
E value 2.0e-28
Match length 62
% identity 98
NCBI Description zein M8 [Zea mays]

Seq. No. 298836
Seq. ID LIB3151-046-Q1-K1-G7
Method BLASTX
NCBI GI g100925
BLAST score 185
E value 4.0e-14
Match length 72
% identity 44
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_ (X58197) 27kDa storage protein, zein [Zea mays]

Seq. No. 298837
Seq. ID LIB3151-046-Q1-K1-H11
Method BLASTX
NCBI GI g141608
BLAST score 178
E value 2.0e-13
Match length 63
% identity 63
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa zein [Zea mays]

Seq. No. 298838
Seq. ID LIB3151-047-P1-K1-D1
Method BLASTN
NCBI GI g168696
BLAST score 60
E value 3.0e-25
Match length 92
% identity 91
NCBI Description Z.mays zein mRNA, 3' end

Seq. No. 298839
Seq. ID LIB3151-047-P1-K1-D4
Method BLASTN
NCBI GI g22549
BLAST score 197
E value 1.0e-107
Match length 337
% identity 90
NCBI Description Maize gene for a 27kDa storage protein, zein

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Seq. No. 298840
Seq. ID LIB3151-047-P1-K1-D6
Method BLASTX
NCBI GI g141597
BLAST score 488
E value 2.0e-50
Match length 142
% identity 77
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 298841
Seq. ID LIB3151-047-P1-K1-F2
Method BLASTN
NCBI GI g168690
BLAST score 77
E value 3.0e-35
Match length 173
% identity 87
NCBI Description Maize zein mRNA, complete cds, clone ZG124

Seq. No. 298842
Seq. ID LIB3151-047-P1-K1-F6
Method BLASTN
NCBI GI g22537
BLAST score 81
E value 9.0e-38
Match length 117
% identity 58
NCBI Description Maize mRNA for zein polypeptide (clone M6)

Seq. No. 298843
Seq. ID LIB3151-047-P1-K1-G12
Method BLASTX
NCBI GI g141609
BLAST score 195
E value 5.0e-15
Match length 112
% identity 46
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi_100944_pir_S15656
zein, 19K - maize >gi_22448_emb_CAA41543_ (X58700) 19 kDa
zein [Zea mays]

Seq. No. 298844
Seq. ID LIB3151-047-P1-K1-H10
Method BLASTX
NCBI GI g16073
BLAST score 293
E value 1.0e-26
Match length 104
% identity 64
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298845

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Seq. ID	LIB3151-048-P1-K1-A1
Method	BLASTX
NCBI GI	g2832247
BLAST score	274
E value	2.0e-24
Match length	101
% identity	61
NCBI Description	(AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.	298846
Seq. ID	LIB3151-048-P1-K1-A12
Method	BLASTN
NCBI GI	g22516
BLAST score	150
E value	8.0e-79
Match length	298
% identity	88
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.	298847
Seq. ID	LIB3151-048-P1-K1-B7
Method	BLASTN
NCBI GI	g22516
BLAST score	92
E value	2.0e-44
Match length	168
% identity	90
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.	298848
Seq. ID	LIB3151-048-P1-K1-B9
Method	BLASTN
NCBI GI	g168573
BLAST score	93
E value	5.0e-45
Match length	183
% identity	93
NCBI Description	Zea mays tryptophan synthase beta-subunit (TSB2) mRNA, complete cds
Seq. No.	298849
Seq. ID	LIB3151-048-P1-K1-C6
Method	BLASTX
NCBI GI	g100940
BLAST score	166
E value	1.0e-11
Match length	74
% identity	49
NCBI Description	zein zA1 - maize
Seq. No.	298850
Seq. ID	LIB3151-048-P1-K1-C7
Method	BLASTX
NCBI GI	g2832243
BLAST score	183
E value	7.0e-14
Match length	54

% identity 72
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298851
Seq. ID LIB3151-048-P1-K1-D5
Method BLASTN
NCBI GI g22516
BLAST score 133
E value 1.0e-68
Match length 303
% identity 89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298852
Seq. ID LIB3151-048-P1-K1-E11
Method BLASTN
NCBI GI g168484
BLAST score 135
E value 6.0e-70
Match length 159
% identity 96
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298853
Seq. ID LIB3151-048-P1-K1-F11
Method BLASTX
NCBI GI g141605
BLAST score 224
E value 2.0e-18
Match length 95
% identity 55
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298854
Seq. ID LIB3151-048-P1-K1-F8
Method BLASTX
NCBI GI g629861
BLAST score 178
E value 4.0e-13
Match length 97
% identity 47
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298855
Seq. ID LIB3151-048-P1-K1-F9
Method BLASTN
NCBI GI g22447
BLAST score 61
E value 5.0e-26
Match length 93
% identity 91
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein

Seq. No. 298856

Seq. ID LIB3151-048-P1-K1-G11
Method BLASTN
NCBI GI g168652
BLAST score 66
E value 3.0e-29
Match length 118
% identity 89
NCBI Description Maize amyloplast-specific transit protein (waxy; wx+ locus), complete cds

Seq. No. 298857
Seq. ID LIB3151-048-P1-K1-G5
Method BLASTN
NCBI GI g168484
BLAST score 76
E value 6.0e-35
Match length 148
% identity 88
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298858
Seq. ID LIB3151-048-P1-K1-G7
Method BLASTX
NCBI GI g16073
BLAST score 233
E value 2.0e-19
Match length 112
% identity 49
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298859
Seq. ID LIB3151-048-P1-K1-G9
Method BLASTX
NCBI GI g72307
BLAST score 185
E value 2.0e-28
Match length 87
% identity 86
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686 (J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 298860
Seq. ID LIB3151-048-P1-K1-H10
Method BLASTN
NCBI GI g168484
BLAST score 260
E value 1.0e-144
Match length 363
% identity 93
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298861
Seq. ID LIB3151-048-P1-K1-H12
Method BLASTX
NCBI GI g168701
BLAST score 427
E value 3.0e-42

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Match length 99
% identity 89
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298862
Seq. ID LIB3151-049-P1-K1-A1
Method BLASTN
NCBI GI g22537
BLAST score 89
E value 1.0e-42
Match length 157
% identity 89
NCBI Description Maize mRNA for zein polypeptide (clone M6)

Seq. No. 298863
Seq. ID LIB3151-049-P1-K1-A10
Method BLASTN
NCBI GI g168673
BLAST score 39
E value 1.0e-12
Match length 91
% identity 86
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 298864
Seq. ID LIB3151-049-P1-K1-A12
Method BLASTN
NCBI GI g168665
BLAST score 203
E value 1.0e-110
Match length 267
% identity 94
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298865
Seq. ID LIB3151-049-P1-K1-A3
Method BLASTX
NCBI GI g168701
BLAST score 252
E value 1.0e-21
Match length 111
% identity 50
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298866
Seq. ID LIB3151-049-P1-K1-A7
Method BLASTX
NCBI GI g224508
BLAST score 167
E value 8.0e-12
Match length 55
% identity 69
NCBI Description zein A20 [Zea mays]

Seq. No. 298867
Seq. ID LIB3151-049-P1-K1-B10
Method BLASTX

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NCBI GI	g168699
BLAST score	144
E value	4.0e-11
Match length	76
% identity	63
NCBI Description	(M60836) zein [Zea mays]
Seq. No.	298868
Seq. ID	LIB3151-049-P1-K1-B2
Method	BLASTX
NCBI GI	g141608
BLAST score	150
E value	2.0e-18
Match length	65
% identity	86
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa zein [Zea mays]
Seq. No.	298869
Seq. ID	LIB3151-049-P1-K1-B5
Method	BLASTN
NCBI GI	g22514
BLAST score	37
E value	5.0e-12
Match length	45
% identity	96
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.	298870
Seq. ID	LIB3151-049-P1-K1-C4
Method	BLASTN
NCBI GI	g168484
BLAST score	321
E value	0.0e+00
Match length	392
% identity	95
NCBI Description	Maize endosperm glutelin-2 gene, complete cds
Seq. No.	298871
Seq. ID	LIB3151-049-P1-K1-D12
Method	BLASTX
NCBI GI	g141605
BLAST score	360
E value	4.0e-36
Match length	123
% identity	73
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) >gi_72312_pir_ZIZM92 19K zein precursor (clone cz19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.	298872
Seq. ID	LIB3151-049-P1-K1-D8
Method	BLASTX
NCBI GI	g3851003
BLAST score	369
E value	2.0e-35

Match length 81
% identity 94
NCBI Description (AF069910) pyruvate dehydrogenase E1 beta subunit isoform 3
[Zea mays]

Seq. No. 298873
Seq. ID LIB3151-049-P1-K1-E3
Method BLASTN
NCBI GI g22549
BLAST score 100
E value 6.0e-49
Match length 120
% identity 96
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298874
Seq. ID LIB3151-049-P1-K1-E7
Method BLASTN
NCBI GI g168652
BLAST score 103
E value 7.0e-51
Match length 167
% identity 91
NCBI Description Maize amyloplast-specific transit protein (waxy; wx+ locus), complete cds

Seq. No. 298875
Seq. ID LIB3151-049-P1-K1-F1
Method BLASTX
NCBI GI g585338
BLAST score 247
E value 6.0e-24
Match length 85
% identity 74
NCBI Description ADENYLYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
>gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza sativa]

Seq. No. 298876
Seq. ID LIB3151-049-P1-K1-F6
Method BLASTN
NCBI GI g168665
BLAST score 164
E value 2.0e-87
Match length 196
% identity 96
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 298877
Seq. ID LIB3151-049-P1-K1-F9
Method BLASTX
NCBI GI g629861
BLAST score 242
E value 9.0e-21
Match length 84
% identity 68
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)

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zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298878
Seq. ID LIB3151-049-P1-K1-G2
Method BLASTN
NCBI GI g22544
BLAST score 69
E value 2.0e-30
Match length 69
% identity 100
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 298879
Seq. ID LIB3151-049-P1-K1-H7
Method BLASTX
NCBI GI g121472
BLAST score 223
E value 2.0e-18
Match length 101
% identity 45
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 298880
Seq. ID LIB3151-049-P1-K1-H8
Method BLASTX
NCBI GI g629861
BLAST score 166
E value 3.0e-12
Match length 78
% identity 63
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298881
Seq. ID LIB3151-050-P1-K1-C10
Method BLASTN
NCBI GI g168484
BLAST score 38
E value 3.0e-12
Match length 98
% identity 85
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298882
Seq. ID LIB3151-050-P1-K1-C11
Method BLASTX
NCBI GI g141601
BLAST score 187
E value 4.0e-14
Match length 106
% identity 45
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)

>gi_82657_pir_S03417 19K zein precursor (clone gZ19AB11) -
maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA
1 - 234) [Zea mays]

Seq. No. 298883
Seq. ID LIB3151-050-P1-K1-C12
Method BLASTN
NCBI GI g168484
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298884
Seq. ID LIB3151-050-P1-K1-C3
Method BLASTX
NCBI GI g141608
BLAST score 248
E value 2.0e-21
Match length 93
% identity 59
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 298885
Seq. ID LIB3151-050-P1-K1-C9
Method BLASTN
NCBI GI g168484
BLAST score 219
E value 1.0e-120
Match length 278
% identity 95
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298886
Seq. ID LIB3151-050-P1-K1-D1
Method BLASTX
NCBI GI g266398
BLAST score 189
E value 7.0e-15
Match length 56
% identity 62
NCBI Description TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
INHIBITOR) (CHFI) >gi_68849_pir_TIZM1 trypsin/factor XIIa
inhibitor precursor - maize >gi_22327_emb_CAA37998_
(X54064) corn Hageman factor inhibitor [Zea mays]

Seq. No. 298887
Seq. ID LIB3151-050-P1-K1-D10
Method BLASTN
NCBI GI g22549
BLAST score 115
E value 4.0e-58
Match length 131
% identity 97

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NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298888
Seq. ID LIB3151-050-P1-K1-D8
Method BLASTX
NCBI GI g22216
BLAST score 144
E value 2.0e-14
Match length 99
% identity 53
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 298889
Seq. ID LIB3151-050-P1-K1-E3
Method BLASTN
NCBI GI g22516
BLAST score 308
E value 1.0e-173
Match length 381
% identity 95
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298890
Seq. ID LIB3151-050-P1-K1-E5
Method BLASTN
NCBI GI g1037129
BLAST score 58
E value 3.0e-24
Match length 78
% identity 95
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298891
Seq. ID LIB3151-050-P1-K1-F10
Method BLASTX
NCBI GI g2832243
BLAST score 277
E value 1.0e-24
Match length 105
% identity 58
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298892
Seq. ID LIB3151-050-P1-K1-G12
Method BLASTN
NCBI GI g168673
BLAST score 119
E value 1.0e-60
Match length 143
% identity 97
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 298893
Seq. ID LIB3151-050-P1-K1-H5
Method BLASTN
NCBI GI g168652

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BLAST score 107
E value 4.0e-53
Match length 207
% identity 88
NCBI Description Maize amyloplast-specific transit protein (waxy; wx+ locus), complete cds

Seq. No. 298894
Seq. ID LIB3151-050-P1-K1-H6
Method BLASTX
NCBI GI g100675
BLAST score 239
E value 2.0e-20
Match length 59
% identity 78
NCBI Description glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) precursor - rice >gi_169759 (J04960) ADP-glucose pyrophosphorylase 51kD subunit (EC 2.7.7.27) [Oryza sativa]

Seq. No. 298895
Seq. ID LIB3151-052-Q1-K1-A2
Method BLASTN
NCBI GI g1037129
BLAST score 151
E value 1.0e-79
Match length 158
% identity 99
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298896
Seq. ID LIB3151-052-Q1-K1-A5
Method BLASTN
NCBI GI g168484
BLAST score 190
E value 1.0e-102
Match length 222
% identity 96
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298897
Seq. ID LIB3151-052-Q1-K1-A8
Method BLASTN
NCBI GI g4140643
BLAST score 118
E value 9.0e-60
Match length 138
% identity 24
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 298898
Seq. ID LIB3151-052-Q1-K1-B6
Method BLASTN
NCBI GI g2832242
BLAST score 91
E value 1.0e-43

Match length 98
% identity 10
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 298899
Seq. ID LIB3151-052-Q1-K1-B7
Method BLASTN
NCBI GI g168675
BLAST score 89
E value 2.0e-42
Match length 139
% identity 94
NCBI Description Maize mutant zein (zE19) gene, complete cds

Seq. No. 298900
Seq. ID LIB3151-052-Q1-K1-C2
Method BLASTX
NCBI GI g16073
BLAST score 339
E value 7.0e-32
Match length 92
% identity 79
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298901
Seq. ID LIB3151-052-Q1-K1-C9
Method BLASTX
NCBI GI g4185308
BLAST score 286
E value 2.0e-35
Match length 91
% identity 93
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]

Seq. No. 298902
Seq. ID LIB3151-052-Q1-K1-E5
Method BLASTN
NCBI GI g3747049
BLAST score 58
E value 5.0e-24
Match length 124
% identity 89
NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds

Seq. No. 298903
Seq. ID LIB3151-052-Q1-K1-E8
Method BLASTN
NCBI GI g168484
BLAST score 96
E value 9.0e-47
Match length 124
% identity 97
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298904
Seq. ID LIB3151-052-Q1-K1-F1
Method BLASTN

NCBI GI g22542
BLAST score 109
E value 2.0e-54
Match length 182
% identity 91
NCBI Description Maize gene for Mr 19000 alpha zein and 5'-flanking region

Seq. No. 298905
Seq. ID LIB3151-052-Q1-K1-F5
Method BLASTN
NCBI GI g22549
BLAST score 160
E value 6.0e-85
Match length 181
% identity 63
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298906
Seq. ID LIB3151-052-Q1-K1-G7
Method BLASTN
NCBI GI g340933
BLAST score 104
E value 8.0e-52
Match length 139
% identity 94
NCBI Description Zea mays 10-kDa zein gene, complete cds

Seq. No. 298907
Seq. ID LIB3151-054-Q1-K1-A12
Method BLASTN
NCBI GI g22549
BLAST score 61
E value 9.0e-26
Match length 292
% identity 80
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 298908
Seq. ID LIB3151-054-Q1-K1-A2
Method BLASTX
NCBI GI g16073
BLAST score 203
E value 4.0e-16
Match length 63
% identity 68
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298909
Seq. ID LIB3151-054-Q1-K1-A5
Method BLASTX
NCBI GI g141603
BLAST score 372
E value 9.0e-36
Match length 86
% identity 91
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize

>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 298910
Seq. ID LIB3151-054-Q1-K1-A8
Method BLASTX
NCBI GI g141603
BLAST score 448
E value 1.0e-44
Match length 107
% identity 92
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 298911
Seq. ID LIB3151-054-Q1-K1-B11
Method BLASTN
NCBI GI g22544
BLAST score 124
E value 2.0e-63
Match length 272
% identity 87
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 298912
Seq. ID LIB3151-054-Q1-K1-B8
Method BLASTX
NCBI GI g2832243
BLAST score 365
E value 5.0e-35
Match length 106
% identity 71
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298913
Seq. ID LIB3151-054-Q1-K1-B9
Method BLASTN
NCBI GI g22516
BLAST score 86
E value 1.0e-40
Match length 210
% identity 85
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298914
Seq. ID LIB3151-054-Q1-K1-C10
Method BLASTX
NCBI GI g16073
BLAST score 286
E value 1.0e-25
Match length 108
% identity 60
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298915
Seq. ID LIB3151-054-Q1-K1-C2
Method BLASTX

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NCBI GI	g2130089
BLAST score	218
E value	8.0e-18
Match length	78
% identity	59
NCBI Description	2-oxoglutarate/malate translocator (clone OMT103), mitochondrial membrane - proso millet >gi_1100743_dbj_BAA08105 (D45075) 2-oxoglutarate/malate translocator [Panicum miliaceum]
Seq. No.	298916
Seq. ID	LIB3151-054-Q1-K1-C9
Method	BLASTN
NCBI GI	g22516
BLAST score	285
E value	1.0e-159
Match length	369
% identity	95
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.	298917
Seq. ID	LIB3151-054-Q1-K1-D11
Method	BLASTX
NCBI GI	g4033424
BLAST score	362
E value	1.0e-34
Match length	84
% identity	89
NCBI Description	SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic pyrophosphatase [Zea mays]
Seq. No.	298918
Seq. ID	LIB3151-054-Q1-K1-D9
Method	BLASTX
NCBI GI	g541546
BLAST score	248
E value	3.0e-21
Match length	101
% identity	13
NCBI Description	ubiquitin precursor - Volvox carteri >gi_395295_emb_CAA52290_ (X74214) polyubiquitin [Volvox carteri]
Seq. No.	298919
Seq. ID	LIB3151-054-Q1-K1-E11
Method	BLASTX
NCBI GI	g141601
BLAST score	385
E value	2.0e-37
Match length	120
% identity	68
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11) >gi_82657_pir_S03417 19K zein precursor (clone gZ19AB11) - maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA 1 - 234) [Zea mays]

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Seq. No.	298920
Seq. ID	LIB3151-054-Q1-K1-E5
Method	BLASTN
NCBI GI	g984524
BLAST score	75
E value	3.0e-34
Match length	250
% identity	86
NCBI Description	Zea mays high-methionine zein DZS18 (dzs18) gene, complete cds
Seq. No.	298921
Seq. ID	LIB3151-054-Q1-K1-E8
Method	BLASTX
NCBI GI	g141603
BLAST score	285
E value	1.0e-25
Match length	103
% identity	66
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20) >gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
Seq. No.	298922
Seq. ID	LIB3151-054-Q1-K1-E9
Method	BLASTX
NCBI GI	g141608
BLAST score	208
E value	3.0e-25
Match length	104
% identity	67
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa zein [Zea mays]
Seq. No.	298923
Seq. ID	LIB3151-054-Q1-K1-G10
Method	BLASTX
NCBI GI	g22220
BLAST score	234
E value	1.0e-19
Match length	91
% identity	56
NCBI Description	(X55723) 22 kD zein [Zea mays]
Seq. No.	298924
Seq. ID	LIB3151-054-Q1-K1-G5
Method	BLASTX
NCBI GI	g82660
BLAST score	304
E value	7.0e-28
Match length	80
% identity	78
NCBI Description	19K zein precursor (clone ZG31A) - maize (fragment) >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
Seq. No.	298925

Sorghum

Seq. ID	LIB3151-054-Q1-K1-G8
Method	BLASTX
NCBI GI	g2735840
BLAST score	318
E value	2.0e-29
Match length	116
% identity	57
NCBI Description	(AF010283) ADP-glucose pyrophosphorylase subunit SH2 [Sorghum bicolor]
Seq. No.	298926
Seq. ID	LIB3151-054-Q1-K1-H10
Method	BLASTX
NCBI GI	g419803
BLAST score	247
E value	4.0e-21
Match length	112
% identity	46
NCBI Description	zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
Seq. No.	298927
Seq. ID	LIB3151-054-Q1-K1-H12
Method	BLASTX
NCBI GI	g22220
BLAST score	280
E value	4.0e-25
Match length	70
% identity	80
NCBI Description	(X55723) 22 kD zein [Zea mays]
Seq. No.	298928
Seq. ID	LIB3151-054-Q1-K1-H7
Method	BLASTX
NCBI GI	g2832246
BLAST score	468
E value	5.0e-47
Match length	120
% identity	82
NCBI Description	(AF031569) 22-kDa alpha zein 8 [Zea mays]
Seq. No.	298929
Seq. ID	LIB3151-054-Q1-K1-H8
Method	BLASTX
NCBI GI	g2832246
BLAST score	143
E value	2.0e-09
Match length	60
% identity	58
NCBI Description	(AF031569) 22-kDa alpha zein 8 [Zea mays]
Seq. No.	298930
Seq. ID	LIB3151-055-Q1-K1-C10
Method	BLASTN
NCBI GI	g22537
BLAST score	70
E value	5.0e-31

Match length 140
% identity 89
NCBI Description Maize mRNA for zein polypeptide (clone M6)

Seq. No. 298931
Seq. ID LIB3151-055-Q1-K1-D10
Method BLASTN
NCBI GI g22445
BLAST score 44
E value 8.0e-16
Match length 94
% identity 85
NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. No. 298932
Seq. ID LIB3151-055-Q1-K1-D9
Method BLASTX
NCBI GI g141608
BLAST score 265
E value 3.0e-23
Match length 63
% identity 86
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 298933
Seq. ID LIB3151-056-Q1-K1-C11
Method BLASTN
NCBI GI g168704
BLAST score 58
E value 4.0e-24
Match length 90
% identity 91
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 298934
Seq. ID LIB3151-057-Q1-K1-A1
Method BLASTX
NCBI GI g2832243
BLAST score 230
E value 4.0e-19
Match length 106
% identity 49
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298935
Seq. ID LIB3151-057-Q1-K1-A12
Method BLASTN
NCBI GI g22516
BLAST score 110
E value 5.0e-55
Match length 282
% identity 85
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298936

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Seq. ID	LIB3151-057-Q1-K1-A9
Method	BLASTN
NCBI GI	g168484
BLAST score	218
E value	1.0e-119
Match length	365
% identity	90
NCBI Description	Maize endosperm glutelin-2 gene, complete cds
Seq. No.	298937
Seq. ID	LIB3151-057-Q1-K1-B1
Method	BLASTX
NCBI GI	g121472
BLAST score	179
E value	3.0e-13
Match length	70
% identity	50
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb CAA37594 (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]
Seq. No.	298938
Seq. ID	LIB3151-057-Q1-K1-B5
Method	BLASTX
NCBI GI	g2832247
BLAST score	225
E value	1.0e-18
Match length	93
% identity	53
NCBI Description	(AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.	298939
Seq. ID	LIB3151-057-Q1-K1-C5
Method	BLASTN
NCBI GI	g218340
BLAST score	45
E value	2.0e-16
Match length	65
% identity	92
NCBI Description	Triticum aestivum mRNA for elongation factor 1 beta'
Seq. No.	298940
Seq. ID	LIB3151-057-Q1-K1-C9
Method	BLASTN
NCBI GI	g22514
BLAST score	227
E value	1.0e-125
Match length	343
% identity	92
NCBI Description	Maize Zcl gene for Zein Zcl (14 kD zein-2)
Seq. No.	298941
Seq. ID	LIB3151-057-Q1-K1-D11
Method	BLASTX

NCBI GI g168701
BLAST score 370
E value 2.0e-35
Match length 98
% identity 79
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298942
Seq. ID LIB3151-057-Q1-K1-D12
Method BLASTX
NCBI GI g168691
BLAST score 200
E value 7.0e-16
Match length 60
% identity 70
NCBI Description (M29628) zein [Zea mays]

Seq. No. 298943
Seq. ID LIB3151-057-Q1-K1-D9
Method BLASTN
NCBI GI g1184775
BLAST score 62
E value 1.0e-26
Match length 90
% identity 92
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4 (gpc4) mRNA, complete cds

Seq. No. 298944
Seq. ID LIB3151-057-Q1-K1-E11
Method BLASTX
NCBI GI g141608
BLAST score 271
E value 7.0e-24
Match length 114
% identity 55
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa zein [Zea mays]

Seq. No. 298945
Seq. ID LIB3151-057-Q1-K1-E3
Method BLASTX
NCBI GI g1542941
BLAST score 148
E value 9.0e-10
Match length 70
% identity 47
NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No. 298946
Seq. ID LIB3151-057-Q1-K1-F2
Method BLASTN
NCBI GI g1037129
BLAST score 258
E value 1.0e-143
Match length 304

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% identity 96
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298947
Seq. ID LIB3151-057-Q1-K1-F5
Method BLASTX
NCBI GI g2130065
BLAST score 146
E value 3.0e-09
Match length 90
% identity 42
NCBI Description alpha-globulin precursor - rice >gi_1783206_dbj_BAA09308_(D50643) 26 kDa globulin [Oryza sativa]

Seq. No. 298948
Seq. ID LIB3151-057-Q1-K1-G11
Method BLASTX
NCBI GI g168701
BLAST score 316
E value 3.0e-29
Match length 79
% identity 82
NCBI Description (M60837) zein [Zea mays]

Seq. No. 298949
Seq. ID LIB3151-057-Q1-K1-H11
Method BLASTN
NCBI GI g22516
BLAST score 155
E value 8.0e-82
Match length 279
% identity 89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 298950
Seq. ID LIB3151-057-Q1-K1-H12
Method BLASTN
NCBI GI g508544
BLAST score 43
E value 6.0e-15
Match length 162
% identity 81
NCBI Description Zea mays 24-kD alpha-zein gene (floury2), complete cds

Seq. No. 298951
Seq. ID LIB3151-058-Q1-K1-B11
Method BLASTX
NCBI GI g99688
BLAST score 317
E value 2.0e-29
Match length 72
% identity 88
NCBI Description translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_(X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No. 298952
Seq. ID LIB3151-058-Q1-K1-C11
Method BLASTX
NCBI GI g451193
BLAST score 143
E value 9.0e-20
Match length 87
% identity 63
NCBI Description (L28008) wali7 [Triticum aestivum]
>gi_1090845_prf_2019486B wali7 gene [Triticum aestivum]

Seq. No. 298953
Seq. ID LIB3151-058-Q1-K1-C2
Method BLASTX
NCBI GI g629861
BLAST score 226
E value 1.0e-18
Match length 100
% identity 51
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 298954
Seq. ID LIB3151-058-Q1-K1-C3
Method BLASTX
NCBI GI g3643607
BLAST score 317
E value 2.0e-29
Match length 113
% identity 58
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 298955
Seq. ID LIB3151-058-Q1-K1-D6
Method BLASTX
NCBI GI gi684855
BLAST score 422
E value 1.0e-41
Match length 85
% identity 21
NCBI Description (U77939) ubiquitin-like protein [Phaseolus vulgaris]

Seq. No. 298956
Seq. ID LIB3151-058-Q1-K1-E12
Method BLASTX
NCBI GI g141608
BLAST score 177
E value 5.0e-17
Match length 78
% identity 71
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 298957
Seq. ID LIB3151-058-Q1-K1-H4
Method BLASTN

NCBI GI g168675
BLAST score 59
E value 1.0e-24
Match length 79
% identity 94
NCBI Description Maize mutant zein (zE19) gene, complete cds

Seq. No. 298958
Seq. ID LIB3151-058-Q1-K1-H5
Method BLASTX
NCBI GI g2832243
BLAST score 242
E value 1.0e-20
Match length 98
% identity 56
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298959
Seq. ID LIB3151-058-Q1-K1-H9
Method BLASTX
NCBI GI g168691
BLAST score 186
E value 5.0e-14
Match length 96
% identity 46
NCBI Description (M29628) zein [Zea mays]

Seq. No. 298960
Seq. ID LIB3151-059-Q1-K1-A8
Method BLASTX
NCBI GI g141616
BLAST score 240
E value 2.0e-20
Match length 71
% identity 62
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 298961
Seq. ID LIB3151-059-Q1-K1-B1
Method BLASTN
NCBI GI g1037129
BLAST score 41
E value 6.0e-14
Match length 216
% identity 82
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298962
Seq. ID LIB3151-059-Q1-K1-B6
Method BLASTN
NCBI GI g168704
BLAST score 54
E value 5.0e-22
Match length 82
% identity 91

NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 298963
Seq. ID LIB3151-059-Q1-K1-B9
Method BLASTX
NCBI GI g2832243
BLAST score 192
E value 9.0e-15
Match length 105
% identity 47
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298964
Seq. ID LIB3151-059-Q1-K1-C2
Method BLASTN
NCBI GI g168425
BLAST score 37
E value 1.0e-11
Match length 61
% identity 90
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 298965
Seq. ID LIB3151-059-Q1-K1-C5
Method BLASTN
NCBI GI g168425
BLAST score 60
E value 1.0e-25
Match length 87
% identity 93
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 298966
Seq. ID LIB3151-059-Q1-K1-C9
Method BLASTN
NCBI GI g1037129
BLAST score 287
E value 1.0e-160
Match length 362
% identity 95
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 298967
Seq. ID LIB3151-059-Q1-K1-D3
Method BLASTX
NCBI GI g4539370
BLAST score 151
E value 3.0e-10
Match length 58
% identity 60
NCBI Description (AL049525) UDP-galactose 4-epimerase-like protein [Arabidopsis thaliana]

Seq. No. 298968
Seq. ID LIB3151-059-Q1-K1-D4
Method BLASTN

NCBI GI g22514
 BLAST score 140
 E value 4.0e-73
 Match length 195
 % identity 93
 NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 298969
 Seq. ID LIB3151-059-Q1-K1-D8
 Method BLASTX
 NCBI GI g141610
 BLAST score 198
 E value 2.0e-15
 Match length 98
 % identity 48
 NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)

Seq. No. 298970
 Seq. ID LIB3151-059-Q1-K1-E4
 Method BLASTN
 NCBI GI g2832242
 BLAST score 168
 E value 1.0e-89
 Match length 204
 % identity 10
 NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 298971
 Seq. ID LIB3151-059-Q1-K1-F3
 Method BLASTX
 NCBI GI g2832246
 BLAST score 229
 E value 5.0e-19
 Match length 107
 % identity 50
 NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 298972
 Seq. ID LIB3151-059-Q1-K1-F5
 Method BLASTN
 NCBI GI g2341060
 BLAST score 33
 E value 4.0e-09
 Match length 61
 % identity 89
 NCBI Description Zea mays translational initiation factor eIF-4A (tif-4A3)
 mRNA, complete cds

Seq. No. 298973
 Seq. ID LIB3151-059-Q1-K1-G9
 Method BLASTX
 NCBI GI g2996096
 BLAST score 140
 E value 4.0e-09
 Match length 31
 % identity 87
 NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1

alpha [Oryza sativa]

Seq. No. 298974
Seq. ID LIB3151-059-Q1-K1-H1
Method BLASTX
NCBI GI g100925
BLAST score 156
E value 1.0e-10
Match length 96
% identity 22
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_(X58197) 27kDa storage protein, zein [Zea mays]

Seq. No. 298975
Seq. ID LIB3151-059-Q1-K1-H2
Method BLASTX
NCBI GI g16073
BLAST score 153
E value 3.0e-10
Match length 53
% identity 62
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 298976
Seq. ID LIB3151-061-Q1-K1-A5
Method BLASTX
NCBI GI g141616
BLAST score 141
E value 8.0e-09
Match length 53
% identity 49
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 298977
Seq. ID LIB3151-061-Q1-K1-B10
Method BLASTX
NCBI GI g141603
BLAST score 434
E value 5.0e-43
Match length 120
% identity 79
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 298978
Seq. ID LIB3151-061-Q1-K1-B5
Method BLASTN
NCBI GI g22485
BLAST score 82
E value 1.0e-38
Match length 146
% identity 90
NCBI Description Maize mRNA for sucrose synthase (EC 2.4.1.13)

Seq. No. 298979

Seq. ID LIB3151-061-Q1-K1-C8
Method BLASTX
NCBI GI g141605
BLAST score 504
E value 4.0e-51
Match length 127
% identity 82
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 298980
Seq. ID LIB3151-061-Q1-K1-D4
Method BLASTX
NCBI GI g141616
BLAST score 142
E value 4.0e-09
Match length 28
% identity 89
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 298981
Seq. ID LIB3151-061-Q1-K1-D5
Method BLASTX
NCBI GI g2501354
BLAST score 206
E value 3.0e-16
Match length 44
% identity 84
NCBI Description TRANSKETOLASE 7 (TK) >gi_1084441_pir_S54301 transketolase
(EC 2.2.1.1) 7 - Craterostigma plantagineum
>gi_664903_emb_CAA86609_ (Z46648) transketolase
[Craterostigma plantagineum]

Seq. No. 298982
Seq. ID LIB3151-061-Q1-K1-D9
Method BLASTX
NCBI GI g168693
BLAST score 220
E value 7.0e-25
Match length 104
% identity 70
NCBI Description (M29627) zein [Zea mays]

Seq. No. 298983
Seq. ID LIB3151-061-Q1-K1-E8
Method BLASTX
NCBI GI g3021357
BLAST score 152
E value 6.0e-10
Match length 39
% identity 74
NCBI Description (AJ005082) UDP-galactose 4-epimerase [Cyamopsis
tetragonoloba]

Seq. No. 298984

Seq. ID LIB3151-061-Q1-K1-E9
Method BLASTX
NCBI GI g541816
BLAST score 196
E value 5.0e-23
Match length 56
% identity 90
NCBI Description protein kinase - common ice plant >gi_457689_emb_CAA82990_(Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No. 298985
Seq. ID LIB3151-061-Q1-K1-F10
Method BLASTX
NCBI GI g2282584
BLAST score 332
E value 5.0e-31
Match length 122
% identity 62
NCBI Description (U76259) elongation factor 1-alpha [Zea mays]

Seq. No. 298986
Seq. ID LIB3151-061-Q1-K1-G10
Method BLASTN
NCBI GI g168652
BLAST score 83
E value 5.0e-39
Match length 123
% identity 92
NCBI Description Maize amyloplast-specific transit protein (waxy; wx+ locus), complete cds

Seq. No. 298987
Seq. ID LIB3151-061-Q1-K1-H10
Method BLASTX
NCBI GI g2832243
BLAST score 220
E value 5.0e-18
Match length 66
% identity 76
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 298988
Seq. ID LIB3151-061-Q1-K1-H9
Method BLASTX
NCBI GI g141603
BLAST score 190
E value 1.0e-14
Match length 72
% identity 61
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2_19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 298989
Seq. ID LIB3151-062-Q1-K1-A2
Method BLASTN
NCBI GI g168704

BLAST score	63
E value	4.0e-27
Match length	115
% identity	89
NCBI Description	Zea mays zein protein gene, complete cds
 Seq. No.	298990
Seq. ID	LIB3151-062-Q1-K1-C11
Method	BLASTX
NCBI GI	g82660
BLAST score	221
E value	4.0e-18
Match length	61
% identity	74
NCBI Description	19K zein precursor (clone ZG31A) - maize (fragment) >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
 Seq. No.	298991
Seq. ID	LIB3151-062-Q1-K1-C9
Method	BLASTN
NCBI GI	g168704
BLAST score	56
E value	7.0e-23
Match length	107
% identity	89
NCBI Description	Zea mays zein protein gene, complete cds
 Seq. No.	298992
Seq. ID	LIB3151-062-Q1-K1-E10
Method	BLASTN
NCBI GI	g168665
BLAST score	198
E value	1.0e-107
Match length	279
% identity	92
NCBI Description	Maize 16-kDa zein-2 mRNA, complete cds
 Seq. No.	298993
Seq. ID	LIB3151-062-Q1-K1-F6
Method	BLASTX
NCBI GI	g1449179
BLAST score	214
E value	3.0e-17
Match length	94
% identity	51
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]
 Seq. No.	298994
Seq. ID	LIB3151-062-Q1-K1-G8
Method	BLASTX
NCBI GI	g141617
BLAST score	279
E value	7.0e-25
Match length	112
% identity	54
NCBI Description	ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)

>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 298995
Seq. ID LIB3152-001-Q1-K1-A3
Method BLASTN
NCBI GI g168484
BLAST score 168
E value 1.0e-89
Match length 264
% identity 91
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 298996
Seq. ID LIB3152-001-Q1-K1-B2
Method BLASTX
NCBI GI g4193320
BLAST score 324
E value 2.0e-30
Match length 77
% identity 78
NCBI Description (AF045473) histone deacetylase [Zea mays]

Seq. No. 298997
Seq. ID LIB3152-001-Q1-K1-C1
Method BLASTX
NCBI GI g141615
BLAST score 248
E value 2.0e-21
Match length 84
% identity 65
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
>gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 298998
Seq. ID LIB3152-001-Q1-K1-C12
Method BLASTX
NCBI GI g141602
BLAST score 343
E value 3.0e-32
Match length 120
% identity 62
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
>gi_82658_pir_A22831 19K zein precursor (clone M6) - maize
>gi_22538_emb_CAA26294_ (X02450) zein precursor [Zea mays]

Seq. No. 298999
Seq. ID LIB3152-001-Q1-K1-C2
Method BLASTX
NCBI GI g2832243
BLAST score 285
E value 2.0e-25
Match length 129
% identity 53
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 299000
Seq. ID LIB3152-001-Q1-K1-C3
Method BLASTX
NCBI GI g224508
BLAST score 330
E value 4.0e-31
Match length 88
% identity 81
NCBI Description zein A20 [Zea mays]

Seq. No. 299001
Seq. ID LIB3152-001-Q1-K1-C4
Method BLASTN
NCBI GI g168681
BLAST score 147
E value 4.0e-77
Match length 255
% identity 89
NCBI Description Maize 19 kDa zein mRNA, clone cz19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 299002
Seq. ID LIB3152-001-Q1-K1-D12
Method BLASTX
NCBI GI g100939
BLAST score 215
E value 1.0e-26
Match length 98
% identity 63
NCBI Description zein precursor - maize

Seq. No. 299003
Seq. ID LIB3152-001-Q1-K1-D3
Method BLASTX
NCBI GI g141608
BLAST score 155
E value 1.0e-10
Match length 63
% identity 62
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 299004
Seq. ID LIB3152-001-Q1-K1-E1
Method BLASTN
NCBI GI g22441
BLAST score 69
E value 1.0e-30
Match length 192
% identity 84
NCBI Description Maize pML2 gene for zein

Seq. No. 299005
Seq. ID LIB3152-001-Q1-K1-E3
Method BLASTN

NCBI GI g22514
BLAST score 150
E value 6.0e-79
Match length 257
% identity 91
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 299006
Seq. ID LIB3152-001-Q1-K1-E4
Method BLASTN
NCBI GI g2832242
BLAST score 69
E value 1.0e-30
Match length 158
% identity 10
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299007
Seq. ID LIB3152-001-Q1-K1-E8
Method BLASTX
NCBI GI g419803
BLAST score 229
E value 3.0e-19
Match length 69
% identity 70
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 299008
Seq. ID LIB3152-001-Q1-K1-F12
Method BLASTX
NCBI GI g2832246
BLAST score 186
E value 4.0e-14
Match length 84
% identity 46
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 299009
Seq. ID LIB3152-001-Q1-K1-H10
Method BLASTX
NCBI GI g168691
BLAST score 237
E value 5.0e-20
Match length 98
% identity 52
NCBI Description (M29628) zein [Zea mays]

Seq. No. 299010
Seq. ID LIB3152-001-Q1-K1-H6
Method BLASTX
NCBI GI g141603
BLAST score 258
E value 1.0e-22
Match length 75
% identity 76
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)

>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 299011
Seq. ID LIB3152-002-Q1-K1-B11
Method BLASTX
NCBI GI g224507
BLAST score 160
E value 5.0e-11
Match length 41
% identity 83
NCBI Description zein A1 [Zea mays]

Seq. No. 299012
Seq. ID LIB3152-002-Q1-K1-D10
Method BLASTX
NCBI GI g82660
BLAST score 189
E value 2.0e-14
Match length 54
% identity 70
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 299013
Seq. ID LIB3152-002-Q1-K1-E6
Method BLASTX
NCBI GI g2281089
BLAST score 292
E value 2.0e-26
Match length 63
% identity 87
NCBI Description (AC002333) Sm protein F isolog [Arabidopsis thaliana]

Seq. No. 299014
Seq. ID LIB3152-002-Q1-K1-F10
Method BLASTX
NCBI GI g2832243
BLAST score 201
E value 5.0e-16
Match length 70
% identity 63
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 299015
Seq. ID LIB3152-002-Q1-K1-F11
Method BLASTN
NCBI GI g2832242
BLAST score 86
E value 6.0e-41
Match length 186
% identity 10
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299016
Seq. ID LIB3152-002-Q1-K1-F3
Method BLASTX

NCBI GI g419803
BLAST score 361
E value 2.0e-34
Match length 116
% identity 66
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 299017
Seq. ID LIB3152-002-Q1-K1-G11
Method BLASTN
NCBI GI g168679
BLAST score 62
E value 1.0e-26
Match length 134
% identity 87
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
>gi_270687_gb_I03334_Sequence 9 from Patent US

Seq. No. 299018
Seq. ID LIB3152-002-Q1-K1-H3
Method BLASTX
NCBI GI g224509
BLAST score 243
E value 1.0e-20
Match length 105
% identity 54
NCBI Description zein E19 [Zea mays]

Seq. No. 299019
Seq. ID LIB3152-002-Q1-K1-H8
Method BLASTN
NCBI GI g22514
BLAST score 104
E value 1.0e-51
Match length 164
% identity 91
NCBI Description Maize Zcl gene for Zein Zcl (14 kD zein-2)

Seq. No. 299020
Seq. ID LIB3152-003-P1-K1-A9
Method BLASTX
NCBI GI g224508
BLAST score 174
E value 2.0e-12
Match length 67
% identity 55
NCBI Description zein A20 [Zea mays]

Seq. No. 299021
Seq. ID LIB3152-003-P1-K1-B11
Method BLASTX
NCBI GI g168691
BLAST score 239
E value 3.0e-20
Match length 107
% identity 54

NCBI Description (M29628) zein [Zea mays]

Seq. No. 299022
Seq. ID LIB3152-003-P1-K1-B9
Method BLASTX
NCBI GI g168699
BLAST score 183
E value 2.0e-18
Match length 81
% identity 72

NCBI Description (M60836) zein [Zea mays]

Seq. No. 299023
Seq. ID LIB3152-003-P1-K1-C4
Method BLASTX
NCBI GI g629861
BLAST score 281
E value 3.0e-25
Match length 107
% identity 61

NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 299024
Seq. ID LIB3152-003-P1-K1-C7
Method BLASTX
NCBI GI g141603
BLAST score 222
E value 3.0e-18
Match length 82
% identity 66

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 299025
Seq. ID LIB3152-003-P1-K1-E6
Method BLASTN
NCBI GI g168681
BLAST score 157
E value 4.0e-83
Match length 300
% identity 89

NCBI Description Maize 19 kDa zein mRNA, clone cz19D1, complete cds.
>gi_270686_gb_I03333_ Sequence 8 from Patent US

Seq. No. 299026
Seq. ID LIB3152-003-P1-K1-E8
Method BLASTX
NCBI GI g168699
BLAST score 269
E value 9.0e-24
Match length 75
% identity 75

NCBI Description (M60836) zein [Zea mays]

Seq. No. 299027

Seq. ID LIB3152-003-P1-K1-F12
Method BLASTN
NCBI GI g22537
BLAST score 48
E value 4.0e-18
Match length 84
% identity 90
NCBI Description Maize mRNA for zein polypeptide (clone M6)

Seq. No. 299028
Seq. ID LIB3152-003-P1-K1-F6
Method BLASTX
NCBI GI g224509
BLAST score 168
E value 9.0e-12
Match length 119
% identity 45
NCBI Description zein E19 [Zea mays]

Seq. No. 299029
Seq. ID LIB3152-003-P1-K1-F7
Method BLASTX
NCBI GI g629861
BLAST score 259
E value 9.0e-23
Match length 73
% identity 75
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 299030
Seq. ID LIB3152-003-P1-K1-G10
Method BLASTN
NCBI GI g22516
BLAST score 169
E value 3.0e-90
Match length 322
% identity 72
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 299031
Seq. ID LIB3152-003-P1-K1-G7
Method BLASTN
NCBI GI g22516
BLAST score 305
E value 1.0e-171
Match length 361
% identity 96
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 299032
Seq. ID LIB3152-003-P1-K1-H10
Method BLASTX
NCBI GI g141597
BLAST score 352
E value 1.0e-34
Match length 111

% identity 75
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 299033
Seq. ID LIB3152-003-P1-K1-H5
Method BLASTX
NCBI GI g141616
BLAST score 364
E value 9.0e-35
Match length 125
% identity 67
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 299034
Seq. ID LIB3152-005-P1-K1-A10
Method BLASTN
NCBI GI g22516
BLAST score 150
E value 6.0e-79
Match length 255
% identity 89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 299035
Seq. ID LIB3152-005-P1-K1-A2
Method BLASTX
NCBI GI g2827524
BLAST score 151
E value 6.0e-10
Match length 36
% identity 69
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 299036
Seq. ID LIB3152-005-P1-K1-A3
Method BLASTN
NCBI GI g168673
BLAST score 92
E value 4.0e-44
Match length 131
% identity 95
NCBI Description Maize 19 kDa zein mRNA, clone cz19B1, complete cds

Seq. No. 299037
Seq. ID LIB3152-005-P1-K1-A7
Method BLASTX
NCBI GI g602076
BLAST score 452
E value 3.0e-45
Match length 98
% identity 21
NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]

Seq. No. 299038
Seq. ID LIB3152-005-P1-K1-C10
Method BLASTX
NCBI GI g141617
BLAST score 249
E value 2.0e-21
Match length 89
% identity 60
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
>gi_168666_(M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299039
Seq. ID LIB3152-005-P1-K1-D11
Method BLASTX
NCBI GI g508545
BLAST score 147
E value 3.0e-15
Match length 91
% identity 59
NCBI Description (L34340) zein [Zea mays]

Seq. No. 299040
Seq. ID LIB3152-005-P1-K1-D3
Method BLASTX
NCBI GI g141617
BLAST score 512
E value 3.0e-52
Match length 128
% identity 74
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
>gi_168666_(M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299041
Seq. ID LIB3152-005-P1-K1-D4
Method BLASTX
NCBI GI g141606
BLAST score 188
E value 3.0e-14
Match length 95
% identity 49
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
>gi_72309_pir_ZIZMD1 19K zein precursor (clone cZ19D1) - maize
>gi_168682_(M12144) 19 kDa zein protein [Zea mays]

Seq. No. 299042
Seq. ID LIB3152-005-P1-K1-D8
Method BLASTX
NCBI GI g141617
BLAST score 320
E value 9.0e-30
Match length 82

% identity 72
 NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
 >gi_100941_pir_S12140 zein Zc1 - maize
 >gi_100945_pir_B29017 zein 2 - maize
 >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
 >gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299043
 Seq. ID LIB3152-005-P1-K1-D9
 Method BLASTX
 NCBI GI g508545
 BLAST score 168
 E value 5.0e-12
 Match length 38
 % identity 89
 NCBI Description (L34340) zein [Zea mays]

Seq. No. 299044
 Seq. ID LIB3152-005-P1-K1-E9
 Method BLASTX
 NCBI GI g72307
 BLAST score 330
 E value 8.0e-31
 Match length 107
 % identity 65
 NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
 (J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 299045
 Seq. ID LIB3152-005-P1-K1-F3
 Method BLASTN
 NCBI GI g168661
 BLAST score 107
 E value 4.0e-53
 Match length 206
 % identity 94
 NCBI Description Maize 15 kDa zein mRNA, clone cz15A3, complete cds

Seq. No. 299046
 Seq. ID LIB3152-005-P1-K1-F6
 Method BLASTX
 NCBI GI g141617
 BLAST score 246
 E value 5.0e-21
 Match length 109
 % identity 50
 NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
 >gi_100941_pir_S12140 zein Zc1 - maize
 >gi_100945_pir_B29017 zein 2 - maize
 >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
 >gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299047
 Seq. ID LIB3152-005-P1-K1-F7
 Method BLASTX
 NCBI GI g224514
 BLAST score 228

E value 2.0e-19
Match length 53
% identity 87
NCBI Description zein M8 [Zea mays]

Seq. No. 299048
Seq. ID LIB3152-005-P1-K1-G2
Method BLASTX
NCBI GI g141608
BLAST score 154
E value 2.0e-12
Match length 86
% identity 50
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 299049
Seq. ID LIB3152-006-P1-K1-B9
Method BLASTN
NCBI GI g168675
BLAST score 219
E value 1.0e-120
Match length 339
% identity 92
NCBI Description Maize mutant zein (zE19) gene, complete cds

Seq. No. 299050
Seq. ID LIB3152-006-P1-K1-D7
Method BLASTX
NCBI GI g135060
BLAST score 232
E value 2.0e-19
Match length 57
% identity 84
NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
(SHRUNKEN-1) >gi_66570_pir_YUZMS sucrose synthase (EC
2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose
synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382)
sucrose synthase [Zea mays]

Seq. No. 299051
Seq. ID LIB3152-006-P1-K1-E8
Method BLASTX
NCBI GI g508545
BLAST score 184
E value 5.0e-20
Match length 71
% identity 80
NCBI Description (L34340) zein [Zea mays]

Seq. No. 299052
Seq. ID LIB3152-006-P1-K1-F12
Method BLASTX
NCBI GI g2832246
BLAST score 207
E value 2.0e-16

Match length 42
% identity 98
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 299053
Seq. ID LIB3152-006-P1-K1-F8
Method BLASTN
NCBI GI g22514
BLAST score 38
E value 2.0e-12
Match length 98
% identity 85
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 299054
Seq. ID LIB3152-006-P1-K1-G5
Method BLASTN
NCBI GI g4185305
BLAST score 195
E value 1.0e-105
Match length 315
% identity 91
NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
(sz22-21) gene, complete cds; retrotransposon Opie-2 gag
protein, polyprotein, and copia protein genes, complete
cds; and unknown genes

Seq. No. 299055
Seq. ID LIB3152-006-P1-K1-H11
Method BLASTX
NCBI GI g2832243
BLAST score 234
E value 8.0e-20
Match length 58
% identity 86
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 299056
Seq. ID LIB3152-006-P1-K1-H12
Method BLASTX
NCBI GI g322870
BLAST score 144
E value 7.0e-21
Match length 57
% identity 93
NCBI Description glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
maize (fragment)

Seq. No. 299057
Seq. ID LIB3152-006-P1-K1-H5
Method BLASTN
NCBI GI g22514
BLAST score 80
E value 3.0e-37
Match length 204
% identity 85
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 299058
Seq. ID LIB3152-006-P1-K1-H7
Method BLASTN
NCBI GI g22516
BLAST score 67
E value 2.0e-29
Match length 115
% identity 90
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 299059
Seq. ID LIB3152-007-P1-K1-A3
Method BLASTN
NCBI GI g22549
BLAST score 268
E value 1.0e-149
Match length 396
% identity 71
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 299060
Seq. ID LIB3152-007-P1-K1-B10
Method BLASTX
NCBI GI g141616
BLAST score 154
E value 1.0e-10
Match length 48
% identity 60
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 299061
Seq. ID LIB3152-007-P1-K1-C2
Method BLASTX
NCBI GI g22216
BLAST score 195
E value 3.0e-15
Match length 61
% identity 66
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 299062
Seq. ID LIB3152-007-P1-K1-C4
Method BLASTX
NCBI GI g419803
BLAST score 230
E value 3.0e-19
Match length 83
% identity 54
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 299063
Seq. ID LIB3152-007-P1-K1-C5
Method BLASTN
NCBI GI g168484

BLAST score 213
E value 1.0e-116
Match length 277
% identity 94
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 299064
Seq. ID LIB3152-007-P1-K1-D12
Method BLASTN
NCBI GI g2832242
BLAST score 60
E value 3.0e-25
Match length 191
% identity 15
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299065
Seq. ID LIB3152-007-P1-K1-D4
Method BLASTX
NCBI GI g22216
BLAST score 266
E value 2.0e-23
Match length 105
% identity 55
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 299066
Seq. ID LIB3152-007-P1-K1-G1
Method BLASTX
NCBI GI g231654
BLAST score 250
E value 1.0e-21
Match length 94
% identity 59
NCBI Description BRITTLE-1 PROTEIN PRECURSOR >gi_82676_pir_JQ1459_Bt1
protein precursor - maize >gi_168426 (M79333) brittle-1
protein [Zea mays]

Seq. No. 299067
Seq. ID LIB3152-007-P1-K1-G3
Method BLASTN
NCBI GI g168698
BLAST score 132
E value 4.0e-68
Match length 174
% identity 94
NCBI Description Z.mays zein mRNA, complete cds

Seq. No. 299068
Seq. ID LIB3152-007-P1-K1-G6
Method BLASTX
NCBI GI g100940
BLAST score 209
E value 8.0e-17
Match length 65
% identity 71
NCBI Description zein zA1 - maize

Seq. No. 299069
Seq. ID LIB3152-007-P1-K1-H11
Method BLASTX
NCBI GI g16073
BLAST score 261
E value 9.0e-23
Match length 62
% identity 82
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 299070
Seq. ID LIB3152-008-P1-K1-A2
Method BLASTN
NCBI GI g168690
BLAST score 116
E value 1.0e-58
Match length 124
% identity 98
NCBI Description Maize zein mRNA, complete cds, clone ZG124

Seq. No. 299071
Seq. ID LIB3152-008-P1-K1-B10
Method BLASTX
NCBI GI g82660
BLAST score 169
E value 5.0e-12
Match length 75
% identity 59
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 299072
Seq. ID LIB3152-008-P1-K1-D3
Method BLASTN
NCBI GI g168692
BLAST score 120
E value 8.0e-61
Match length 206
% identity 64
NCBI Description Maize zein mRNA, complete cds, clone ZG7

Seq. No. 299073
Seq. ID LIB3152-008-P1-K1-E10
Method BLASTX
NCBI GI g2832243
BLAST score 226
E value 6.0e-19
Match length 68
% identity 72
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 299074
Seq. ID LIB3152-008-P1-K1-H10
Method BLASTX
NCBI GI g168701
BLAST score 245

E value 7.0e-21
 Match length 100
 % identity 57
 NCBI Description (M60837) zein [Zea mays]

Seq. No. 299075
 Seq. ID LIB3152-008-P1-K1-H2
 Method BLASTN
 NCBI GI g2832242
 BLAST score 228
 E value 1.0e-125
 Match length 343
 % identity 12
 NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299076
 Seq. ID LIB3152-008-P1-K1-H6
 Method BLASTX
 NCBI GI g4586107
 BLAST score 313
 E value 8.0e-29
 Match length 114
 % identity 16
 NCBI Description (AL049638) putative disease resistance protein [Arabidopsis thaliana]

Seq. No. 299077
 Seq. ID LIB3152-009-P1-K1-A7
 Method BLASTX
 NCBI GI g121472
 BLAST score 188
 E value 4.0e-14
 Match length 60
 % identity 63
 NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
 (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
 >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
 maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
 [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea mays] >gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 299078
 Seq. ID LIB3152-009-P1-K1-B8
 Method BLASTX
 NCBI GI g508545
 BLAST score 241
 E value 2.0e-20
 Match length 109
 % identity 50
 NCBI Description (L34340) zein [Zea mays]

Seq. No. 299079
 Seq. ID LIB3152-009-P1-K1-D12
 Method BLASTN
 NCBI GI g168690
 BLAST score 99
 E value 2.0e-48

Match length 175
% identity 90
NCBI Description Maize zein mRNA, complete cds, clone ZG124

Seq. No. 299080
Seq. ID LIB3152-009-P1-K1-D3
Method BLASTX
NCBI GI g419803
BLAST score 351
E value 2.0e-33
Match length 98
% identity 66
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 299081
Seq. ID LIB3152-009-P1-K1-D9
Method BLASTN
NCBI GI g4185305
BLAST score 112
E value 3.0e-56
Match length 220
% identity 89
NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

Seq. No. 299082
Seq. ID LIB3152-009-P1-K1-E6
Method BLASTX
NCBI GI g168699
BLAST score 166
E value 2.0e-25
Match length 93
% identity 60
NCBI Description (M60836) zein [Zea mays]

Seq. No. 299083
Seq. ID LIB3152-009-P1-K1-F9
Method BLASTX
NCBI GI g16073
BLAST score 452
E value 3.0e-45
Match length 101
% identity 89
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 299084
Seq. ID LIB3152-009-P1-K1-G1
Method BLASTX
NCBI GI g141612
BLAST score 430
E value 1.0e-42
Match length 107
% identity 82
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)

>gi_72306_pir_ZIZMC2 22K zein precursor (clone cZ22C2) -
maize (fragment) >gi_168688 (M12141) 22 kDa zein protein
[Zea mays]

Seq. No. 299085
Seq. ID LIB3152-010-P1-K1-B11
Method BLASTX
NCBI GI g168693
BLAST score 306
E value 3.0e-28
Match length 88
% identity 74
NCBI Description (M29627) zein [Zea mays]

Seq. No. 299086
Seq. ID LIB3152-010-P1-K1-C10
Method BLASTN
NCBI GI g168698
BLAST score 120
E value 6.0e-61
Match length 291
% identity 87
NCBI Description Z.mays zein mRNA, complete cds

Seq. No. 299087
Seq. ID LIB3152-010-P1-K1-D3
Method BLASTX
NCBI GI g141612
BLAST score 340
E value 6.0e-32
Match length 135
% identity 67
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)
>gi_72306_pir_ZIZMC2 22K zein precursor (clone cZ22C2) -
maize (fragment) >gi_168688 (M12141) 22 kDa zein protein
[Zea mays]

Seq. No. 299088
Seq. ID LIB3152-010-P1-K1-E11
Method BLASTN
NCBI GI g168681
BLAST score 144
E value 3.0e-75
Match length 311
% identity 88
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 299089
Seq. ID LIB3152-010-P1-K1-G5
Method BLASTX
NCBI GI g168703
BLAST score 205
E value 3.0e-16
Match length 69
% identity 64
NCBI Description (M86591) 22 kDa zein protein [Zea mays]

BIBLIOGRAPHY

Seq. No. 299090
 Seq. ID LIB3152-010-P1-K1-G8
 Method BLASTX
 NCBI GI g2244785
 BLAST score 369
 E value 2.0e-35
 Match length 104
 % identity 65
 NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

 Seq. No. 299091
 Seq. ID LIB3152-010-P1-K1-H11
 Method BLASTX
 NCBI GI g72307
 BLAST score 261
 E value 8.0e-23
 Match length 102
 % identity 57
 NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686 (J01246) 26.99 kd zein protein [Zea mays]

 Seq. No. 299092
 Seq. ID LIB3152-012-P1-K1-C8
 Method BLASTX
 NCBI GI g2832247
 BLAST score 148
 E value 2.0e-10
 Match length 58
 % identity 61
 NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

 Seq. No. 299093
 Seq. ID LIB3152-012-P1-K1-D10
 Method BLASTN
 NCBI GI g168681
 BLAST score 89
 E value 2.0e-42
 Match length 149
 % identity 90
 NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds. >gi_270686_gb_I03333_Sequence 8 from Patent US

 Seq. No. 299094
 Seq. ID LIB3152-012-P1-K1-D11
 Method BLASTX
 NCBI GI g1345587
 BLAST score 255
 E value 3.0e-22
 Match length 92
 % identity 63
 NCBI Description 14-3-3-LIKE PROTEIN GF14-6 >gi_998430_bbs_164522 (S77133) GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261 aa] [Zea mays]

 Seq. No. 299095
 Seq. ID LIB3152-012-P1-K1-D7

Method BLASTX
 NCBI GI g141597
 BLAST score 316
 E value 3.0e-29
 Match length 72
 % identity 86
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
 >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
 >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
 [Zea mays]

Seq. No. 299096
 Seq. ID LIB3152-012-P1-K1-F6
 Method BLASTX
 NCBI GI g22216
 BLAST score 282
 E value 3.0e-25
 Match length 79
 % identity 76
 NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 299097
 Seq. ID LIB3152-012-P1-K1-F7
 Method BLASTN
 NCBI GI g168702
 BLAST score 69
 E value 1.0e-30
 Match length 161
 % identity 86
 NCBI Description Corn 22 kDa zein protein gene, complete cds

Seq. No. 299098
 Seq. ID LIB3152-012-P1-K1-G11
 Method BLASTX
 NCBI GI g141605
 BLAST score 258
 E value 1.0e-22
 Match length 73
 % identity 75
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
 >gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize
 >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 299099
 Seq. ID LIB3152-014-P1-K1-A1
 Method BLASTX
 NCBI GI g16073
 BLAST score 184
 E value 3.0e-27
 Match length 120
 % identity 63
 NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 299100
 Seq. ID LIB3152-014-P1-K1-A11
 Method BLASTX
 NCBI GI g468516

BLAST score 143
E value 5.0e-09
Match length 34
% identity 85
NCBI Description (X55724) zein [Zea mays]

Seq. No. 299101
Seq. ID LIB3152-014-P1-K1-B12
Method BLASTN
NCBI GI g168681
BLAST score 61
E value 5.0e-26
Match length 153
% identity 85
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 299102
Seq. ID LIB3152-014-P1-K1-C11
Method BLASTX
NCBI GI g168699
BLAST score 171
E value 1.0e-18
Match length 81
% identity 74
NCBI Description (M60836) zein [Zea mays]

Seq. No. 299103
Seq. ID LIB3152-014-P1-K1-D2
Method BLASTX
NCBI GI g16073
BLAST score 293
E value 1.0e-26
Match length 68
% identity 88
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 299104
Seq. ID LIB3152-014-P1-K1-E9
Method BLASTN
NCBI GI g168665
BLAST score 94
E value 1.0e-45
Match length 225
% identity 88
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 299105
Seq. ID LIB3152-014-P1-K1-G11
Method BLASTN
NCBI GI g2832242
BLAST score 56
E value 8.0e-23
Match length 158
% identity 16
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299106
Seq. ID LIB3152-014-P1-K1-G2
Method BLASTX
NCBI GI g168699
BLAST score 354
E value 1.0e-33
Match length 73
% identity 99
NCBI Description (M60836) zein [Zea mays]

Seq. No. 299107
Seq. ID LIB3152-014-P1-K1-H3
Method BLASTN
NCBI GI g168675
BLAST score 60
E value 4.0e-25
Match length 128
% identity 88
NCBI Description Maize mutant zein (zE19) gene, complete cds

Seq. No. 299108
Seq. ID LIB3152-014-P1-K1-H7
Method BLASTN
NCBI GI g168398
BLAST score 226
E value 1.0e-124
Match length 234
% identity 99
NCBI Description Zea mays auxin-binding protein (abp4) gene, exons 1-5 and complete cds

Seq. No. 299109
Seq. ID LIB3152-015-P1-K1-B1
Method BLASTX
NCBI GI g141608
BLAST score 188
E value 2.0e-15
Match length 98
% identity 54
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 299110
Seq. ID LIB3152-015-P1-K1-D9
Method BLASTX
NCBI GI g168699
BLAST score 267
E value 2.0e-23
Match length 82
% identity 71
NCBI Description (M60836) zein [Zea mays]

Seq. No. 299111
Seq. ID LIB3152-015-P1-K1-F11
Method BLASTX
NCBI GI g141616

BLAST score	241
E value	3.0e-20
Match length	98
% identity	61
NCBI Description	ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3) >gi_168662 (M12147) 15 kDa zein protein [Zea mays]
Seq. No.	299112
Seq. ID	LIB3152-015-P1-K1-H8
Method	BLASTX
NCBI GI	g461498
BLAST score	227
E value	5.0e-19
Match length	46
% identity	96
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir_S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]
Seq. No.	299113
Seq. ID	LIB3152-016-P1-K1-A1
Method	BLASTX
NCBI GI	g4140644
BLAST score	324
E value	4.0e-30
Match length	90
% identity	76
NCBI Description	(AF090447) 22-kDa zein protein 12 [Zea mays]
Seq. No.	299114
Seq. ID	LIB3152-016-P1-K1-A11
Method	BLASTN
NCBI GI	g4140643
BLAST score	43
E value	4.0e-15
Match length	175
% identity	82
NCBI Description	Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	299115
Seq. ID	LIB3152-016-P1-K1-A7
Method	BLASTX
NCBI GI	g3694807
BLAST score	223
E value	1.0e-18
Match length	55
% identity	84
NCBI Description	(AF055898) alanine aminotransferase [Zea mays]
Seq. No.	299116
Seq. ID	LIB3152-016-P1-K1-C11
Method	BLASTN
NCBI GI	g168685
BLAST score	51

E value 7.0e-20
Match length 182
% identity 86
NCBI Description Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA

Seq. No. 299117
Seq. ID LIB3152-016-P1-K1-E3
Method BLASTX
NCBI GI g4263695
BLAST score 162
E value 4.0e-11
Match length 119
% identity 30
NCBI Description (AC006223) putative myosin II heavy chain [Arabidopsis thaliana]

Seq. No. 299118
Seq. ID LIB3152-016-P1-K1-E9
Method BLASTX
NCBI GI g22220
BLAST score 252
E value 1.0e-21
Match length 110
% identity 51
NCBI Description (X55723) 22 kD zein [Zea mays]

Seq. No. 299119
Seq. ID LIB3152-016-P1-K1-G2
Method BLASTX
NCBI GI g141600
BLAST score 168
E value 7.0e-12
Match length 61
% identity 57
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) -
maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 299120
Seq. ID LIB3152-016-P1-K1-G8
Method BLASTX
NCBI GI g22216
BLAST score 280
E value 4.0e-25
Match length 96
% identity 65
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 299121
Seq. ID LIB3152-016-P1-K1-H1
Method BLASTN
NCBI GI g22516
BLAST score 261
E value 1.0e-145
Match length 360
% identity 94
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 299122
Seq. ID LIB3152-017-P1-K1-A3
Method BLASTN
NCBI GI g22326
BLAST score 120
E value 6.0e-61
Match length 160
% identity 94
NCBI Description Z.mays gene for Hageman factor inhibitor

Seq. No. 299123
Seq. ID LIB3152-017-P1-K1-B11
Method BLASTX
NCBI GI g141603
BLAST score 416
E value 6.0e-41
Match length 96
% identity 92
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2_19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_(V01476) zein [Zea mays]

Seq. No. 299124
Seq. ID LIB3152-017-P1-K1-B5
Method BLASTX
NCBI GI g121472
BLAST score 223
E value 9.0e-23
Match length 75
% identity 76
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize
>gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor [Zea mays]
>gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea mays]
>gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 299125
Seq. ID LIB3152-017-P1-K1-C10
Method BLASTX
NCBI GI g22220
BLAST score 178
E value 2.0e-13
Match length 71
% identity 55
NCBI Description (X55723) 22 kd zein [Zea mays]

Seq. No. 299126
Seq. ID LIB3152-017-P1-K1-C5
Method BLASTX
NCBI GI g533086
BLAST score 171
E value 3.0e-12
Match length 46
% identity 74
NCBI Description (U07605) precursor delta-9-stearoyl-acyl carrier protein

desaturase [Thunbergia alata]

Seq. No. 299127
Seq. ID LIB3152-017-P1-K1-D11
Method BLASTX
NCBI GI g141603
BLAST score 244
E value 2.0e-31
Match length 99
% identity 80
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2_19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 299128
Seq. ID LIB3152-017-P1-K1-F11
Method BLASTX
NCBI GI g141614
BLAST score 174
E value 1.0e-17
Match length 89
% identity 63
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
>gi_82662_pir_B22831_22K zein precursor (clone M1) - maize
>gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea mays]
>gi_224510_prf_1107201D zein M1 [Zea mays]

Seq. No. 299129
Seq. ID LIB3152-017-P1-K1-F3
Method BLASTN
NCBI GI g303854
BLAST score 82
E value 1.0e-38
Match length 114
% identity 93
NCBI Description Rice mRNA for ribosomal protein L7A, complete cds

Seq. No. 299130
Seq. ID LIB3152-017-P1-K1-F5
Method BLASTX
NCBI GI g224508
BLAST score 302
E value 1.0e-27
Match length 109
% identity 67
NCBI Description zein A20 [Zea mays]

Seq. No. 299131
Seq. ID LIB3152-017-P1-K1-F7
Method BLASTX
NCBI GI g168699
BLAST score 256
E value 3.0e-27
Match length 105
% identity 70
NCBI Description (M60836) zein [Zea mays]

Seq. No. 299132
Seq. ID LIB3152-017-P1-K1-G7
Method BLASTN
NCBI GI g168704
BLAST score 57
E value 1.0e-23
Match length 119
% identity 92
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 299133
Seq. ID LIB3152-017-P1-K1-H11
Method BLASTX
NCBI GI g2832246
BLAST score 308
E value 3.0e-28
Match length 110
% identity 60
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 299134
Seq. ID LIB3152-017-P1-K1-H3
Method BLASTN
NCBI GI g2828011
BLAST score 41
E value 6.0e-14
Match length 61
% identity 92
NCBI Description Zea mays starch synthase I precursor (Ss1) mRNA, nuclear gene encoding plastid protein, complete cds

Seq. No. 299135
Seq. ID LIB3152-017-P1-K1-H7
Method BLASTN
NCBI GI g2832242
BLAST score 70
E value 3.0e-31
Match length 142
% identity 14
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299136
Seq. ID LIB3152-017-P1-K1-H9
Method BLASTX
NCBI GI g141614
BLAST score 290
E value 8.0e-30
Match length 110
% identity 39
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
>gi_82662_pir_B22831 22K zein precursor (clone M1) - maize
>gi_22527_emb_CAA24722 (V01475) reading frame zein [Zea mays] >gi_224510_prf_1107201D zein M1 [Zea mays]

Seq. No. 299137
Seq. ID LIB3152-018-P1-K1-A11
Method BLASTX

NCBI GI g141603
BLAST score 290
E value 4.0e-26
Match length 116
% identity 58
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 299138
Seq. ID LIB3152-018-P1-K1-E6
Method BLASTN
NCBI GI g168681
BLAST score 92
E value 3.0e-44
Match length 124
% identity 94
NCBI Description Maize 19 kDa zein mRNA, clone cz19D1, complete cds.
>gi_270686_gb_I03333_ Sequence 8 from Patent US

Seq. No. 299139
Seq. ID LIB3152-018-P1-K1-F6
Method BLASTX
NCBI GI g224508
BLAST score 188
E value 1.0e-28
Match length 89
% identity 88
NCBI Description zein A20 [Zea mays]

Seq. No. 299140
Seq. ID LIB3152-019-P1-K1-C8
Method BLASTX
NCBI GI g141617
BLAST score 236
E value 7.0e-20
Match length 44
% identity 95
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299141
Seq. ID LIB3152-019-P1-K1-D8
Method BLASTX
NCBI GI g141605
BLAST score 144
E value 5.0e-13
Match length 76
% identity 58
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cz19C2) - maize
>gi_168680_ (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 299142

DRAFT

Seq. ID	LIB3152-019-P1-K1-E11
Method	BLASTX
NCBI GI	g1076791
BLAST score	251
E value	1.0e-37
Match length	122
% identity	70
NCBI Description	calcium-binding protein - maize >gi_2119370_pir_S58170 Calreticulin precursor - maize >gi_577612_emb_CAA86728_ (Z46772) calcium-binding protein [Zea mays] >gi_927572_emb_CAA61939_ (X89813) Calreticulin precursor [Zea mays] >gi_1587033_prf_2205314A calreticulin [Zea mays]
Seq. No.	299143
Seq. ID	LIB3152-019-P1-K1-F1
Method	BLASTN
NCBI GI	g168673
BLAST score	121
E value	1.0e-61
Match length	136
% identity	98
NCBI Description	Maize 19 kDa zein mRNA, clone cz19B1, complete cds
Seq. No.	299144
Seq. ID	LIB3152-019-P1-K1-G11
Method	BLASTX
NCBI GI	g141600
BLAST score	171
E value	3.0e-12
Match length	84
% identity	50
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1) >gi_72315_pir_ZIZMB1 19K zein precursor (clone cz19B1) - maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]
Seq. No.	299145
Seq. ID	LIB3152-019-P1-K1-H6
Method	BLASTN
NCBI GI	g168652
BLAST score	42
E value	2.0e-14
Match length	86
% identity	87
NCBI Description	Maize amyloplast-specific transit protein (waxy; wx+ locus), complete cds
Seq. No.	299146
Seq. ID	LIB3152-020-P1-K1-A7
Method	BLASTX
NCBI GI	g82660
BLAST score	361
E value	2.0e-34
Match length	128
% identity	60
NCBI Description	19K zein precursor (clone ZG31A) - maize (fragment) >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 299147
 Seq. ID LIB3152-020-P1-K1-B12
 Method BLASTX
 NCBI GI g629861
 BLAST score 159
 E value 6.0e-11
 Match length 47
 % identity 68
 NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_(X67203)
 zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 299148
 Seq. ID LIB3152-020-P1-K1-C2
 Method BLASTX
 NCBI GI g3122071
 BLAST score 326
 E value 5.0e-42
 Match length 122
 % identity 73
 NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
 >gi_2130148_pir_S66339 translation elongation factor eEF-1
 alpha chain - maize >gi_1321656_dbj_BAA08249_(D45408)
 alpha subunit of tlation elongation factor 1 [Zea mays]

Seq. No. 299149
 Seq. ID LIB3152-020-P1-K1-D12
 Method BLASTX
 NCBI GI g168695
 BLAST score 231
 E value 1.0e-19
 Match length 63
 % identity 70
 NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
 zein gamma [Zea mays]

Seq. No. 299150
 Seq. ID LIB3152-020-P1-K1-D3
 Method BLASTX
 NCBI GI g508545
 BLAST score 222
 E value 3.0e-18
 Match length 99
 % identity 56
 NCBI Description (L34340) zein [Zea mays]

Seq. No. 299151
 Seq. ID LIB3152-020-P1-K1-F1
 Method BLASTX
 NCBI GI g2130065
 BLAST score 173
 E value 2.0e-12
 Match length 54
 % identity 72
 NCBI Description alpha-globulin precursor - rice >gi_1783206_dbj_BAA09308_(D50643) 26 kDa globulin [Oryza sativa]

Seq. No. 299152
 Seq. ID LIB3152-020-P1-K1-G1
 Method BLASTN
 NCBI GI g2253277
 BLAST score 41
 E value 9.0e-14
 Match length 92
 % identity 86
 NCBI Description Oryza sativa bZIP transcriptional activator RF2a (rf2a) mRNA, complete cds

Seq. No. 299153
 Seq. ID LIB3152-020-P1-K1-H11
 Method BLASTX
 NCBI GI g141603
 BLAST score 304
 E value 7.0e-28
 Match length 72
 % identity 88
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
 >gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
 >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 299154
 Seq. ID LIB3152-020-P1-K1-H5
 Method BLASTX
 NCBI GI g141615
 BLAST score 222
 E value 3.0e-18
 Match length 64
 % identity 73
 NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
 >gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 299155
 Seq. ID LIB3152-021-P1-K1-A11
 Method BLASTX
 NCBI GI g121472
 BLAST score 154
 E value 1.0e-10
 Match length 57
 % identity 58
 NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
 (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
 >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize
 >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays]
 >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays]
 >gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 299156
 Seq. ID LIB3152-021-P1-K1-A9
 Method BLASTX
 NCBI GI g141597
 BLAST score 231
 E value 2.0e-19
 Match length 58
 % identity 81

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
 >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
 >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
 [Zea mays]

Seq. No.	299157
Seq. ID	LIB3152-021-P1-K1-B10
Method	BLASTN
NCBI GI	g22514
BLAST score	185
E value	1.0e-100
Match length	253
% identity	93
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.	299158
Seq. ID	LIB3152-021-P1-K1-B11
Method	BLASTN
NCBI GI	g22514
BLAST score	136
E value	1.0e-70
Match length	192
% identity	93
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.	299159
Seq. ID	LIB3152-021-P1-K1-C11
Method	BLASTN
NCBI GI	g22326
BLAST score	135
E value	5.0e-70
Match length	167
% identity	95
NCBI Description	Z.mays gene for Hageman factor inhibitor
Seq. No.	299160
Seq. ID	LIB3152-021-P1-K1-C12
Method	BLASTN
NCBI GI	g463151
BLAST score	180
E value	8.0e-97
Match length	264
% identity	92
NCBI Description	Zea mays high sulfur zein gene, complete cds
Seq. No.	299161
Seq. ID	LIB3152-021-P1-K1-C2
Method	BLASTX
NCBI GI	g141616
BLAST score	191
E value	1.0e-14
Match length	42
% identity	86
NCBI Description	ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3) >gi_168662 (M12147) 15 kDa zein protein [Zea mays]
Seq. No.	299162

Seq. ID LIB3152-021-P1-K1-C5
 Method BLASTX
 NCBI GI g141598
 BLAST score 297
 E value 5.0e-27
 Match length 98
 % identity 66
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE ZG99)
 >gi_72313_pir_ZIZM99_19K zein precursor (clone ZG99) -
 maize >gi_22519_emb_CAA24717_ (V01470) zein [Zea mays]
 >gi_22534_emb_CAA24726_ (V01479) zein [Zea mays]

Seq. No. 299163
 Seq. ID LIB3152-021-P1-K1-D11
 Method BLASTX
 NCBI GI g508545
 BLAST score 243
 E value 1.0e-20
 Match length 124
 % identity 50
 NCBI Description (L34340) zein [Zea mays]

Seq. No. 299164
 Seq. ID LIB3152-021-P1-K1-F11
 Method BLASTX
 NCBI GI g82654
 BLAST score 170
 E value 1.0e-12
 Match length 55
 % identity 64
 NCBI Description 10K zein precursor - maize >gi_22541_emb_CAA30409_ (X07535)
 10kDa zein (AA 1 - 150) [Zea mays]

Seq. No. 299165
 Seq. ID LIB3152-021-P1-K1-G5
 Method BLASTX
 NCBI GI g629861
 BLAST score 239
 E value 3.0e-20
 Match length 102
 % identity 53
 NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
 zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 299166
 Seq. ID LIB3152-021-P1-K1-H1
 Method BLASTX
 NCBI GI g1177320
 BLAST score 345
 E value 1.0e-32
 Match length 98
 % identity 64
 NCBI Description (X89891) EFA27 for EF hand, abscisic acid, 27kD [Oryza sativa]

Seq. No. 299167
 Seq. ID LIB3152-021-P1-K1-H10

Method BLASTN
NCBI GI g22544
BLAST score 76
E value 1.0e-34
Match length 277
% identity 82
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 299168
Seq. ID LIB3152-021-P1-K1-H2
Method BLASTX
NCBI GI g1177320
BLAST score 226
E value 1.0e-18
Match length 93
% identity 49
NCBI Description (X89891) EFA27 for EF hand, abscisic acid, 27kD [Oryza sativa]

Seq. No. 299169
Seq. ID LIB3152-021-P1-K1-H9
Method BLASTN
NCBI GI g248336
BLAST score 44
E value 6.0e-16
Match length 116
% identity 84
NCBI Description polyubiquitin [maize, Genomic, 3841 nt]

Seq. No. 299170
Seq. ID LIB3152-022-P1-K1-A8
Method BLASTX
NCBI GI g168697
BLAST score 321
E value 9.0e-30
Match length 78
% identity 87
NCBI Description (M60835) zein [Zea mays]

Seq. No. 299171
Seq. ID LIB3152-022-P1-K1-D1
Method BLASTX
NCBI GI g2564066
BLAST score 184
E value 8.0e-14
Match length 69
% identity 59
NCBI Description (D45900) LEDI-3 protein [Lithospermum erythrorhizon]

Seq. No. 299172
Seq. ID LIB3152-022-P1-K1-D7
Method BLASTX
NCBI GI g224513
BLAST score 207
E value 5.0e-35
Match length 107
% identity 79

NCBI Description zein M6 [Zea mays]

Seq. No. 299173
Seq. ID LIB3152-022-P1-K1-F4
Method BLASTX
NCBI GI g141603
BLAST score 251
E value 1.0e-21
Match length 87
% identity 67
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 299174
Seq. ID LIB3152-022-P1-K1-G7
Method BLASTX
NCBI GI g2244866
BLAST score 165
E value 1.0e-13
Match length 59
% identity 68
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 299175
Seq. ID LIB3152-023-P1-K1-A12
Method BLASTN
NCBI GI g2832242
BLAST score 78
E value 3.0e-36
Match length 162
% identity 12
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299176
Seq. ID LIB3152-023-P1-K1-A2
Method BLASTX
NCBI GI g2245020
BLAST score 381
E value 5.0e-37
Match length 93
% identity 76
NCBI Description (Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No. 299177
Seq. ID LIB3152-023-P1-K1-A6
Method BLASTX
NCBI GI g72307
BLAST score 290
E value 4.0e-26
Match length 104
% identity 61
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
(J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 299178
Seq. ID LIB3152-023-P1-K1-C8

Method BLASTN
NCBI GI g22099
BLAST score 41
E value 4.0e-14
Match length 69
% identity 90
NCBI Description Z.mays 27kDa zein locus DNA

Seq. No. 299179
Seq. ID LIB3152-023-P1-K1-D4
Method BLASTX
NCBI GI g121472
BLAST score 219
E value 7.0e-18
Match length 61
% identity 70
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 299180
Seq. ID LIB3152-023-P1-K1-E12
Method BLASTN
NCBI GI g22544
BLAST score 171
E value 2.0e-91
Match length 251
% identity 92
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 299181
Seq. ID LIB3152-023-P1-K1-F9
Method BLASTN
NCBI GI g1419369
BLAST score 114
E value 2.0e-57
Match length 224
% identity 97
NCBI Description Z.mays ZmABP3 mRNA for actin depolymerizing factor

Seq. No. 299182
Seq. ID LIB3152-023-P1-K1-G6
Method BLASTX
NCBI GI g141614
BLAST score 147
E value 2.0e-09
Match length 52
% identity 67
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
>gi_82662_pir_B22831 22K zein precursor (clone M1) - maize
>gi_22527_emb_CAA24722 (V01475) reading frame zein [Zea
mays] >gi_224510_prf_I107201D zein M1 [Zea mays]

Seq. No. 299183

Seq. ID LIB3152-024-P1-K1-A1
 Method BLASTN
 NCBI GI g168704
 BLAST score 38
 E value 3.0e-12
 Match length 102
 % identity 84
 NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 299184
 Seq. ID LIB3152-024-P1-K1-A12
 Method BLASTN
 NCBI GI g22514
 BLAST score 55
 E value 2.0e-22
 Match length 91
 % identity 90
 NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 299185
 Seq. ID LIB3152-024-P1-K1-C4
 Method BLASTX
 NCBI GI g168701
 BLAST score 323
 E value 4.0e-30
 Match length 95
 % identity 73
 NCBI Description (M60837) zein [Zea mays]

Seq. No. 299186
 Seq. ID LIB3152-024-P1-K1-C6
 Method BLASTX
 NCBI GI g141603
 BLAST score 266
 E value 2.0e-23
 Match length 78
 % identity 76
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
 >gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
 >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 299187
 Seq. ID LIB3152-024-P1-K1-D7
 Method BLASTN
 NCBI GI g4140643
 BLAST score 58
 E value 4.0e-24
 Match length 94
 % identity 91
 NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299188
 Seq. ID LIB3152-024-P1-K1-F10
 Method BLASTX
 NCBI GI g168701
 BLAST score 341

E value 2.0e-32
Match length 81
% identity 85
NCBI Description (M60837) zein [Zea mays]

Seq. No. 299189
Seq. ID LIB3152-024-P1-K1-G9
Method BLASTX
NCBI GI g224509
BLAST score 186
E value 4.0e-14
Match length 95
% identity 52
NCBI Description zein E19 [Zea mays]

Seq. No. 299190
Seq. ID LIB3152-026-P1-K1-B3
Method BLASTN
NCBI GI g22514
BLAST score 53
E value 4.0e-21
Match length 121
% identity 88
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 299191
Seq. ID LIB3152-026-P1-K1-C1
Method BLASTX
NCBI GI g224507
BLAST score 207
E value 1.0e-16
Match length 59
% identity 73
NCBI Description zein A1 [Zea mays]

Seq. No. 299192
Seq. ID LIB3152-026-P1-K1-C8
Method BLASTN
NCBI GI g168484
BLAST score 108
E value 9.0e-54
Match length 164
% identity 92
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 299193
Seq. ID LIB3152-026-P1-K1-D11
Method BLASTX
NCBI GI g508545
BLAST score 263
E value 8.0e-25
Match length 111
% identity 65
NCBI Description (L34340) zein [Zea mays]

Seq. No. 299194
Seq. ID LIB3152-026-P1-K1-D2

Method BLASTX
 NCBI GI g629861
 BLAST score 368
 E value 2.0e-35
 Match length 119
 % identity 65
 NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
 zein Zd1 (19 kDa zein) [Zea mays]

 Seq. No. 299195
 Seq. ID LIB3152-026-P1-K1-E7
 Method BLASTN
 NCBI GI g4140643
 BLAST score 100
 E value 4.0e-49
 Match length 207
 % identity 47
 NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
 complete sequence

 Seq. No. 299196
 Seq. ID LIB3152-026-P1-K1-F5
 Method BLASTX
 NCBI GI g141616
 BLAST score 186
 E value 5.0e-16
 Match length 76
 % identity 64
 NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
 >gi_168662 (M12147) 15 kDa zein protein [Zea mays]

 Seq. No. 299197
 Seq. ID LIB3152-027-P1-K2-A3
 Method BLASTX
 NCBI GI g141603
 BLAST score 207
 E value 2.0e-16
 Match length 70
 % identity 67
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
 >gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
 >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

 Seq. No. 299198
 Seq. ID LIB3152-027-P1-K2-A7
 Method BLASTX
 NCBI GI g141597
 BLAST score 267
 E value 2.0e-23
 Match length 105
 % identity 57
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
 >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
 >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
 [Zea mays]

 Seq. No. 299199

Seq. ID LIB3152-027-P1-K2-B7
Method BLASTN
NCBI GI g22326
BLAST score 43
E value 7.0e-15
Match length 59
% identity 93
NCBI Description Z.mays gene for Hageman factor inhibitor

Seq. No. 299200
Seq. ID LIB3152-027-P1-K2-C10
Method BLASTX
NCBI GI g168701
BLAST score 275
E value 1.0e-24
Match length 72
% identity 81
NCBI Description (M60837) zein [Zea mays]

Seq. No. 299201
Seq. ID LIB3152-027-P1-K2-D2
Method BLASTN
NCBI GI g168665
BLAST score 324
E value 0.0e+00
Match length 344
% identity 99
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 299202
Seq. ID LIB3152-027-P1-K2-D5
Method BLASTX
NCBI GI g141605
BLAST score 251
E value 1.0e-21
Match length 66
% identity 77
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 299203
Seq. ID LIB3152-027-P1-K2-E7
Method BLASTX
NCBI GI g141613
BLAST score 291
E value 1.0e-26
Match length 81
% identity 80
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
>gi_72305_pir_ZIZM21 22K zein precursor (clone pZ22.1) -
maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]

Seq. No. 299204
Seq. ID LIB3152-027-P1-K2-H7
Method BLASTX
NCBI GI g4416301

BLAST score 379
 E value 1.0e-36
 Match length 116
 % identity 70
 NCBI Description (AF105716) gag protein [Zea mays]

Seq. No. 299205
 Seq. ID LIB3152-028-P1-K1-A1
 Method BLASTX
 NCBI GI g141607
 BLAST score 152
 E value 5.0e-10
 Match length 104
 % identity 38
 NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
 >gi_22521_emb_CAA24718_(V01471) zein [Zea mays] >gi_168672
 (J01244) zein 19 kd protein (partial) [Zea mays]

Seq. No. 299206
 Seq. ID LIB3152-028-P1-K1-B4
 Method BLASTN
 NCBI GI g508544
 BLAST score 63
 E value 4.0e-27
 Match length 182
 % identity 90
 NCBI Description Zea mays 24-kD alpha-zein gene (floury2), complete cds

Seq. No. 299207
 Seq. ID LIB3152-028-P1-K1-D6
 Method BLASTX
 NCBI GI g141617
 BLAST score 246
 E value 5.0e-21
 Match length 47
 % identity 89
 NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
 >gi_100941_pir_S12140 zein Zc1 - maize
 >gi_100945_pir_B29017 zein 2 - maize
 >gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
 >gi_168666_(M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299208
 Seq. ID LIB3152-028-P1-K1-E5
 Method BLASTX
 NCBI GI g266398
 BLAST score 275
 E value 1.0e-24
 Match length 82
 % identity 61
 NCBI Description TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR
 INHIBITOR) (CHFI) >gi_68849_pir_TIZM1 trypsin/factor XIIa
 inhibitor precursor - maize >gi_22327_emb_CAA37998_
 (X54064) corn Hageman factor inhibitor [Zea mays]

Seq. No. 299209
 Seq. ID LIB3152-028-P1-K1-G10

DRAFT

Method BLASTX
NCBI GI g260042
BLAST score 332
E value 4.0e-31
Match length 80
% identity 82
NCBI Description (S48563) endosperm ADP-glucose pyrophosphorylase subunit homolog=Sh2 [maize, Peptide Partial, 542 aa] [Zea mays]

Seq. No. 299210
Seq. ID LIB3152-028-P1-K1-H5
Method BLASTX
NCBI GI g100846
BLAST score 263
E value 5.0e-23
Match length 95
% identity 65
NCBI Description 22K zein precursor (clone gZ22.8H3) - maize
>gi_22179_emb_CAA43399 (X61085) 22 kD alpha-zein [Zea mays]

Seq. No. 299211
Seq. ID LIB3152-029-P1-K1-C1
Method BLASTX
NCBI GI g22220
BLAST score 216
E value 2.0e-17
Match length 97
% identity 54
NCBI Description (X55723) 22 kD zein [Zea mays]

Seq. No. 299212
Seq. ID LIB3152-029-P1-K1-C6
Method BLASTX
NCBI GI g4185308
BLAST score 262
E value 7.0e-23
Match length 77
% identity 70
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]

Seq. No. 299213
Seq. ID LIB3152-029-P1-K1-C8
Method BLASTX
NCBI GI g224509
BLAST score 165
E value 5.0e-12
Match length 58
% identity 62
NCBI Description zein E19 [Zea mays]

Seq. No. 299214
Seq. ID LIB3152-029-P1-K1-D1
Method BLASTX
NCBI GI g100938
BLAST score 187
E value 4.0e-14

Match length 69
% identity 62
NCBI Description zein precursor - maize >gi_22442_emb_CAA32513_ (X14335)
zein precursor (AA -21 to 90) [Zea mays]

Seq. No. 299215
Seq. ID LIB3152-029-P1-K1-E1
Method BLASTX
NCBI GI g72307
BLAST score 260
E value 4.0e-26
Match length 90
% identity 79
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
(J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 299216
Seq. ID LIB3152-029-P1-K1-F1
Method BLASTX
NCBI GI g141608
BLAST score 186
E value 2.0e-26
Match length 112
% identity 65
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 299217
Seq. ID LIB3152-029-P1-K1-F11
Method BLASTX
NCBI GI g141597
BLAST score 236
E value 6.0e-20
Match length 68
% identity 72
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 299218
Seq. ID LIB3152-029-P1-K1-F4
Method BLASTX
NCBI GI g2832247
BLAST score 367
E value 3.0e-35
Match length 95
% identity 83
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 299219
Seq. ID LIB3152-029-P1-K1-F8
Method BLASTX
NCBI GI g2832246
BLAST score 254
E value 5.0e-22

Match length 55
% identity 95
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 299220
Seq. ID LIB3152-030-P1-K1-C6
Method BLASTX
NCBI GI g224507
BLAST score 249
E value 2.0e-21
Match length 94
% identity 60
NCBI Description zein A1 [Zea mays]

Seq. No. 299221
Seq. ID LIB3152-030-P1-K1-D2
Method BLASTN
NCBI GI g168673
BLAST score 90
E value 5.0e-43
Match length 90
% identity 100
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 299222
Seq. ID LIB3152-030-P1-K1-F8
Method BLASTX
NCBI GI g2832247
BLAST score 192
E value 1.0e-14
Match length 98
% identity 48
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 299223
Seq. ID LIB3152-031-P1-K1-B2
Method BLASTX
NCBI GI g82696
BLAST score 382
E value 6.0e-37
Match length 82
% identity 90
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]

Seq. No. 299224
Seq. ID LIB3152-031-P1-K1-B3
Method BLASTN
NCBI GI g168681
BLAST score 86
E value 7.0e-41
Match length 138
% identity 91
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 299225

Seq. ID LIB3152-031-P1-K1-B9
Method BLASTX
NCBI GI g141605
BLAST score 435
E value 3.0e-43
Match length 103
% identity 88
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 299226
Seq. ID LIB3152-031-P1-K1-F12
Method BLASTX
NCBI GI g168695
BLAST score 162
E value 3.0e-11
Match length 43
% identity 63
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
zein gamma [Zea mays]

Seq. No. 299227
Seq. ID LIB3152-031-P1-K1-F9
Method BLASTX
NCBI GI g322870
BLAST score 532
E value 2.0e-61
Match length 120
% identity 99
NCBI Description glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
maize (fragment)

Seq. No. 299228
Seq. ID LIB3152-031-P1-K1-G6
Method BLASTN
NCBI GI g168484
BLAST score 295
E value 1.0e-165
Match length 359
% identity 96
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 299229
Seq. ID LIB3152-031-P1-K1-H11
Method BLASTX
NCBI GI g508545
BLAST score 245
E value 2.0e-29
Match length 98
% identity 77
NCBI Description (L34340) zein [Zea mays]

Seq. No. 299230
Seq. ID LIB3152-031-P1-K1-H4
Method BLASTX
NCBI GI g168695

BLAST score 213
E value 4.0e-17
Match length 37
% identity 100
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
zein gamma [Zea mays]

Seq. No. 299231
Seq. ID LIB3152-031-P1-K1-H8
Method BLASTX
NCBI GI g2739333
BLAST score 359
E value 1.0e-34
Match length 79
% identity 24
NCBI Description (U74318) polyubiquitin [Schizophyllum commune]

Seq. No. 299232
Seq. ID LIB3152-032-P1-K1-B12
Method BLASTX
NCBI GI g168691
BLAST score 168
E value 6.0e-12
Match length 97
% identity 49
NCBI Description (M29628) zein [Zea mays]

Seq. No. 299233
Seq. ID LIB3152-032-P1-K1-C10
Method BLASTN
NCBI GI g2832242
BLAST score 275
E value 1.0e-153
Match length 351
% identity 10
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299234
Seq. ID LIB3152-032-P1-K1-D3
Method BLASTN
NCBI GI g168675
BLAST score 164
E value 3.0e-87
Match length 352
% identity 87
NCBI Description Maize mutant zein (zE19) gene, complete cds

Seq. No. 299235
Seq. ID LIB3152-032-P1-K1-F11
Method BLASTN
NCBI GI g2995383
BLAST score 80
E value 3.0e-37
Match length 128
% identity 92
NCBI Description Zea mays mays mRNA for cytochrome P450 monooxygenase, partial

Seq. No. 299236
Seq. ID LIB3152-032-P1-K1-H9
Method BLASTX
NCBI GI g100940
BLAST score 264
E value 3.0e-23
Match length 97
% identity 63
NCBI Description zein zA1 - maize

Seq. No. 299237
Seq. ID LIB3152-033-P1-K1-A3
Method BLASTX
NCBI GI g224508
BLAST score 220
E value 7.0e-18
Match length 47
% identity 98
NCBI Description zein A20 [Zea mays]

Seq. No. 299238
Seq. ID LIB3152-033-P1-K1-C12
Method BLASTX
NCBI GI g141617
BLAST score 189
E value 8.0e-22
Match length 52
% identity 98
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
>gi_168666_(M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299239
Seq. ID LIB3152-033-P1-K1-C4
Method BLASTX
NCBI GI g168699
BLAST score 318
E value 5.0e-43
Match length 106
% identity 92
NCBI Description (M60836) zein [Zea mays]

Seq. No. 299240
Seq. ID LIB3152-033-P1-K1-E4
Method BLASTN
NCBI GI g22537
BLAST score 79
E value 8.0e-37
Match length 111
% identity 61
NCBI Description Maize mRNA for zein polypeptide (clone M6)

Seq. No. 299241
Seq. ID LIB3152-033-P1-K1-F1

C O D E R O U T P U T

Method BLASTN
NCBI GI g168704
BLAST score 208
E value 1.0e-113
Match length 215
% identity 100
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 299242
Seq. ID LIB3152-033-P1-K1-G1
Method BLASTX
NCBI GI g141617
BLAST score 240
E value 3.0e-20
Match length 58
% identity 78
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays]
>gi_168666_(M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299243
Seq. ID LIB3152-033-P1-K1-G10
Method BLASTN
NCBI GI g22514
BLAST score 132
E value 2.0e-68
Match length 180
% identity 94
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 299244
Seq. ID LIB3152-033-P1-K1-G12
Method BLASTX
NCBI GI g2393775
BLAST score 435
E value 4.0e-43
Match length 115
% identity 73
NCBI Description (U82230) prolamin box binding factor [Zea mays]

Seq. No. 299245
Seq. ID LIB3152-033-P1-K1-H2
Method BLASTN
NCBI GI g168679
BLAST score 87
E value 2.0e-41
Match length 118
% identity 95
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
>gi_270687_gb_I03334_Sequence 9 from Patent US

Seq. No. 299246
Seq. ID LIB3152-033-P1-K1-H8
Method BLASTX
NCBI GI g4185308

BLAST score 258
E value 1.0e-22
Match length 68
% identity 79
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]

Seq. No. 299247
Seq. ID LIB3152-034-P1-K1-A2
Method BLASTX
NCBI GI g168701
BLAST score 256
E value 3.0e-22
Match length 84
% identity 69
NCBI Description (M60837) zein [Zea mays]

Seq. No. 299248
Seq. ID LIB3152-034-P1-K1-A5
Method BLASTX
NCBI GI g508545
BLAST score 261
E value 2.0e-25
Match length 135
% identity 64
NCBI Description (L34340) zein [Zea mays]

Seq. No. 299249
Seq. ID LIB3152-034-P1-K1-A6
Method BLASTX
NCBI GI g141603
BLAST score 251
E value 1.0e-28
Match length 92
% identity 89
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 299250
Seq. ID LIB3152-034-P1-K1-B12
Method BLASTX
NCBI GI g121472
BLAST score 276
E value 2.0e-24
Match length 104
% identity 54
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize
>gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor [Zea mays]
>gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea mays]
>gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 299251
Seq. ID LIB3152-034-P1-K1-B3
Method BLASTN
NCBI GI g22514

BLAST score 123
E value 8.0e-63
Match length 183
% identity 92
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 299252
Seq. ID LIB3152-034-P1-K1-C6
Method BLASTX
NCBI GI g141608
BLAST score 230
E value 2.0e-19
Match length 62
% identity 77
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 299253
Seq. ID LIB3152-034-P1-K1-C7
Method BLASTX
NCBI GI g168701
BLAST score 303
E value 1.0e-27
Match length 73
% identity 86
NCBI Description (M60837) zein [Zea mays]

Seq. No. 299254
Seq. ID LIB3152-034-P1-K1-D11
Method BLASTN
NCBI GI g168665
BLAST score 238
E value 1.0e-131
Match length 266
% identity 97
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 299255
Seq. ID LIB3152-034-P1-K1-D7
Method BLASTX
NCBI GI g22216
BLAST score 246
E value 6.0e-25
Match length 100
% identity 69
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 299256
Seq. ID LIB3152-034-P1-K1-D8
Method BLASTX
NCBI GI g2832243
BLAST score 226
E value 6.0e-19
Match length 70
% identity 71
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

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Seq. No.	299257
Seq. ID	LIB3152-034-P1-K1-D9
Method	BLASTX
NCBI GI	g100938
BLAST score	216
E value	1.0e-17
Match length	76
% identity	64
NCBI Description	zein precursor - maize >gi_22442_emb_CAA32513_ (X14335) zein precursor (AA -21 to 90) [Zea mays]
Seq. No.	299258
Seq. ID	LIB3152-034-P1-K1-E8
Method	BLASTX
NCBI GI	g118926
BLAST score	274
E value	2.0e-24
Match length	102
% identity	50
NCBI Description	DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR >gi_320600_pir_E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781_prf_1710351E abscisic acid responsive protein E [Craterostigma plantagineum]
Seq. No.	299259
Seq. ID	LIB3152-034-P1-K1-F4
Method	BLASTX
NCBI GI	g508545
BLAST score	232
E value	6.0e-25
Match length	104
% identity	63
NCBI Description	(L34340) zein [Zea mays]
Seq. No.	299260
Seq. ID	LIB3152-034-P1-K1-F6
Method	BLASTN
NCBI GI	g1276923
BLAST score	39
E value	7.0e-13
Match length	171
% identity	80
NCBI Description	Zea perennis USDA Ames 21881 ITS1, 5.8S ribosomal RNA, ITS2
Seq. No.	299261
Seq. ID	LIB3152-034-P1-K1-G1
Method	BLASTX
NCBI GI	g4140644
BLAST score	366
E value	5.0e-35
Match length	100
% identity	77
NCBI Description	(AF090447) 22-kDa zein protein 12 [Zea mays]

DO NOT DESTROY

Seq. No. 299262
Seq. ID LIB3152-034-P1-K1-G7
Method BLASTX
NCBI GI g224507
BLAST score 198
E value 3.0e-20
Match length 98
% identity 63
NCBI Description zein A1 [Zea mays]

Seq. No. 299263
Seq. ID LIB3152-034-P1-K1-H7
Method BLASTX
NCBI GI g141607
BLAST score 286
E value 8.0e-26
Match length 66
% identity 89
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
>gi_22521_emb_CAA24718_(V01471) zein [Zea mays] >gi_168672
(J01244) zein 19 kd protein (partial) [Zea mays]

Seq. No. 299264
Seq. ID LIB3152-035-P1-K1-A8
Method BLASTN
NCBI GI g22544
BLAST score 62
E value 1.0e-26
Match length 206
% identity 78
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 299265
Seq. ID LIB3152-035-P1-K1-C7
Method BLASTX
NCBI GI g72307
BLAST score 373
E value 8.0e-36
Match length 115
% identity 70
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
(J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 299266
Seq. ID LIB3152-035-P1-K1-C9
Method BLASTN
NCBI GI g22516
BLAST score 50
E value 2.0e-19
Match length 142
% identity 82
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 299267
Seq. ID LIB3152-035-P1-K1-D12
Method BLASTX
NCBI GI g1351303

BLAST score 211
E value 4.0e-17
Match length 91
% identity 47
NCBI Description INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS)
>gi_619732 (U18770) indole-3-glycerol phosphate synthase
[Arabidopsis thaliana]

Seq. No. 299268
Seq. ID LIB3152-035-P1-K1-E5
Method BLASTN
NCBI GI g3342031
BLAST score 53
E value 2.0e-21
Match length 65
% identity 97
NCBI Description Oryza sativa 18S small subunit ribosomal RNA gene, complete sequence

Seq. No. 299269
Seq. ID LIB3152-035-P1-K1-E7
Method BLASTX
NCBI GI g629861
BLAST score 205
E value 1.0e-28
Match length 101
% identity 66
NCBI Description zein Zd1, 19K - maize >gi_535020 emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 299270
Seq. ID LIB3152-036-P1-K1-A1
Method BLASTN
NCBI GI g4140643
BLAST score 190
E value 1.0e-103
Match length 206
% identity 25
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299271
Seq. ID LIB3152-036-P1-K1-A12
Method BLASTN
NCBI GI g22326
BLAST score 67
E value 2.0e-29
Match length 115
% identity 90
NCBI Description Z.mays gene for Hageman factor inhibitor

Seq. No. 299272
Seq. ID LIB3152-036-P1-K1-B4
Method BLASTX
NCBI GI g168701
BLAST score 434
E value 6.0e-43

Match length 120
% identity 78
NCBI Description (M60837) zein [Zea mays]

Seq. No. 299273
Seq. ID LIB3152-036-P1-K1-E5
Method BLASTX
NCBI GI g22216
BLAST score 177
E value 2.0e-13
Match length 59
% identity 64
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 299274
Seq. ID LIB3152-036-P1-K1-E7
Method BLASTX
NCBI GI g22216
BLAST score 149
E value 5.0e-10
Match length 85
% identity 55
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 299275
Seq. ID LIB3152-036-P1-K1-H9
Method BLASTX
NCBI GI g141615
BLAST score 252
E value 7.0e-22
Match length 78
% identity 68
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
>gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 299276
Seq. ID LIB3152-039-P1-K1-D4
Method BLASTN
NCBI GI g22447
BLAST score 217
E value 1.0e-119
Match length 225
% identity 99
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein

Seq. No. 299277
Seq. ID LIB3152-039-P1-K1-D7
Method BLASTX
NCBI GI g141617
BLAST score 239
E value 3.0e-20
Match length 107
% identity 50
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]

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>gi_168666 (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299278
Seq. ID LIB3152-039-P1-K1-F2
Method BLASTN
NCBI GI g168685
BLAST score 117
E value 4.0e-59
Match length 181
% identity 94
NCBI Description Maize 22 kd (Mw=26.99 kd) zein protein 3, mRNA

Seq. No. 299279
Seq. ID LIB3152-039-P1-K1-H4
Method BLASTN
NCBI GI g168484
BLAST score 109
E value 2.0e-54
Match length 113
% identity 99
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 299280
Seq. ID LIB3152-040-P1-K1-A10
Method BLASTX
NCBI GI g2832247
BLAST score 235
E value 1.0e-19
Match length 104
% identity 52
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 299281
Seq. ID LIB3152-040-P1-K1-C3
Method BLASTX
NCBI GI g141603
BLAST score 483
E value 8.0e-49
Match length 118
% identity 86
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 299282
Seq. ID LIB3152-040-P1-K1-C5
Method BLASTX
NCBI GI g67155
BLAST score 345
E value 8.0e-33
Match length 88
% identity 84
NCBI Description pyruvate,orthophosphate dikinase (EC 2.7.9.1) precursor - maize

Seq. No. 299283
Seq. ID LIB3152-040-P1-K1-D8

DRAFT

Method BLASTX
NCBI GI g2832246
BLAST score 226
E value 8.0e-19
Match length 58
% identity 84
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 299284
Seq. ID LIB3152-040-P1-K1-E9
Method BLASTX
NCBI GI g3643809
BLAST score 144
E value 4.0e-09
Match length 79
% identity 42
NCBI Description (AF062346) zinc finger protein 216 splice variant 1 [Homo sapiens] >gi_3643811 (AF062347) zinc finger protein 216 splice variant 2 [Homo sapiens] >gi_3668066 (AF062072) zinc finger protein 216 [Homo sapiens]

Seq. No. 299285
Seq. ID LIB3152-040-P1-K1-F11
Method BLASTX
NCBI GI g141614
BLAST score 205
E value 3.0e-16
Match length 78
% identity 60
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1)
>gi_82662_pir_B22831 22K zein precursor (clone M1) - maize
>gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea mays] >gi_224510_prf_1107201D zein M1 [Zea mays]

Seq. No. 299286
Seq. ID LIB3152-040-P1-K1-G2
Method BLASTN
NCBI GI g22445
BLAST score 52
E value 1.0e-20
Match length 80
% identity 91
NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. No. 299287
Seq. ID LIB3152-040-P1-K1-G3
Method BLASTX
NCBI GI g141602
BLAST score 149
E value 4.0e-10
Match length 35
% identity 80
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6)
>gi_82658_pir_A22831 19K zein precursor (clone M6) - maize
>gi_22538_emb_CAA26294_ (X02450) zein precursor [Zea mays]

Seq. No. 299288

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Seq. ID	LIB3152-041-P1-K1-A8
Method	BLASTX
NCBI GI	g141605
BLAST score	142
E value	7.0e-18
Match length	64
% identity	71
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) >gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.	299289
Seq. ID	LIB3152-041-P1-K1-B12
Method	BLASTX
NCBI GI	g22216
BLAST score	230
E value	3.0e-19
Match length	98
% identity	53
NCBI Description	(X55722) 22kD zein [Zea mays]
Seq. No.	299290
Seq. ID	LIB3152-041-P1-K1-B2
Method	BLASTX
NCBI GI	g1742187
BLAST score	177
E value	6.0e-13
Match length	101
% identity	41
NCBI Description	(D90771) ORF_ID:o260#14; similar to [SwissProt Accession Number P11666] [Escherichia coli] >gi_1742198_dbj_BAA14933_(D90772) ORF_ID:o260#14; similar to [SwissProt Accession Number P11666] [Escherichia coli] >gi_1787591 (AE000231) orf, hypothetical protein [Escherichia coli]
Seq. No.	299291
Seq. ID	LIB3152-041-P1-K1-C5
Method	BLASTX
NCBI GI	g168701
BLAST score	387
E value	2.0e-37
Match length	111
% identity	77
NCBI Description	(M60837) zein [Zea mays]
Seq. No.	299292
Seq. ID	LIB3152-041-P1-K1-D2
Method	BLASTX
NCBI GI	g224507
BLAST score	161
E value	5.0e-11
Match length	123
% identity	34
NCBI Description	zein A1 [Zea mays]
Seq. No.	299293
Seq. ID	LIB3152-041-P1-K1-F12

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Method	BLASTX
NCBI GI	g3063449
BLAST score	247
E value	4.0e-21
Match length	56
% identity	84
NCBI Description	(AC003981) F22013.11 [Arabidopsis thaliana]
Seq. No.	299294
Seq. ID	LIB3152-041-P1-K1-F2
Method	BLASTX
NCBI GI	g3024552
BLAST score	237
E value	5.0e-20
Match length	89
% identity	64
NCBI Description	RAS-RELATED PROTEIN RGP2 (GTP-BINDING REGULATORY PROTEIN RGP2) >gi_419797_pir_S30273 GTP-binding protein rgp2 - rice >gi_218204_dbj_BAA02437 (D13152) GTP binding protein [Oryza sativa] >gi_446772_prf_1912297A rgp2 gene [Oryza sativa]
Seq. No.	299295
Seq. ID	LIB3152-041-P1-K1-G6
Method	BLASTX
NCBI GI	g72307
BLAST score	213
E value	3.0e-17
Match length	65
% identity	69
NCBI Description	22K zein precursor (clone pZ22.3) - maize >gi_168686 (J01246) 26.99 kd zein protein [Zea mays]
Seq. No.	299296
Seq. ID	LIB3152-041-P1-K1-H3
Method	BLASTX
NCBI GI	g141617
BLAST score	265
E value	3.0e-23
Match length	48
% identity	98
NCBI Description	ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) >gi_100941_pir_S12140 zein Zc1 - maize >gi_100945_pir_B29017 zein 2 - maize >gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays] >gi_168666_(M16460) 16-kDa zein protein [Zea mays]
Seq. No.	299297
Seq. ID	LIB3152-041-P1-K1-H7
Method	BLASTX
NCBI GI	g141617
BLAST score	238
E value	4.0e-20
Match length	81
% identity	59
NCBI Description	ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) >gi_100941_pir_S12140 zein Zc1 - maize

>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299298
Seq. ID LIB3152-042-P1-K1-A1
Method BLASTX
NCBI GI g2832246
BLAST score 177
E value 7.0e-13
Match length 93
% identity 46
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 299299
Seq. ID LIB3152-042-P1-K1-A10
Method BLASTX
NCBI GI g72307
BLAST score 216
E value 5.0e-18
Match length 51
% identity 86
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686 (J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 299300
Seq. ID LIB3152-042-P1-K1-B1
Method BLASTX
NCBI GI g141617
BLAST score 222
E value 3.0e-18
Match length 45
% identity 89
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299301
Seq. ID LIB3152-042-P1-K1-B12
Method BLASTX
NCBI GI g1703108
BLAST score 418
E value 3.0e-41
Match length 104
% identity 76
NCBI Description ACTIN 2/7 >gi_2129525_pir_S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir_S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No. 299302
Seq. ID LIB3152-042-P1-K1-B5
Method BLASTN
NCBI GI g22544

BLAST score 75
E value 4.0e-34
Match length 243
% identity 84
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 299303
Seq. ID LIB3152-042-P1-K1-D3
Method BLASTX
NCBI GI g141597
BLAST score 163
E value 3.0e-11
Match length 63
% identity 60
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3_19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 299304
Seq. ID LIB3152-042-P1-K1-D6
Method BLASTX
NCBI GI g72307
BLAST score 185
E value 6.0e-14
Match length 51
% identity 76
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
(J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 299305
Seq. ID LIB3152-042-P1-K1-F6
Method BLASTN
NCBI GI g168704
BLAST score 216
E value 1.0e-118
Match length 252
% identity 96
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 299306
Seq. ID LIB3152-042-P1-K1-H12
Method BLASTN
NCBI GI g22516
BLAST score 189
E value 1.0e-102
Match length 258
% identity 95
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 299307
Seq. ID LIB3152-042-P1-K1-H4
Method BLASTN
NCBI GI g168700
BLAST score 154
E value 3.0e-81
Match length 210

% identity 94
NCBI Description Z.mays zein mRNA, complete cds

Seq. No. 299308
Seq. ID LIB3152-043-P1-K1-B1
Method BLASTX
NCBI GI g168701
BLAST score 238
E value 3.0e-20
Match length 68
% identity 72
NCBI Description (M60837) zein [Zea mays]

Seq. No. 299309
Seq. ID LIB3152-043-P1-K1-C8
Method BLASTN
NCBI GI g22518
BLAST score 62
E value 2.0e-26
Match length 134
% identity 89
NCBI Description Zea mays gene encoding a zein gene (clone lambda-ZG99)

Seq. No. 299310
Seq. ID LIB3152-043-P1-K1-D12
Method BLASTN
NCBI GI g168681
BLAST score 165
E value 6.0e-88
Match length 237
% identity 77
NCBI Description Maize 19 kDa zein mRNA, clone cz19D1, complete cds.
[>gi_270686_gb_I03333_Sequence 8 from Patent US](#)

Seq. No. 299311
Seq. ID LIB3152-043-P1-K1-D3
Method BLASTN
NCBI GI g168679
BLAST score 100
E value 5.0e-49
Match length 302
% identity 88
NCBI Description Maize 19 kDa zein mRNA, clone cz19C2, complete cds.
[>gi_270687_gb_I03334_Sequence 9 from Patent US](#)

Seq. No. 299312
Seq. ID LIB3152-043-P1-K1-D4
Method BLASTN
NCBI GI g16072
BLAST score 163
E value 8.0e-87
Match length 219
% identity 94
NCBI Description Acetabularia mediterranea zein gene

Seq. No. 299313
Seq. ID LIB3152-043-P1-K1-D5

Method BLASTN
NCBI GI g4185305
BLAST score 45
E value 2.0e-16
Match length 77
% identity 90
NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
(sz22-21) gene, complete cds; retrotransposon Opie-2 gag
protein, polyprotein, and copia protein genes, complete
cds; and unknown genes

Seq. No. 299314
Seq. ID LIB3152-043-P1-K1-E2
Method BLASTX
NCBI GI g419803
BLAST score 454
E value 2.0e-45
Match length 118
% identity 80
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea
mays]

Seq. No. 299315
Seq. ID LIB3152-043-P1-K1-G12
Method BLASTN
NCBI GI g535019
BLAST score 55
E value 3.0e-22
Match length 91
% identity 46
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)

Seq. No. 299316
Seq. ID LIB3152-043-P1-K1-G5
Method BLASTX
NCBI GI g511870
BLAST score 206
E value 3.0e-16
Match length 36
% identity 100
NCBI Description (M23537) zein protein [Zea mays]

Seq. No. 299317
Seq. ID LIB3152-043-P1-K1-G7
Method BLASTN
NCBI GI g4185305
BLAST score 118
E value 9.0e-60
Match length 238
% identity 88
NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
(sz22-21) gene, complete cds; retrotransposon Opie-2 gag
protein, polyprotein, and copia protein genes, complete
cds; and unknown genes

Seq. No. 299318
Seq. ID LIB3152-043-P1-K1-H6

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Method BLASTN
NCBI GI g22540
BLAST score 54
E value 4.0e-22
Match length 66
% identity 95
NCBI Description Maize mRNA for 10kDa zein

Seq. No. 299319
Seq. ID LIB3152-044-P1-K1-A5
Method BLASTX
NCBI GI g2832247
BLAST score 213
E value 6.0e-24
Match length 85
% identity 71
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 299320
Seq. ID LIB3152-044-P1-K1-B5
Method BLASTX
NCBI GI g121472
BLAST score 210
E value 3.0e-17
Match length 67
% identity 58
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 299321
Seq. ID LIB3152-044-P1-K1-B7
Method BLASTN
NCBI GI g508544
BLAST score 90
E value 5.0e-43
Match length 94
% identity 99
NCBI Description Zea mays 24-kD alpha-zein gene (floury2), complete cds

Seq. No. 299322
Seq. ID LIB3152-044-P1-K1-C11
Method BLASTX
NCBI GI g16073
BLAST score 235
E value 6.0e-20
Match length 62
% identity 81
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 299323
Seq. ID LIB3152-044-P1-K1-C5
Method BLASTX
NCBI GI g4539660

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BLAST score 197
E value 3.0e-15
Match length 117
% identity 36
NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 299324
Seq. ID LIB3152-044-P1-K1-D2
Method BLASTX
NCBI GI g629862
BLAST score 148
E value 2.0e-09
Match length 78
% identity 51
NCBI Description zein Zd1, 19K - maize >gi_535021_emb_CAA47640_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 299325
Seq. ID LIB3152-044-P1-K1-D9
Method BLASTN
NCBI GI g168673
BLAST score 52
E value 8.0e-21
Match length 136
% identity 85
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 299326
Seq. ID LIB3152-044-P1-K1-E2
Method BLASTN
NCBI GI g168681
BLAST score 104
E value 2.0e-51
Match length 216
% identity 87
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 299327
Seq. ID LIB3152-044-P1-K1-F12
Method BLASTX
NCBI GI g141617
BLAST score 286
E value 1.0e-25
Match length 113
% identity 54
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666_(M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299328
Seq. ID LIB3152-044-P1-K1-F5
Method BLASTX
NCBI GI g4140644
BLAST score 342

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E value	3.0e-32
Match length	94
% identity	77
NCBI Description	(AF090447) 22-kDa zein protein 12 [Zea mays]
Seq. No.	299329
Seq. ID	LIB3152-044-P1-K1-G11
Method	BLASTX
NCBI GI	g141602
BLAST score	202
E value	2.0e-23
Match length	84
% identity	66
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6) >gi_82658_pir_A22831 19K zein precursor (clone M6) - maize >gi_22538_emb_CAA26294_ (X02450) zein precursor [Zea mays]
Seq. No.	299330
Seq. ID	LIB3152-044-P1-K1-G9
Method	BLASTX
NCBI GI	g2642636
BLAST score	144
E value	1.0e-09
Match length	42
% identity	76
NCBI Description	(AF032471) ADP-glucose pyrophosphorylase small subunit [Citrullus lanatus]
Seq. No.	299331
Seq. ID	LIB3152-045-P1-K1-A12
Method	BLASTX
NCBI GI	g141608
BLAST score	192
E value	3.0e-15
Match length	44
% identity	86
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa zein [Zea mays]
Seq. No.	299332
Seq. ID	LIB3152-045-P1-K1-C12
Method	BLASTN
NCBI GI	g22514
BLAST score	233
E value	1.0e-128
Match length	289
% identity	95
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.	299333
Seq. ID	LIB3152-045-P1-K1-D10
Method	BLASTX
NCBI GI	g508545
BLAST score	178
E value	6.0e-13
Match length	107

DRAFT Sequence

% identity 45
NCBI Description (L34340) zein [Zea mays]

Seq. No. 299334
Seq. ID LIB3152-045-P1-K1-H11
Method BLASTN
NCBI GI g22516
BLAST score 62
E value 2.0e-26
Match length 174
% identity 84
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 299335
Seq. ID LIB3152-045-P1-K1-H2
Method BLASTN
NCBI GI g22524
BLAST score 72
E value 2.0e-32
Match length 130
% identity 93
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)

Seq. No. 299336
Seq. ID LIB3152-046-P1-K1-A2
Method BLASTN
NCBI GI g168679
BLAST score 73
E value 5.0e-33
Match length 97
% identity 94
NCBI Description Maize 19 kDa zein mRNA, clone cz19C2, complete cds.
>gi_270687_gb_I03334_Sequence 9 from Patent US

Seq. No. 299337
Seq. ID LIB3152-046-P1-K1-E6
Method BLASTX
NCBI GI g121472
BLAST score 185
E value 7.0e-14
Match length 101
% identity 39
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 299338
Seq. ID LIB3152-046-P1-K1-F1
Method BLASTX
NCBI GI g72307
BLAST score 194
E value 6.0e-15
Match length 112
% identity 43

BIOEDIT

NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
(J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 299339
Seq. ID LIB3152-046-P1-K1-H2
Method BLASTX
NCBI GI g168701
BLAST score 289
E value 1.0e-32
Match length 116
% identity 75
NCBI Description (M60837) zein [Zea mays]

Seq. No. 299340
Seq. ID LIB3152-047-P1-K1-A9
Method BLASTN
NCBI GI g22524
BLAST score 277
E value 1.0e-154
Match length 325
% identity 98
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)

Seq. No. 299341
Seq. ID LIB3152-047-P1-K1-C2
Method BLASTN
NCBI GI g22445
BLAST score 141
E value 2.0e-73
Match length 149
% identity 99
NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. No. 299342
Seq. ID LIB3152-047-P1-K1-C4
Method BLASTX
NCBI GI g508545
BLAST score 176
E value 4.0e-27
Match length 106
% identity 73
NCBI Description (L34340) zein [Zea mays]

Seq. No. 299343
Seq. ID LIB3152-047-P1-K1-D2
Method BLASTX
NCBI GI g72307
BLAST score 161
E value 3.0e-21
Match length 107
% identity 65
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686
(J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 299344
Seq. ID LIB3152-047-P1-K1-E7
Method BLASTN

Q32000

NCBI GI	g22544
BLAST score	94
E value	1.0e-45
Match length	193
% identity	93
NCBI Description	Maize mRNA (clone A30) for zein (a plant storage protein)
Seq. No.	299345
Seq. ID	LIB3152-047-P1-K1-F6
Method	BLASTN
NCBI GI	g22522
BLAST score	237
E value	1.0e-130
Match length	319
% identity	94
NCBI Description	Zea mays gene encoding a zein (clone Z4)
Seq. No.	299346
Seq. ID	LIB3152-048-P1-K1-A11
Method	BLASTX
NCBI GI	g141617
BLAST score	394
E value	2.0e-38
Match length	110
% identity	67
NCBI Description	ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) >gi_100941_pir_S12140 zein Zc1 - maize >gi_100945_pir_B29017 zein 2 - maize >gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays] >gi_168666_(M16460) 16-kDa zein protein [Zea mays]
Seq. No.	299347
Seq. ID	LIB3152-048-P1-K1-C3
Method	BLASTX
NCBI GI	g2832246
BLAST score	287
E value	1.0e-25
Match length	96
% identity	65
NCBI Description	(AF031569) 22-kDa alpha zein 8 [Zea mays]
Seq. No.	299348
Seq. ID	LIB3152-048-P1-K1-C4
Method	BLASTX
NCBI GI	g2194132
BLAST score	179
E value	4.0e-13
Match length	129
% identity	36
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]
Seq. No.	299349
Seq. ID	LIB3152-048-P1-K1-D9
Method	BLASTX
NCBI GI	g100846
BLAST score	319
E value	1.0e-29

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Match length 89
% identity 75
NCBI Description 22K zein precursor (clone gZ22.8H3) - maize
>gi_22179_emb_CAA43399_ (X61085) 22 kD alpha-zein [Zea mays]

Seq. No. 299350
Seq. ID LIB3152-048-P1-K1-F4
Method BLASTX
NCBI GI g4519539
BLAST score 280
E value 6.0e-25
Match length 86
% identity 60
NCBI Description (AB016256) NAD-dependent sorbitol dehydrogenase [Malus domestica]

Seq. No. 299351
Seq. ID LIB3152-048-P1-K1-H10
Method BLASTN
NCBI GI g168704
BLAST score 171
E value 2.0e-91
Match length 351
% identity 84
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 299352
Seq. ID LIB3152-048-P1-K1-H12
Method BLASTX
NCBI GI g141605
BLAST score 202
E value 4.0e-16
Match length 80
% identity 59
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 299353
Seq. ID LIB3152-048-P1-K1-H4
Method BLASTX
NCBI GI g168695
BLAST score 262
E value 3.0e-23
Match length 67
% identity 69
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A zein gamma [Zea mays]

Seq. No. 299354
Seq. ID LIB3152-048-P1-K1-H9
Method BLASTX
NCBI GI g141603
BLAST score 452
E value 4.0e-45
Match length 95

% identity 98
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize.
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 299355
Seq. ID LIB3152-049-P1-K1-C1
Method BLASTN
NCBI GI g168694
BLAST score 110
E value 6.0e-55
Match length 162
% identity 92
NCBI Description Maize gamma zein mRNA, partial cds

Seq. No. 299356
Seq. ID LIB3152-049-P1-K1-C2
Method BLASTX
NCBI GI g141607
BLAST score 272
E value 5.0e-24
Match length 66
% identity 82
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
>gi_22521_emb_CAA24718_ (V01471) zein [Zea mays] >gi_168672
(J01244) zein 19 kd protein (partial) [Zea mays]

Seq. No. 299357
Seq. ID LIB3152-049-P1-K1-F6
Method BLASTN
NCBI GI g168681
BLAST score 292
E value 1.0e-163
Match length 371
% identity 97
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_ Sequence 8 from Patent US

Seq. No. 299358
Seq. ID LIB3152-049-P1-K1-F9
Method BLASTN
NCBI GI g22537
BLAST score 69
E value 1.0e-30
Match length 125
% identity 90
NCBI Description Maize mRNA for zein polypeptide (clone M6)

Seq. No. 299359
Seq. ID LIB3152-049-P1-K1-H6
Method BLASTN
NCBI GI g168480
BLAST score 78
E value 7.0e-36
Match length 146
% identity 88
NCBI Description Maize embryo globulin S allele (7S-like) mRNA, complete cds

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Seq. No.	299360
Seq. ID	LIB3152-049-P1-K1-H9
Method	BLASTX
NCBI GI	g141597
BLAST score	150
E value	3.0e-10
Match length	37
% identity	81
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30) >gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2] [Zea mays]
Seq. No.	299361
Seq. ID	LIB3152-050-P1-K1-B3
Method	BLASTX
NCBI GI	g141617
BLAST score	317
E value	2.0e-29
Match length	107
% identity	59
NCBI Description	ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) >gi_100941_pir_S12140 zein Zc1 - maize >gi_100945_pir_B29017 zein 2 - maize >gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays] >gi_168666_(M16460) 16-kDa zein protein [Zea mays]
Seq. No.	299362
Seq. ID	LIB3152-050-P1-K1-D10
Method	BLASTN
NCBI GI	g2832242
BLAST score	196
E value	1.0e-106
Match length	322
% identity	11
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	299363
Seq. ID	LIB3152-050-P1-K1-E5
Method	BLASTN
NCBI GI	g535019
BLAST score	73
E value	3.0e-33
Match length	85
% identity	48
NCBI Description	Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
Seq. No.	299364
Seq. ID	LIB3152-050-P1-K1-F4
Method	BLASTN
NCBI GI	g22548
BLAST score	194
E value	1.0e-105
Match length	194
% identity	100
NCBI Description	Maize chimeric zein/beta-phaseolin gene 3'end region

Seq. No. 299365
Seq. ID LIB3152-050-P1-K1-G5
Method BLASTN
NCBI GI g535019
BLAST score 52
E value 1.0e-20
Match length 76
% identity 46
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)

Seq. No. 299366
Seq. ID LIB3152-050-P1-K1-G8
Method BLASTX
NCBI GI g2911059
BLAST score 162
E value 3.0e-11
Match length 75
% identity 45
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 299367
Seq. ID LIB3152-050-P1-K1-H10
Method BLASTN
NCBI GI g22514
BLAST score 116
E value 1.0e-58
Match length 228
% identity 89
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 299368
Seq. ID LIB3152-051-P1-K1-A11
Method BLASTX
NCBI GI g168691
BLAST score 274
E value 2.0e-24
Match length 82
% identity 65
NCBI Description (M29628) zein [Zea mays]

Seq. No. 299369
Seq. ID LIB3152-051-P1-K1-A5
Method BLASTX
NCBI GI g141606
BLAST score 315
E value 4.0e-29
Match length 112
% identity 62
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
>gi_72309_pir_ZIZMD1 19K zein precursor (clone cZ19D1) -
maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]

Seq. No. 299370
Seq. ID LIB3152-051-P1-K1-C11
Method BLASTX
NCBI GI g168701

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BLAST score 303
E value 9.0e-28
Match length 93
% identity 72
NCBI Description (M60837) zein [Zea mays]

Seq. No. 299371
Seq. ID LIB3152-051-P1-K1-C12
Method BLASTX
NCBI GI g2832243
BLAST score 184
E value 2.0e-25
Match length 98
% identity 73
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 299372
Seq. ID LIB3152-051-P1-K1-C2
Method BLASTN
NCBI GI g22549
BLAST score 94
E value 2.0e-45
Match length 260
% identity 84
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 299373
Seq. ID LIB3152-051-P1-K1-D11
Method BLASTN
NCBI GI g2832242
BLAST score 118
E value 7.0e-60
Match length 226
% identity 12
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299374
Seq. ID LIB3152-051-P1-K1-D4
Method BLASTX
NCBI GI g141597
BLAST score 258
E value 2.0e-22
Match length 96
% identity 62
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 299375
Seq. ID LIB3152-051-P1-K1-F5
Method BLASTX
NCBI GI g2832243
BLAST score 198
E value 3.0e-15
Match length 104
% identity 54

Sequence Data

NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 299376
Seq. ID LIB3152-051-P1-K1-G3
Method BLASTX
NCBI GI g141604
BLAST score 231
E value 2.0e-19
Match length 89
% identity 58
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C1)
>gi_72310_pir_ZIZM91 19K zein precursor (clone cZ19C1) -
maize >gi_168678 (M12146) 19 kDa zein protein [Zea mays]

Seq. No. 299377
Seq. ID LIB3152-051-P1-K1-G7
Method BLASTX
NCBI GI g224513
BLAST score 145
E value 2.0e-11
Match length 74
% identity 61
NCBI Description zein M6 [Zea mays]

Seq. No. 299378
Seq. ID LIB3152-053-P1-K1-A8
Method BLASTN
NCBI GI g168681
BLAST score 39
E value 5.0e-13
Match length 115
% identity 83
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 299379
Seq. ID LIB3152-053-P1-K1-B1
Method BLASTX
NCBI GI g22220
BLAST score 249
E value 1.0e-21
Match length 70
% identity 76
NCBI Description (X55723) 22 kD zein [Zea mays]

Seq. No. 299380
Seq. ID LIB3152-053-P1-K1-B6
Method BLASTX
NCBI GI g141601
BLAST score 237
E value 6.0e-20
Match length 63
% identity 76
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
>gi_82657_pir_S03417 19K zein precursor (clone gZ19AB11) -
maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA
1 - 234) [Zea mays]

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Seq. No. 299381
Seq. ID LIB3152-053-P1-K1-B9
Method BLASTN
NCBI GI g340933
BLAST score 37
E value 9.0e-12
Match length 77
% identity 87
NCBI Description Zea mays 10-kDa zein gene, complete cds

Seq. No. 299382
Seq. ID LIB3152-053-P1-K1-D12
Method BLASTX
NCBI GI g168703
BLAST score 205
E value 1.0e-16
Match length 55
% identity 76
NCBI Description (M86591) 22 kDa zein protein [Zea mays]

Seq. No. 299383
Seq. ID LIB3152-053-P1-K1-D6
Method BLASTN
NCBI GI g168484
BLAST score 115
E value 4.0e-58
Match length 166
% identity 94
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 299384
Seq. ID LIB3152-053-P1-K1-E4
Method BLASTN
NCBI GI g2832242
BLAST score 159
E value 2.0e-84
Match length 191
% identity 11
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299385
Seq. ID LIB3152-053-P1-K1-F10
Method BLASTX
NCBI GI g3790102
BLAST score 276
E value 2.0e-26
Match length 110
% identity 57
NCBI Description (AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No. 299386
Seq. ID LIB3152-053-P1-K1-G4
Method BLASTN
NCBI GI g168661
BLAST score 96

Sequence Data

E value 2.0e-46
Match length 308
% identity 91
NCBI Description Maize 15 kDa zein mRNA, clone cZ15A3, complete cds

Seq. No. 299387
Seq. ID LIB3152-054-P1-K1-A10
Method BLASTN
NCBI GI g2393774
BLAST score 197
E value 1.0e-107
Match length 269
% identity 94
NCBI Description Zea mays endosperm-specific prolamin box binding factor (PBF) mRNA, complete cds

Seq. No. 299388
Seq. ID LIB3152-054-P1-K1-B2
Method BLASTX
NCBI GI g629861
BLAST score 289
E value 4.0e-26
Match length 85
% identity 74
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 299389
Seq. ID LIB3152-054-P1-K1-B6
Method BLASTN
NCBI GI g4140643
BLAST score 73
E value 4.0e-33
Match length 133
% identity 36
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299390
Seq. ID LIB3152-054-P1-K1-C8
Method BLASTN
NCBI GI g22445
BLAST score 142
E value 4.0e-74
Match length 310
% identity 86
NCBI Description Zea mays ZMPMS1 gene for 19 kDa zein protein

Seq. No. 299391
Seq. ID LIB3152-054-P1-K1-D9
Method BLASTN
NCBI GI g22516
BLAST score 72
E value 1.0e-32
Match length 128
% identity 89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

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Seq. No.	299392
Seq. ID	LIB3152-054-P1-K1-E2
Method	BLASTX
NCBI GI	g168699
BLAST score	564
E value	3.0e-58
Match length	123
% identity	95
NCBI Description	(M60836) zein [Zea mays]
Seq. No.	299393
Seq. ID	LIB3152-054-P1-K1-E3
Method	BLASTX
NCBI GI	g141608
BLAST score	195
E value	3.0e-15
Match length	47
% identity	81
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa zein [Zea mays]
Seq. No.	299394
Seq. ID	LIB3152-054-P1-K1-E5
Method	BLASTX
NCBI GI	g531829
BLAST score	156
E value	5.0e-11
Match length	61
% identity	59
NCBI Description	(U12390) beta-galactosidase alpha peptide [cloning vector pSport1]
Seq. No.	299395
Seq. ID	LIB3152-054-P1-K1-F2
Method	BLASTX
NCBI GI	g141608
BLAST score	223
E value	3.0e-18
Match length	56
% identity	86
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa zein [Zea mays]
Seq. No.	299396
Seq. ID	LIB3152-054-P1-K1-F3
Method	BLASTX
NCBI GI	g419803
BLAST score	275
E value	1.0e-24
Match length	89
% identity	57
NCBI Description	zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

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Seq. No. 299397
Seq. ID LIB3152-054-P1-K1-G6
Method BLASTN
NCBI GI g22514
BLAST score 205
E value 1.0e-111
Match length 312
% identity 92
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 299398
Seq. ID LIB3152-054-P1-K1-G7
Method BLASTX
NCBI GI g141615
BLAST score 171
E value 2.0e-12
Match length 56
% identity 71
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
>gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 299399
Seq. ID LIB3152-054-P1-K1-G9
Method BLASTX
NCBI GI g141605
BLAST score 317
E value 2.0e-29
Match length 90
% identity 78
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 299400
Seq. ID LIB3152-054-P1-K1-H2
Method BLASTN
NCBI GI g22540
BLAST score 137
E value 3.0e-71
Match length 156
% identity 98
NCBI Description Maize mRNA for 10kDa zein

Seq. No. 299401
Seq. ID LIB3152-054-P1-K1-H6
Method BLASTX
NCBI GI g141616
BLAST score 380
E value 9.0e-37
Match length 84
% identity 81
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 299402
Seq. ID LIB3152-056-P1-K1-B3
Method BLASTN

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NCBI GI g168675
BLAST score 246
E value 1.0e-136
Match length 336
% identity 94
NCBI Description Maize mutant zein (zE19) gene, complete cds

Seq. No. 299403
Seq. ID LIB3152-056-P1-K1-C6
Method BLASTN
NCBI GI g168681
BLAST score 227
E value 1.0e-125
Match length 320
% identity 93
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 299404
Seq. ID LIB3152-056-P1-K1-E6
Method BLASTN
NCBI GI g22514
BLAST score 293
E value 1.0e-164
Match length 335
% identity 97
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 299405
Seq. ID LIB3152-056-P1-K1-H6
Method BLASTX
NCBI GI g168664
BLAST score 233
E value 2.0e-19
Match length 90
% identity 53
NCBI Description (M13507) zein protein precursor [Zea mays]

Seq. No. 299406
Seq. ID LIB3152-057-P1-K1-A1
Method BLASTN
NCBI GI g22537
BLAST score 54
E value 6.0e-22
Match length 142
% identity 85
NCBI Description Maize mRNA for zein polypeptide (clone M6)

Seq. No. 299407
Seq. ID LIB3152-057-P1-K1-A2
Method BLASTX
NCBI GI g2832246
BLAST score 224
E value 7.0e-19
Match length 102
% identity 61
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

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Seq. No.	299408
Seq. ID	LIB3152-057-P1-K1-A3
Method	BLASTN
NCBI GI	g662367
BLAST score	83
E value	6.0e-39
Match length	159
% identity	88
NCBI Description	Zea mays farnesyl pyrophosphate synthetase (fps) mRNA, complete cds
Seq. No.	299409
Seq. ID	LIB3152-057-P1-K1-A6
Method	BLASTX
NCBI GI	g168699
BLAST score	223
E value	2.0e-18
Match length	68
% identity	68
NCBI Description	(M60836) zein [Zea mays]
Seq. No.	299410
Seq. ID	LIB3152-057-P1-K1-B1
Method	BLASTN
NCBI GI	g535019
BLAST score	64
E value	2.0e-27
Match length	96
% identity	37
NCBI Description	Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
Seq. No.	299411
Seq. ID	LIB3152-057-P1-K1-B10
Method	BLASTX
NCBI GI	g141603
BLAST score	144
E value	6.0e-09
Match length	52
% identity	73
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20) >gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
Seq. No.	299412
Seq. ID	LIB3152-057-P1-K1-B2
Method	BLASTX
NCBI GI	g141605
BLAST score	215
E value	1.0e-17
Match length	68
% identity	66
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2) >gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.	299413

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Seq. ID	LIB3152-057-P1-K1-B3
Method	BLASTX
NCBI GI	g508545
BLAST score	229
E value	6.0e-19
Match length	95
% identity	57
NCBI Description	(L34340) zein [Zea mays]
Seq. No.	299414
Seq. ID	LIB3152-057-P1-K1-B5
Method	BLASTX
NCBI GI	g224514
BLAST score	225
E value	1.0e-18
Match length	63
% identity	76
NCBI Description	zein M8 [Zea mays]
Seq. No.	299415
Seq. ID	LIB3152-057-P1-K1-B7
Method	BLASTX
NCBI GI	g629861
BLAST score	225
E value	1.0e-18
Match length	79
% identity	61
NCBI Description	zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203) zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.	299416
Seq. ID	LIB3152-057-P1-K1-B8
Method	BLASTN
NCBI GI	g168484
BLAST score	147
E value	5.0e-77
Match length	159
% identity	98
NCBI Description	Maize endosperm glutelin-2 gene, complete cds
Seq. No.	299417
Seq. ID	LIB3152-057-P1-K1-C2
Method	BLASTX
NCBI GI	g168699
BLAST score	393
E value	3.0e-38
Match length	102
% identity	79
NCBI Description	(M60836) zein [Zea mays]
Seq. No.	299418
Seq. ID	LIB3152-057-P1-K1-C4
Method	BLASTX
NCBI GI	g168699
BLAST score	185
E value	3.0e-14
Match length	73

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% identity 62
NCBI Description (M60836) zein [Zea mays]

Seq. No. 299419
Seq. ID LIB3152-057-P1-K1-C5
Method BLASTX
NCBI GI g72307
BLAST score 336
E value 2.0e-31
Match length 113
% identity 65
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686 (J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 299420
Seq. ID LIB3152-057-P1-K1-C6
Method BLASTX
NCBI GI g141603
BLAST score 235
E value 8.0e-20
Match length 81
% identity 68
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 299421
Seq. ID LIB3152-057-P1-K1-C7
Method BLASTX
NCBI GI g168701
BLAST score 150
E value 6.0e-10
Match length 74
% identity 49
NCBI Description (M60837) zein [Zea mays]

Seq. No. 299422
Seq. ID LIB3152-057-P1-K1-C8
Method BLASTX
NCBI GI g82659
BLAST score 294
E value 1.0e-26
Match length 75
% identity 79
NCBI Description 19K zein precursor (clone Z4) - maize
>gi_4388702_emb_CAA24719_ (V01472) zein [Zea mays]

Seq. No. 299423
Seq. ID LIB3152-057-P1-K1-D1
Method BLASTN
NCBI GI g22528
BLAST score 117
E value 3.0e-59
Match length 292
% identity 85
NCBI Description Zea mays mRNA encoding a zein (clone A20)

Seq. No. 299424
Seq. ID LIB3152-057-P1-K1-D10
Method BLASTX
NCBI GI g168693
BLAST score 359
E value 3.0e-34
Match length 114
% identity 67
NCBI Description (M29627) zein [Zea mays]

Seq. No. 299425
Seq. ID LIB3152-057-P1-K1-D5
Method BLASTN
NCBI GI g2828011
BLAST score 46
E value 5.0e-17
Match length 102
% identity 86
NCBI Description Zea mays starch synthase I precursor (Ss1) mRNA, nuclear gene encoding plastid protein, complete cds

Seq. No. 299426
Seq. ID LIB3152-057-P1-K1-D6
Method BLASTX
NCBI GI g141616
BLAST score 316
E value 4.0e-29
Match length 93
% identity 68
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 299427
Seq. ID LIB3152-057-P1-K1-D8
Method BLASTX
NCBI GI g168703
BLAST score 221
E value 4.0e-18
Match length 56
% identity 79
NCBI Description (M86591) 22 kDa zein protein [Zea mays]

Seq. No. 299428
Seq. ID LIB3152-057-P1-K1-E12
Method BLASTX
NCBI GI g2832243
BLAST score 152
E value 2.0e-10
Match length 42
% identity 67
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 299429
Seq. ID LIB3152-057-P1-K1-E2
Method BLASTX
NCBI GI g141617
BLAST score 257

E value 2.0e-22
Match length 108
% identity 52
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 299430
Seq. ID LIB3152-057-P1-K1-E3
Method BLASTN
NCBI GI g168679
BLAST score 47
E value 2.0e-17
Match length 127
% identity 84
NCBI Description Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
>gi_270687_gb_I03334_ Sequence 9 from Patent US

Seq. No. 299431
Seq. ID LIB3152-057-P1-K1-E4
Method BLASTX
NCBI GI g224508
BLAST score 273
E value 2.0e-24
Match length 79
% identity 76
NCBI Description zein A20 [Zea mays]

Seq. No. 299432
Seq. ID LIB3152-057-P1-K1-E5
Method BLASTX
NCBI GI g22216
BLAST score 271
E value 4.0e-24
Match length 67
% identity 79
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 299433
Seq. ID LIB3152-057-P1-K1-F11
Method BLASTX
NCBI GI g399414
BLAST score 159
E value 4.0e-11
Match length 39
% identity 85
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
>gi_322865_pir_JC1454 translation elongation factor eEF-1 alpha chain - wheat >gi_170776_ (M90077) translation elongation factor 1 alpha-subunit [Triticum aestivum]
>gi_949878_emb_CAA90651_ (Z50789) elongation factor 1-alpha [Hordeum vulgare]

Seq. No. 299434
Seq. ID LIB3152-057-P1-K1-F3

Method BLASTX
NCBI GI g16073
BLAST score 175
E value 9.0e-13
Match length 64
% identity 61
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 299435
Seq. ID LIB3152-057-P1-K1-F4
Method BLASTX
NCBI GI g2832243
BLAST score 167
E value 1.0e-11
Match length 90
% identity 44
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 299436
Seq. ID LIB3152-057-P1-K1-F7
Method BLASTX
NCBI GI g2832243
BLAST score 203
E value 4.0e-16
Match length 81
% identity 59
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 299437
Seq. ID LIB3152-057-P1-K1-F8
Method BLASTN
NCBI GI g2832242
BLAST score 38
E value 3.0e-12
Match length 173
% identity 81
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299438
Seq. ID LIB3152-057-P1-K1-H10
Method BLASTN
NCBI GI g168673
BLAST score 50
E value 2.0e-19
Match length 70
% identity 93
NCBI Description Maize 19 kDa zein mRNA, clone cz19B1, complete cds

Seq. No. 299439
Seq. ID LIB3153-004-Q1-K1-E5
Method BLASTN
NCBI GI g22516
BLAST score 51
E value 4.0e-20
Match length 143
% identity 84
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

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Seq. No. 299440
Seq. ID LIB3153-005-Q1-K1-B5
Method BLASTX
NCBI GI g70774
BLAST score 273
E value 2.0e-24
Match length 55
% identity 100
NCBI Description histone H4 (TH091) - wheat >gi_170747 (M12277) histone H4 [Triticum aestivum]

Seq. No. 299441
Seq. ID LIB3153-005-Q1-K1-E4
Method BLASTX
NCBI GI g119355
BLAST score 192
E value 3.0e-15
Match length 39
% identity 97
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
>gi_100869_pir_S16257 phosphopyruvate hydratase (EC
4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
[Zea mays]

Seq. No. 299442
Seq. ID LIB3153-005-Q1-K1-E8
Method BLASTN
NCBI GI g459896
BLAST score 54
E value 7.0e-22
Match length 86
% identity 91
NCBI Description Zea mays triosephosphate isomerase 1 gene, exon

Seq. No. 299443
Seq. ID LIB3153-005-Q1-K1-F3
Method BLASTX
NCBI GI g1084481
BLAST score 262
E value 2.0e-23
Match length 57
% identity 89
NCBI Description heat shock protein 70 - Maize

Seq. No. 299444
Seq. ID LIB3153-005-Q1-K1-G8
Method BLASTN
NCBI GI g168500
BLAST score 51
E value 4.0e-20
Match length 83
% identity 90
NCBI Description Maize (Zea mays) histone H4 gene (H4C14), complete cds

Seq. No. 299445

Seq. ID LIB3153-006-Q1-K1-B9
Method BLASTX
NCBI GI g129916
BLAST score 204
E value 2.0e-16
Match length 51
% identity 82
NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir_TVWTGY
phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
>gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
(AA 1 - 401) [Triticum aestivum]

Seq. No. 299446
Seq. ID LIB3153-006-Q1-K1-C4
Method BLASTX
NCBI GI g3746060
BLAST score 215
E value 3.0e-17
Match length 72
% identity 58
NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 299447
Seq. ID LIB3153-007-Q1-K1-D11
Method BLASTX
NCBI GI g141608
BLAST score 192
E value 2.0e-19
Match length 66
% identity 83
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 299448
Seq. ID LIB3153-008-Q1-K1-H7
Method BLASTX
NCBI GI g4115371
BLAST score 275
E value 8.0e-25
Match length 76
% identity 75
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 299449
Seq. ID LIB3153-009-Q1-K1-D4
Method BLASTX
NCBI GI g119355
BLAST score 240
E value 7.0e-21
Match length 47
% identity 100
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
>gi_100869_pir_S16257 phosphopyruvate hydratase (EC
4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
[Zea mays]

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Seq. No. 299450
Seq. ID LIB3153-009-Q1-K1-G11
Method BLASTX
NCBI GI g3445207
BLAST score 345
E value 9.0e-33
Match length 101
% identity 58
NCBI Description (AC004786) unknown protein [Arabidopsis thaliana]

Seq. No. 299451
Seq. ID LIB3153-010-Q1-K1-C1
Method BLASTX
NCBI GI g3128177
BLAST score 230
E value 3.0e-19
Match length 94
% identity 52
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 299452
Seq. ID LIB3153-010-Q1-K1-D4
Method BLASTX
NCBI GI g3914368
BLAST score 313
E value 3.0e-29
Match length 69
% identity 77
NCBI Description GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
>gi_167519 (M80571) glycerol-3-phosphate acyltransferase
[Cucumis sativus] >gi_444331_prf_1906380A glycerol
phosphate acyltransferase [Cucumis sativus]

Seq. No. 299453
Seq. ID LIB3153-011-Q1-K1-A4
Method BLASTN
NCBI GI g474009
BLAST score 54
E value 6.0e-22
Match length 110
% identity 87
NCBI Description Rice mRNA, partial homologous to ribosomal protein S19 gene

Seq. No. 299454
Seq. ID LIB3153-011-Q1-K1-C4
Method BLASTX
NCBI GI g3128231
BLAST score 202
E value 8.0e-16
Match length 134
% identity 12
NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]
>gi_3337370 (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 299455

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Seq. ID LIB3153-011-Q1-K1-D6
Method BLASTX
NCBI GI g3150406
BLAST score 242
E value 1.0e-20
Match length 97
% identity 48
NCBI Description (AC004165) putative indole-3-acetate
beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No. 299456
Seq. ID LIB3153-011-Q1-K1-G1
Method BLASTX
NCBI GI g1362009
BLAST score 390
E value 6.0e-38
Match length 85
% identity 50
NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No. 299457
Seq. ID LIB3153-011-Q1-K1-H5
Method BLASTX
NCBI GI g2982259
BLAST score 327
E value 9.0e-31
Match length 74
% identity 82
NCBI Description (AF051212) probable 60s ribosomal protein L13a [Picea
mariana]

Seq. No. 299458
Seq. ID LIB3153-012-Q1-K1-E3
Method BLASTX
NCBI GI g1169476
BLAST score 566
E value 2.0e-58
Match length 116
% identity 93
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632)
vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No. 299459
Seq. ID LIB3153-012-Q1-K1-F12
Method BLASTX
NCBI GI g3135274
BLAST score 323
E value 5.0e-30
Match length 102
% identity 59
NCBI Description (AC003058) putative beta-1,3-endoglucanase [Arabidopsis
thaliana]

Seq. No. 299460
Seq. ID LIB3153-013-Q1-K1-D7
Method BLASTN

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NCBI GI	g3821780
BLAST score	36
E value	8.0e-11
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	299461
Seq. ID	LIB3154-001-Q1-K1-A12
Method	BLASTX
NCBI GI	g1169475
BLAST score	665
E value	8.0e-74
Match length	146
% identity	99
NCBI Description	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR TU) (EF-TU) >gi_556301 (M22432) elongation factor Tu [Mus musculus]
Seq. No.	299462
Seq. ID	LIB3154-001-Q1-K1-A2
Method	BLASTN
NCBI GI	g163349
BLAST score	33
E value	4.0e-09
Match length	33
% identity	100
NCBI Description	Bovine MHC class I BoLA gene, complete cds, clone BL3-6
Seq. No.	299463
Seq. ID	LIB3154-001-Q1-K1-A4
Method	BLASTX
NCBI GI	g2501654
BLAST score	701
E value	3.0e-74
Match length	152
% identity	88
NCBI Description	VILLIN >gi_202366 (M98454) villin [Mus musculus]
Seq. No.	299464
Seq. ID	LIB3154-001-Q1-K1-B10
Method	BLASTX
NCBI GI	g3068759
BLAST score	232
E value	2.0e-19
Match length	50
% identity	92
NCBI Description	(AF059185) Mi-2 [Xenopus laevis]
Seq. No.	299465
Seq. ID	LIB3154-001-Q1-K1-B11
Method	BLASTN
NCBI GI	g353
BLAST score	173
E value	8.0e-93
Match length	197
% identity	97

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NCBI Description Bovine mRNA encoding fibromodulin.

Seq. No. 299466
Seq. ID LIB3154-001-Q1-K1-B3
Method BLASTN
NCBI GI g2981246
BLAST score 40
E value 4.0e-13
Match length 52
% identity 94
NCBI Description Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC library) contains Bmx gene, complete sequence [Homo sapiens]

Seq. No. 299467
Seq. ID LIB3154-001-Q1-K1-B6
Method BLASTN
NCBI GI g163460
BLAST score 123
E value 4.0e-63
Match length 127
% identity 99
NCBI Description Bovine osteonectin mRNA, complete cds

Seq. No. 299468
Seq. ID LIB3154-001-Q1-K1-C10
Method BLASTX
NCBI GI g4506515
BLAST score 541
E value 2.0e-55
Match length 115
% identity 91
NCBI Description regulator of G-protein signalling 1
>gi_728728_sp_Q08116_RGS1_HUMAN REGULATOR OF G-PROTEIN SIGNALING 1 (RGS1) (EARLY RESPONSE PROTEIN 1R20) (B-CELL ACTIVATION PROTEIN BL34) >gi_631051_pir_S43436 B-cell activation protein 1r20 - human >gi_313215_emb_CAA51826_(X73427) 1r20 [Homo sapiens]

Seq. No. 299469
Seq. ID LIB3154-001-Q1-K1-C11
Method BLASTX
NCBI GI g4503483
BLAST score 650
E value 2.0e-68
Match length 128
% identity 95
NCBI Description eukaryotic translation elongation factor 2
>gi_119172_sp_P13639_EF2_HUMAN ELONGATION FACTOR 2 (EF-2)
>gi_2144947_pir_EFHU2 translation elongation factor eEF-2 - human >gi_31106_emb_CAA35829_(X51466) elongation factor 2 [Homo sapiens] >gi_31108_emb_CAA77750_(Z11692) human elongation factor 2 [Homo sapiens]

Seq. No. 299470
Seq. ID LIB3154-001-Q1-K1-C12
Method BLASTX

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NCBI GI	g3242231
BLAST score	155
E value	3.0e-10
Match length	33
% identity	88
NCBI Description	(AJ006486) RNA binding protein [Mus musculus]
Seq. No.	299471
Seq. ID	LIB3154-001-Q1-K1-C3
Method	BLASTN
NCBI GI	g1276618
BLAST score	34
E value	8.0e-10
Match length	98
% identity	84
NCBI Description	Bos taurus clone 14 immunoglobulin lambda light chain variable region (Vlambda1b) mRNA, partial cds
Seq. No.	299472
Seq. ID	LIB3154-001-Q1-K1-C5
Method	BLASTN
NCBI GI	g1848270
BLAST score	55
E value	5.0e-22
Match length	83
% identity	92
NCBI Description	Human calcium and integrin binding protein CIB mRNA, complete cds
Seq. No.	299473
Seq. ID	LIB3154-001-Q1-K1-C6
Method	BLASTX
NCBI GI	g2460124
BLAST score	609
E value	1.0e-63
Match length	126
% identity	97
NCBI Description	(AF017789) putative transcription factor CA150 [Homo sapiens]
Seq. No.	299474
Seq. ID	LIB3154-001-Q1-K1-D1
Method	BLASTX
NCBI GI	g4557387
BLAST score	702
E value	2.0e-74
Match length	147
% identity	82
NCBI Description	complement component 7 precursor >gi_116610_sp_P10643_CO7_HUMAN COMPLEMENT COMPONENT C7 PRECURSOR >gi_87197_pir_A27340 complement C7 precursor - human >gi_179716 (J03507) complement protein C7 precursor [Homo sapiens]
Seq. No.	299475
Seq. ID	LIB3154-001-Q1-K1-D10
Method	BLASTX

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NCBI GI g2494890
BLAST score 485
E value 6.0e-49
Match length 87
% identity 100
NCBI Description CORONIN-LIKE PROTEIN P57 >gi_2136796_pir_S65666 p57
protein - bovine >gi_927647_dbj_BAA07939_ (D44496) bovine
p57 [Bos taurus]

Seq. No. 299476
Seq. ID LIB3154-001-Q1-K1-D11
Method BLASTX
NCBI GI g1665859
BLAST score 470
E value 2.0e-47
Match length 92
% identity 93
NCBI Description (Y09205) MHC class I molecule [Bos taurus]

Seq. No. 299477
Seq. ID LIB3154-001-Q1-K1-D12
Method BLASTN
NCBI GI g3688100
BLAST score 85
E value 6.0e-40
Match length 417
% identity 87
NCBI Description Homo sapiens chromosome 17, clone hRPK.178_C_3, complete
sequence [Homo sapiens]

Seq. No. 299478
Seq. ID LIB3154-001-Q1-K1-D4
Method BLASTX
NCBI GI g3820482
BLAST score 260
E value 2.0e-22
Match length 55
% identity 93
NCBI Description (AF032922) syntaxin 4 binding protein UNC-18c [Homo
sapiens]

Seq. No. 299479
Seq. ID LIB3154-001-Q1-K1-D7
Method BLASTX
NCBI GI g123332
BLAST score 700
E value 4.0e-74
Match length 137
% identity 94
NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE, CYTOPLASMIC (HMG-COA
SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
>gi_90200_pir_A25332 hydroxymethylglutaryl-CoA synthase
(EC 4.1.3.5) - Chinese hamster >gi_387072 (L00334)
3-hydroxy-3-methylglutaryl coenzyme A synthase (HMG CoA)
[Mesocricetus auratus]

Seq. No. 299480

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Seq. ID LIB3154-001-Q1-K1-D9
Method BLASTX
NCBI GI g2134796
BLAST score 260
E value 2.0e-22
Match length 57
% identity 84
NCBI Description B cell activation protein BL34 - human
>gi_299705_bbs_129951 (S59049) BL34=B cell activation gene
[human, Peptide, 196 aa] [Homo sapiens]

Seq. No. 299481
Seq. ID LIB3154-001-Q1-K1-E1
Method BLASTX
NCBI GI g731046
BLAST score 605
E value 5.0e-63
Match length 126
% identity 89
NCBI Description PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME) (KIAA0055)
>gi_473945_dbj_BAA06225 (D29956) This gene is similar to tre oncogene(X63547). [Homo sapiens]

Seq. No. 299482
Seq. ID LIB3154-001-Q1-K1-E2
Method BLASTX
NCBI GI g399012
BLAST score 618
E value 2.0e-64
Match length 121
% identity 100
NCBI Description ADP,ATP CARRIER PROTEIN, ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
>gi_280900_pir_B43646 ADP,ATP carrier protein T2 - bovine
>gi_529417 (M24103) translocase [Bos taurus]

Seq. No. 299483
Seq. ID LIB3154-001-Q1-K1-E3
Method BLASTN
NCBI GI g2582198
BLAST score 45
E value 4.0e-16
Match length 57
% identity 95
NCBI Description Bos taurus locus UW76 polymorphic microsatellite

Seq. No. 299484
Seq. ID LIB3154-001-Q1-K1-E4
Method BLASTN
NCBI GI g178996
BLAST score 99
E value 3.0e-48
Match length 195
% identity 89
NCBI Description Human arginine-rich nuclear protein mRNA, complete cds

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Seq. No.	299485
Seq. ID	LIB3154-001-Q1-K1-E6
Method	BLASTX
NCBI GI	g2353754
BLAST score	315
E value	6.0e-29
Match length	125
% identity	51
NCBI Description	(AF015504) immunoglobulin variable region [Bos taurus]
Seq. No.	299486
Seq. ID	LIB3154-001-Q1-K1-E7
Method	BLASTX
NCBI GI	g3914346
BLAST score	500
E value	1.0e-50
Match length	108
% identity	87
NCBI Description	POLYMERIC-IMMUNOGLOBULIN RECEPTOR PRECURSOR (PLGR) [CONTAINS: SECRETORY COMPONENT] >gi_388280 (L04797) polymeric immunoglobulin receptor [Bos taurus] >gi_1095524_prf_2109248A polymeric Ig receptor [Bos taurus]
Seq. No.	299487
Seq. ID	LIB3154-001-Q1-K1-F1
Method	BLASTX
NCBI GI	g120742
BLAST score	406
E value	7.0e-41
Match length	114
% identity	80
NCBI Description	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi_68446_pir_NUPG glucose-6-phosphate isomerase (EC 5.3.1.9) - pig >gi_2043_emb_CAA30295_ (X07382) muscle phosphohexose isomerase (AA 1 - 558) [Sus scrofa]
Seq. No.	299488
Seq. ID	LIB3154-001-Q1-K1-F10
Method	BLASTX
NCBI GI	g432627
BLAST score	567
E value	2.0e-60
Match length	149
% identity	81
NCBI Description	(X62917) anti-testosterone antibody [Bos taurus]
Seq. No.	299489
Seq. ID	LIB3154-001-Q1-K1-F12
Method	BLASTX
NCBI GI	g4240299
BLAST score	723
E value	8.0e-77
Match length	149
% identity	95

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NCBI Description (AB020712) KIAA0905 protein [Homo sapiens]

Seq. No. 299490
Seq. ID LIB3154-001-Q1-K1-F3
Method BLASTX
NCBI GI g3915129
BLAST score 652
E value 2.0e-68
Match length 150
% identity 86
NCBI Description TRANSMEMBRANE PROTEIN TMP21 PRECURSOR (INTEGRAL MEMBRANE PROTEIN P23) >gi_1370279_emb_CAA66947_ (X98303)
transmembrane protein [Oryctolagus cuniculus]

Seq. No. 299491
Seq. ID LIB3154-001-Q1-K1-F4
Method BLASTX
NCBI GI g2146954
BLAST score 411
E value 3.0e-40
Match length 151
% identity 60
NCBI Description hevin precursor - human >gi_758066_emb_CAA57650_ (X82157)
hevin [Homo sapiens]

Seq. No. 299492
Seq. ID LIB3154-001-Q1-K1-F7
Method BLASTN
NCBI GI g2864757
BLAST score 112
E value 5.0e-56
Match length 313
% identity 88
NCBI Description Bos taurus gene for MHC class I heavy chain, partial cds,
clone 303F.10g

Seq. No. 299493
Seq. ID LIB3154-001-Q1-K1-F9
Method BLASTN
NCBI GI g3360459
BLAST score 91
E value 1.0e-43
Match length 297
% identity 87
NCBI Description Homo sapiens clone 24733 mRNA sequence

Seq. No. 299494
Seq. ID LIB3154-001-Q1-K1-G1
Method BLASTX
NCBI GI g1905974
BLAST score 333
E value 4.0e-31
Match length 78
% identity 82
NCBI Description (U80628) thymidine kinase 2 isoform B [Homo sapiens]

Seq. No. 299495

Seq. ID LIB3154-001-Q1-K1-G11
 Method BLASTN
 NCBI GI g1374680
 BLAST score 315
 E value 1.0e-177
 Match length 315
 % identity 100
 NCBI Description Bovine mRNA for invariant chain, complete cds

Seq. No. 299496
 Seq. ID LIB3154-001-Q1-K1-G3
 Method BLASTX
 NCBI GI g1209255
 BLAST score 351
 E value 3.0e-33
 Match length 71
 % identity 92
 NCBI Description (L20311) immunoglobulin J-chain [Bos taurus] >gi_1408167
 (U02301) immunoglobulin J chain [Bos taurus]

Seq. No. 299497
 Seq. ID LIB3154-001-Q1-K1-G5
 Method BLASTX
 NCBI GI g2429083
 BLAST score 469
 E value 5.0e-47
 Match length 89
 % identity 96
 NCBI Description (D89730) T16 [Rattus rattus]

Seq. No. 299498
 Seq. ID LIB3154-001-Q1-K1-G6
 Method BLASTX
 NCBI GI g1345649
 BLAST score 253
 E value 1.0e-27
 Match length 89
 % identity 71
 NCBI Description PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR
 >gi_71411_pir_CGHU4B collagen alpha 1(IV) chain precursor
 - human >gi_180803 (M26576) alpha-1 type IV collagen [Homo sapiens]

Seq. No. 299499
 Seq. ID LIB3154-001-Q1-K1-G7
 Method BLASTX
 NCBI GI g547902
 BLAST score 185
 E value 1.0e-13
 Match length 50
 % identity 68
 NCBI Description PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24
 (MULTI-GLYCOSYLATED CORE PROTEIN 24) (MGC-24) (MUC-24)
 (CD164 ANTIGEN) >gi_422794_pir_JX0235 core protein MGC-24
 - human >gi_219925_dbj_BAA03130_ (D14043) MGC-24 precursor
 [Homo sapiens]

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Seq. No.	299500
Seq. ID	LIB3154-001-Q1-K1-G9
Method	BLASTX
NCBI GI	g2088714
BLAST score	269
E value	1.0e-23
Match length	147
% identity	37
NCBI Description	(AF003139) strong similarity to NADPH oxidases; partial CDS, the gene begins in the neighboring clone [Caenorhabditis elegans]
Seq. No.	299501
Seq. ID	LIB3154-001-Q1-K1-H12
Method	BLASTN
NCBI GI	g181154
BLAST score	136
E value	2.0e-70
Match length	200
% identity	93
NCBI Description	Human casein kinase II beta subunit mRNA, complete cds
Seq. No.	299502
Seq. ID	LIB3154-001-Q1-K1-H5
Method	BLASTX
NCBI GI	g3831588
BLAST score	208
E value	4.0e-17
Match length	55
% identity	75
NCBI Description	(AF064741) carboxylesterase [Sus scrofa]
Seq. No.	299503
Seq. ID	LIB3154-001-Q1-K1-H7
Method	BLASTN
NCBI GI	g3882158
BLAST score	192
E value	1.0e-104
Match length	394
% identity	87
NCBI Description	Homo sapiens mRNA for KIAA0719 protein, complete cds
Seq. No.	299504
Seq. ID	LIB3154-001-Q1-K1-H8
Method	BLASTX
NCBI GI	g128905
BLAST score	211
E value	9.0e-17
Match length	45
% identity	100
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 9 KD SUBUNIT PRECURSOR (COMPLEX I-9KD) (CI-9KD) >gi_108827_pir_S15107 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 10K chain - bovine >gi_220_emb_CAA41775_(X59048) NADH dehydrogenase (ubiquinone) [Bos taurus]
Seq. No.	299505

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Seq. ID	LIB3154-002-Q1-K1-C1
Method	BLASTX
NCBI GI	g141601
BLAST score	343
E value	3.0e-32
Match length	137
% identity	58
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11) >gi_82657_pir_S03417 19K zein precursor (clone gZ19AB11) - maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA 1 - 234) [Zea mays]
Seq. No.	299506
Seq. ID	LIB3154-003-Q1-K1-D1
Method	BLASTX
NCBI GI	g419803
BLAST score	204
E value	3.0e-16
Match length	95
% identity	44
NCBI Description	zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
Seq. No.	299507
Seq. ID	LIB3154-003-Q1-K1-E2
Method	BLASTX
NCBI GI	g141612
BLAST score	165
E value	1.0e-11
Match length	62
% identity	60
NCBI Description	ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2) >gi_72306_pir_ZIZMC2 22K zein precursor (clone cZ22C2) - maize (fragment) >gi_168688 (M12141) 22 kDa zein protein [Zea mays]
Seq. No.	299508
Seq. ID	LIB3154-003-Q1-K1-F8
Method	BLASTN
NCBI GI	g22531
BLAST score	147
E value	5.0e-77
Match length	350
% identity	86
NCBI Description	Zea mays mRNA encoding a zein (clone pZ22.1) >gi_270688_gb_I03336_ Sequence 10 from Patent US 4885357 >gi_270741_gb_I03273_ Sequence 2 from Patent US
Seq. No.	299509
Seq. ID	LIB3154-004-Q1-K1-A9
Method	BLASTX
NCBI GI	g168699
BLAST score	192
E value	1.0e-14
Match length	85
% identity	59
NCBI Description	(M60836) zein [Zea mays]

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Seq. No. 299510
Seq. ID LIB3154-004-Q1-K1-B1
Method BLASTN
NCBI GI g22544
BLAST score 215
E value 1.0e-117
Match length 303
% identity 93
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 299511
Seq. ID LIB3154-004-Q1-K1-B12
Method BLASTX
NCBI GI g971143
BLAST score 149
E value 4.0e-10
Match length 55
% identity 60
NCBI Description (D63842) modified alpha peptide of E. coli
beta-galactosidase [Cloning vector pKF298]
>gi_971155_dbj_BAA09909_ (D63846) modified alpha peptide of
E. coli beta-galactosidase [Cloning vector pKF18k]
>gi_3953639_dbj_BAA34741_ (AB019603) beta-galactosidase
alpha-peptide [Cloning vector pKF28wt]
>gi_3953643_dbj_BAA34744_ (AB019604) beta-galactosidase
alpha-peptide [Cloning vector pKF28ts1]
>gi_3953647_dbj_BAA34747_ (AB019605) beta-galactosidase
alpha-peptide [Cloning vector pKF28ts5]

Seq. No. 299512
Seq. ID LIB3154-004-Q1-K1-B7
Method BLASTN
NCBI GI g2832242
BLAST score 35
E value 3.0e-10
Match length 63
% identity 89
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299513
Seq. ID LIB3154-004-Q1-K1-D7
Method BLASTX
NCBI GI g121472
BLAST score 167
E value 1.0e-11
Match length 101
% identity 40
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb CAA37594_ (X53514) zein Zc2 [Zea
mays] >gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 299514
Seq. ID LIB3154-004-Q1-K1-E5

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Method	BLASTX
NCBI GI	g141614
BLAST score	144
E value	4.0e-09
Match length	63
% identity	51
NCBI Description	ZEIN-ALPHA PRECURSOR (22 KD) (CLONE ZA1 OR M1) >gi_82662_pir_B22831 22K zein precursor (clone M1) - maize >gi_22527_emb_CAA24722_ (V01475) reading frame zein [Zea mays] >gi_224510_prf_1107201D zein M1 [Zea mays]
Seq. No.	299515
Seq. ID	LIB3154-004-Q1-K1-E9
Method	BLASTX
NCBI GI	g2832243
BLAST score	354
E value	1.0e-33
Match length	116
% identity	65
NCBI Description	(AF031569) 22-kDa alpha zein 4 [Zea mays]
Seq. No.	299516
Seq. ID	LIB3154-004-Q1-K1-F4
Method	BLASTX
NCBI GI	g168699
BLAST score	306
E value	5.0e-28
Match length	83
% identity	80
NCBI Description	(M60836) zein [Zea mays]
Seq. No.	299517
Seq. ID	LIB3154-004-Q1-K1-G1
Method	BLASTX
NCBI GI	g141608
BLAST score	274
E value	1.0e-29
Match length	107
% identity	71
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa zein [Zea mays]
Seq. No.	299518
Seq. ID	LIB3154-005-Q1-K1-A1
Method	BLASTN
NCBI GI	g22514
BLAST score	58
E value	5.0e-24
Match length	190
% identity	83
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.	299519
Seq. ID	LIB3154-005-Q1-K1-A2
Method	BLASTN
NCBI GI	g168690

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BLAST score	91
E value	1.0e-43
Match length	91
% identity	100
NCBI Description	Maize zein mRNA, complete cds, clone ZG124
Seq. No.	299520
Seq. ID	LIB3154-005-Q1-K1-A6
Method	BLASTX
NCBI GI	g82660
BLAST score	286
E value	1.0e-25
Match length	104
% identity	60
NCBI Description	19K zein precursor (clone ZG31A) - maize (fragment) >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
Seq. No.	299521
Seq. ID	LIB3154-005-Q1-K1-B11
Method	BLASTX
NCBI GI	g419803
BLAST score	226
E value	4.0e-19
Match length	62
% identity	69
NCBI Description	zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
Seq. No.	299522
Seq. ID	LIB3154-005-Q1-K1-B6
Method	BLASTX
NCBI GI	g168664
BLAST score	209
E value	1.0e-16
Match length	110
% identity	47
NCBI Description	(M13507) zein protein precursor [Zea mays]
Seq. No.	299523
Seq. ID	LIB3154-005-Q1-K1-C5
Method	BLASTX
NCBI GI	g168699
BLAST score	468
E value	5.0e-47
Match length	132
% identity	77
NCBI Description	(M60836) zein [Zea mays]
Seq. No.	299524
Seq. ID	LIB3154-005-Q1-K1-E8
Method	BLASTX
NCBI GI	g141597
BLAST score	396
E value	1.0e-38
Match length	105
% identity	78
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)

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>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 299525
Seq. ID LIB3154-005-Q1-K1-E9
Method BLASTX
NCBI GI g100925
BLAST score 203
E value 3.0e-16
Match length 67
% identity 55
NCBI Description zein, 27K - maize (fragment) >gi_22550_emb_CAA41175_
(X58197) 27kDa storage protein, zein [Zea mays]

Seq. No. 299526
Seq. ID LIB3154-005-Q1-K1-G3
Method BLASTX
NCBI GI g2262105
BLAST score 186
E value 6.0e-14
Match length 74
% identity 49
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 299527
Seq. ID LIB3154-005-Q1-K1-G6
Method BLASTX
NCBI GI g168699
BLAST score 202
E value 9.0e-16
Match length 60
% identity 72
NCBI Description (M60836) zein [Zea mays]

Seq. No. 299528
Seq. ID LIB3154-005-Q1-K1-H1
Method BLASTX
NCBI GI g531829
BLAST score 185
E value 5.0e-14
Match length 81
% identity 51
NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector
pSport1]

Seq. No. 299529
Seq. ID LIB3154-005-Q1-K1-H9
Method BLASTN
NCBI GI g22537
BLAST score 127
E value 2.0e-65
Match length 175
% identity 68
NCBI Description Maize mRNA for zein polypeptide (clone M6)

Seq. No. 299530

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Seq. ID LIB3154-006-Q1-K1-C12
Method BLASTX
NCBI GI g82660
BLAST score 190
E value 6.0e-18
Match length 91
% identity 62
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 299531
Seq. ID LIB3154-006-Q1-K1-C3
Method BLASTN
NCBI GI g168704
BLAST score 87
E value 3.0e-41
Match length 161
% identity 91
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 299532
Seq. ID LIB3154-006-Q1-K1-E5
Method BLASTX
NCBI GI g224508
BLAST score 360
E value 2.0e-34
Match length 103
% identity 75
NCBI Description zein A20 [Zea mays]

Seq. No. 299533
Seq. ID LIB3154-007-Q1-K1-C1
Method BLASTN
NCBI GI g168425
BLAST score 187
E value 1.0e-101
Match length 215
% identity 97
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 299534
Seq. ID LIB3154-007-Q1-K1-C4
Method BLASTX
NCBI GI g141603
BLAST score 418
E value 4.0e-41
Match length 115
% identity 79
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 299535
Seq. ID LIB3154-007-Q1-K1-D6
Method BLASTX
NCBI GI g224508
BLAST score 338

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E value 8.0e-32
Match length 81
% identity 89
NCBI Description zein A20 [Zea mays]

Seq. No. 299536
Seq. ID LIB3154-007-Q1-K1-E3
Method BLASTX
NCBI GI g419803
BLAST score 196
E value 2.0e-15
Match length 80
% identity 53
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 299537
Seq. ID LIB3154-007-Q1-K1-E6
Method BLASTX
NCBI GI g168691
BLAST score 273
E value 3.0e-24
Match length 99
% identity 58
NCBI Description (M29628) zein [Zea mays]

Seq. No. 299538
Seq. ID LIB3154-007-Q1-K1-E8
Method BLASTX
NCBI GI g121472
BLAST score 140
E value 4.0e-18
Match length 69
% identity 68
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 299539
Seq. ID LIB3154-007-Q1-K1-E9
Method BLASTN
NCBI GI g4140643
BLAST score 71
E value 9.0e-32
Match length 231
% identity 58
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
complete sequence

Seq. No. 299540
Seq. ID LIB3154-007-Q1-K1-F6
Method BLASTX
NCBI GI g141617
BLAST score 356

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E value	5.0e-34
Match length	106
% identity	62
NCBI Description	ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) >gi_100941_pir_S12140 zein Zc1 - maize >gi_100945_pir_B29017 zein 2 - maize >gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays] >gi_168666_(M16460) 16-kDa zein protein [Zea mays]
Seq. No.	299541
Seq. ID	LIB3154-007-Q1-K1-G1
Method	BLASTN
NCBI GI	g22516
BLAST score	111
E value	1.0e-55
Match length	219
% identity	88
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)
Seq. No.	299542
Seq. ID	LIB3154-007-Q1-K1-G6
Method	BLASTN
NCBI GI	g168665
BLAST score	162
E value	5.0e-86
Match length	346
% identity	87
NCBI Description	Maize 16-kDa zein-2 mRNA, complete cds
Seq. No.	299543
Seq. ID	LIB3154-008-Q1-K1-B12
Method	BLASTN
NCBI GI	g168690
BLAST score	43
E value	4.0e-15
Match length	91
% identity	87
NCBI Description	Maize zein mRNA, complete cds, clone ZG124
Seq. No.	299544
Seq. ID	LIB3154-010-Q1-K1-A7
Method	BLASTN
NCBI GI	g535019
BLAST score	43
E value	6.0e-15
Match length	53
% identity	48
NCBI Description	Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
Seq. No.	299545
Seq. ID	LIB3154-010-Q1-K1-B1
Method	BLASTN
NCBI GI	g168673
BLAST score	156
E value	2.0e-82
Match length	189
% identity	97

NCBI Description Maize 19 kDa zein mRNA, clone cz19B1, complete cds

Seq. No. 299546
Seq. ID LIB3154-010-Q1-K1-B6
Method BLASTX
NCBI GI g141608
BLAST score 143
E value 5.0e-09
Match length 46
% identity 63
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 299547
Seq. ID LIB3154-010-Q1-K1-C3
Method BLASTX
NCBI GI g2832243
BLAST score 203
E value 7.0e-16
Match length 40
% identity 100
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 299548
Seq. ID LIB3154-010-Q1-K1-F5
Method BLASTX
NCBI GI g1182065
BLAST score 198
E value 3.0e-15
Match length 53
% identity 77
NCBI Description (X55661) 22 kD zein [Zea mays]

Seq. No. 299549
Seq. ID LIB3154-010-Q1-K1-F6
Method BLASTN
NCBI GI g168690
BLAST score 54
E value 2.0e-21
Match length 62
% identity 98
NCBI Description Maize zein mRNA, complete cds, clone ZG124

Seq. No. 299550
Seq. ID LIB3154-010-Q1-K1-G5
Method BLASTX
NCBI GI g508545
BLAST score 168
E value 7.0e-12
Match length 49
% identity 73
NCBI Description (L34340) zein [Zea mays]

Seq. No. 299551
Seq. ID LIB3154-010-Q1-K1-H8
Method BLASTX

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NCBI GI g141597
BLAST score 192
E value 1.0e-14
Match length 49
% identity 76
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 299552
Seq. ID LIB3154-011-Q1-K1-C12
Method BLASTN
NCBI GI g1037129
BLAST score 308
E value 1.0e-173
Match length 392
% identity 95
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 299553
Seq. ID LIB3154-011-Q1-K1-D4
Method BLASTX
NCBI GI g82654
BLAST score 161
E value 2.0e-11
Match length 53
% identity 60
NCBI Description 10K zein precursor - maize >gi_22541_emb_CAA30409_ (X07535)
10kDa zein (AA 1 - 150) [Zea mays]

Seq. No. 299554
Seq. ID LIB3154-011-Q1-K1-F9
Method BLASTX
NCBI GI g141608
BLAST score 251
E value 2.0e-21
Match length 103
% identity 54
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655
zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa
zein [Zea mays]

Seq. No. 299555
Seq. ID LIB3154-011-Q1-K1-G7
Method BLASTX
NCBI GI g141601
BLAST score 168
E value 7.0e-12
Match length 66
% identity 62
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
>gi_82657_pir_S03417 19K zein precursor (clone gZ19AB11) -
maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA
1 - 234) [Zea mays]

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Seq. No.	299556
Seq. ID	LIB3154-013-Q1-K1-A1
Method	BLASTN
NCBI GI	g22514
BLAST score	69
E value	1.0e-30
Match length	264
% identity	81
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.	299557
Seq. ID	LIB3154-013-Q1-K1-B12
Method	BLASTN
NCBI GI	g22514
BLAST score	67
E value	2.0e-29
Match length	255
% identity	82
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.	299558
Seq. ID	LIB3154-013-Q1-K1-B6
Method	BLASTN
NCBI GI	g1061304
BLAST score	54
E value	7.0e-22
Match length	142
% identity	85
NCBI Description	Z.mays ZSF4C5 gene for zein
Seq. No.	299559
Seq. ID	LIB3154-013-Q1-K1-C5
Method	BLASTX
NCBI GI	g2832247
BLAST score	267
E value	2.0e-23
Match length	87
% identity	66
NCBI Description	(AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.	299560
Seq. ID	LIB3154-013-Q1-K1-C7
Method	BLASTN
NCBI GI	g22514
BLAST score	252
E value	1.0e-139
Match length	340
% identity	94
NCBI Description	Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.	299561
Seq. ID	LIB3154-013-Q1-K1-E1
Method	BLASTX
NCBI GI	g419803
BLAST score	278
E value	9.0e-25
Match length	108

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% identity 53
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 299562
Seq. ID LIB3154-013-Q1-K1-E5
Method BLASTX
NCBI GI g4519539
BLAST score 207
E value 2.0e-16
Match length 86
% identity 52
NCBI Description (AB016256) NAD-dependent sorbitol dehydrogenase [Malus domestica]

Seq. No. 299563
Seq. ID LIB3154-013-Q1-K1-G1
Method BLASTX
NCBI GI g141603
BLAST score 476
E value 6.0e-48
Match length 119
% identity 85
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20)
>gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize
>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

Seq. No. 299564
Seq. ID LIB3154-014-Q1-K1-B2
Method BLASTN
NCBI GI g168652
BLAST score 114
E value 2.0e-57
Match length 261
% identity 90
NCBI Description Maize amyloplast-specific transit protein (waxy; wx+ locus), complete cds

Seq. No. 299565
Seq. ID LIB3154-014-Q1-K1-C4
Method BLASTX
NCBI GI g567893
BLAST score 176
E value 6.0e-13
Match length 79
% identity 48
NCBI Description (L37382) beta-galactosidase-complementation protein [Cloning vector]

Seq. No. 299566
Seq. ID LIB3154-014-Q1-K1-D10
Method BLASTX
NCBI GI g168701
BLAST score 167
E value 4.0e-12
Match length 66
% identity 59

NCBI Description (M60837) zein [Zea mays]

Seq. No. 299567
Seq. ID LIB3154-014-Q1-K1-D2
Method BLASTX
NCBI GI g567893
BLAST score 157
E value 1.0e-10
Match length 77
% identity 45
NCBI Description (L37382) beta-galactosidase-complementation protein
[Cloning vector]

Seq. No. 299568
Seq. ID LIB3154-014-Q1-K1-D7
Method BLASTX
NCBI GI g168701
BLAST score 464
E value 1.0e-46
Match length 111
% identity 87
NCBI Description (M60837) zein [Zea mays]

Seq. No. 299569
Seq. ID LIB3154-014-Q1-K1-E10
Method BLASTX
NCBI GI g168691
BLAST score 240
E value 1.0e-20
Match length 86
% identity 62
NCBI Description (M29628) zein [Zea mays]

Seq. No. 299570
Seq. ID LIB3154-014-Q1-K1-E7
Method BLASTN
NCBI GI g22447
BLAST score 101
E value 9.0e-50
Match length 116
% identity 97
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein

Seq. No. 299571
Seq. ID LIB3154-014-Q1-K1-H1
Method BLASTN
NCBI GI g4185305
BLAST score 85
E value 4.0e-40
Match length 317
% identity 82
NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
(sz22-21) gene, complete cds; retrotransposon Opie-2 gag
protein, polyprotein, and copia protein genes, complete
cds; and unknown genes

Seq. No. 299572

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Seq. ID LIB3154-014-Q1-K1-H10
Method BLASTX
NCBI GI g168664
BLAST score 308
E value 2.0e-28
Match length 78
% identity 78
NCBI Description (M13507) zein protein precursor [Zea mays]

Seq. No. 299573
Seq. ID LIB3154-014-Q1-K1-H11
Method BLASTN
NCBI GI g168665
BLAST score 81
E value 5.0e-38
Match length 109
% identity 95
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 299574
Seq. ID LIB3156-001-Q1-K1-A10
Method BLASTX
NCBI GI g72287
BLAST score 528
E value 5.0e-54
Match length 117
% identity 90
NCBI Description beta-globulin A precursor (clone 94) - upland cotton (fragment) >gi_167377 (M16905) legumin precursor [Gossypium hirsutum]

Seq. No. 299575
Seq. ID LIB3156-001-Q1-K1-A11
Method BLASTN
NCBI GI g2642323
BLAST score 38
E value 3.0e-12
Match length 46
% identity 96
NCBI Description Zea mays profilin (PRO4) mRNA, complete cds

Seq. No. 299576
Seq. ID LIB3156-001-Q1-K1-A9
Method BLASTX
NCBI GI g1561774
BLAST score 504
E value 3.0e-51
Match length 109
% identity 85
NCBI Description (U67426) malate dehydrogenase [Vitis vinifera]

Seq. No. 299577
Seq. ID LIB3156-001-Q1-K1-B12
Method BLASTX
NCBI GI g4588906
BLAST score 167
E value 4.0e-12

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Match length 65
% identity 58
NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]

Seq. No. 299578
Seq. ID LIB3156-001-Q1-K1-C10
Method BLASTX
NCBI GI g131015
BLAST score 469
E value 4.0e-47
Match length 112
% identity 73
NCBI Description PATHOGENESIS-RELATED PROTEIN R MAJOR FORM PRECURSOR
(THAUMATIN-LIKE PROTEIN E22) >gi_100385_pir_JH0230
pathogenesis-related protein R precursor - common tobacco
>gi_19855_emb_CAA33293 (X15224) thaumatin-like protein
[Nicotiana tabacum] >gi_19980_emb_CAA31235 (X12739)
pathogenesis-related protein R (AA 1 - 226) [Nicotiana
tabacum]

Seq. No. 299579
Seq. ID LIB3156-001-Q1-K1-C11
Method BLASTX
NCBI GI g3850999
BLAST score 245
E value 8.0e-21
Match length 79
% identity 71
NCBI Description (AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1
[Zea mays]

Seq. No. 299580
Seq. ID LIB3156-001-Q1-K1-D10
Method BLASTX
NCBI GI g1350956
BLAST score 230
E value 2.0e-19
Match length 62
% identity 85
NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No. 299581
Seq. ID LIB3156-001-Q1-K1-D9
Method BLASTX
NCBI GI g2618721
BLAST score 155
E value 3.0e-10
Match length 70
% identity 46
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]

Seq. No. 299582
Seq. ID LIB3156-001-Q1-K1-F9
Method BLASTX
NCBI GI g1419370
BLAST score 302
E value 2.0e-27

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Match length 70
% identity 84
NCBI Description (X97726) actin depolymerizing factor [Zea mays]

Seq. No. 299583
Seq. ID LIB3156-001-Q1-K1-G9
Method BLASTX
NCBI GI g2462927
BLAST score 241
E value 2.0e-20
Match length 90
% identity 53
NCBI Description (Y10342) putative amidase [Arabidopsis thaliana]

Seq. No. 299584
Seq. ID LIB3156-001-Q1-K1-H12
Method BLASTX
NCBI GI g1107526
BLAST score 310
E value 1.0e-28
Match length 85
% identity 68
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]

Seq. No. 299585
Seq. ID LIB3156-001-Q1-K1-H9
Method BLASTX
NCBI GI g2467088
BLAST score 181
E value 2.0e-13
Match length 65
% identity 60
NCBI Description (AJ001911) putative Ckc2 [Arabidopsis thaliana]

Seq. No. 299586
Seq. ID LIB3156-002-Q1-K1-A12
Method BLASTX
NCBI GI g2673918
BLAST score 194
E value 7.0e-15
Match length 46
% identity 78
NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]

Seq. No. 299587
Seq. ID LIB3156-002-Q1-K1-B6
Method BLASTN
NCBI GI g2208987
BLAST score 100
E value 4.0e-49
Match length 178
% identity 90
NCBI Description Z.mays mRNA for signal recognition particle subunit

Seq. No. 299588
Seq. ID LIB3156-002-Q1-K1-D4
Method BLASTX

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NCBI GI	g1173194
BLAST score	322
E value	8.0e-30
Match length	88
% identity	68
NCBI Description	30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13) >gi_2119093_pir_S59594 ribosomal protein S13 precursor, chloroplast - Arabidopsis thaliana >gi_16767_emb_CAA79013 (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_662869_emb_CAA88028 (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana] >gi_1107483_emb_CAA63021 (X91955) 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_1515107_emb_CAA60413 (X86734) plastid ribosomal protein S13 [Arabidopsis thaliana]
Seq. No.	299589
Seq. ID	LIB3156-002-Q1-K1-E10
Method	BLASTN
NCBI GI	g603189
BLAST score	88
E value	6.0e-42
Match length	140
% identity	91
NCBI Description	Zea mays translation initiation factor eIF-4A mRNA, complete cds
Seq. No.	299590
Seq. ID	LIB3156-002-Q1-K1-F5
Method	BLASTN
NCBI GI	g1177368
BLAST score	246
E value	1.0e-136
Match length	338
% identity	94
NCBI Description	Z.mays mRNA for ribosomal protein L39
Seq. No.	299591
Seq. ID	LIB3156-002-Q1-K1-H7
Method	BLASTX
NCBI GI	g2668742
BLAST score	335
E value	2.0e-31
Match length	86
% identity	79
NCBI Description	(AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.	299592
Seq. ID	LIB3156-002-Q1-K2-A12
Method	BLASTX
NCBI GI	g2673918
BLAST score	157
E value	2.0e-10
Match length	46
% identity	65
NCBI Description	(AC002561) unkwnon protein [Arabidopsis thaliana]

Seq. No. 299593
Seq. ID LIB3156-002-Q1-K2-B10
Method BLASTX
NCBI GI g1172818
BLAST score 218
E value 1.0e-17
Match length 45
% identity 91
NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal protein S16 [Oryza sativa] >gi_1096552_prf_2111468A ribosomal protein S16 [Oryza sativa]

Seq. No. 299594
Seq. ID LIB3156-002-Q1-K2-B11
Method BLASTX
NCBI GI g1172818
BLAST score 203
E value 5.0e-16
Match length 45
% identity 87
NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal protein S16 [Oryza sativa] >gi_1096552_prf_2111468A ribosomal protein S16 [Oryza sativa]

Seq. No. 299595
Seq. ID LIB3156-002-Q1-K2-G8
Method BLASTX
NCBI GI g3080420
BLAST score 167
E value 4.0e-12
Match length 50
% identity 64
NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No. 299596
Seq. ID LIB3156-003-Q1-K1-D11
Method BLASTN
NCBI GI g168577
BLAST score 69
E value 2.0e-30
Match length 158
% identity 91
NCBI Description Maize phospholipid transfer protein mRNA, 3' end

Seq. No. 299597
Seq. ID LIB3156-003-Q1-K1-D5
Method BLASTN
NCBI GI g4218534
BLAST score 37
E value 1.0e-11
Match length 61
% identity 90
NCBI Description Triticum sp. mRNA for GRAB1 protein

Seq. No. 299598
Seq. ID LIB3156-003-Q1-K1-E4

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Method	BLASTX
NCBI GI	g2618699
BLAST score	191
E value	1.0e-14
Match length	101
% identity	38
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]
Seq. No.	299599
Seq. ID	LIB3156-003-Q1-K1-F3
Method	BLASTX
NCBI GI	g1040877
BLAST score	477
E value	4.0e-48
Match length	121
% identity	69
NCBI Description	(U30460) expansin S2 precursor [Cucumis sativus]
Seq. No.	299600
Seq. ID	LIB3156-004-Q1-K1-B12
Method	BLASTX
NCBI GI	g1172813
BLAST score	149
E value	5.0e-10
Match length	45
% identity	64
NCBI Description	60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPPRESSOR SG12) >gi_1076752_pir_S49596 ribosomal protein L10.e, cytosolic - rice >gi_575357_emb_CAA57340_ (X81692) putative tumor supressor [Oryza sativa]
Seq. No.	299601
Seq. ID	LIB3156-004-Q1-K1-B4
Method	BLASTX
NCBI GI	g3395938
BLAST score	241
E value	2.0e-20
Match length	103
% identity	29
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]
Seq. No.	299602
Seq. ID	LIB3156-004-Q1-K1-C1
Method	BLASTX
NCBI GI	g4104056
BLAST score	520
E value	4.0e-53
Match length	113
% identity	81
NCBI Description	(AF031194) S276 [Triticum aestivum]
Seq. No.	299603
Seq. ID	LIB3156-004-Q1-K1-C10
Method	BLASTN
NCBI GI	g168436
BLAST score	82

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E value 3.0e-38
Match length 142
% identity 89
NCBI Description Zea mays catalase (Cat3) gene, complete cds

Seq. No. 299604
Seq. ID LIB3156-004-Q1-K1-C3
Method BLASTX
NCBI GI g2344871
BLAST score 225
E value 1.0e-18
Match length 92
% identity 48
NCBI Description (AJ001270) purple acid phosphatase precursor [Phaseolus vulgaris]

Seq. No. 299605
Seq. ID LIB3156-004-Q1-K1-C6
Method BLASTX
NCBI GI g1732511
BLAST score 410
E value 4.0e-40
Match length 124
% identity 65
NCBI Description (U62742) Ran binding protein 1 homolog [Arabidopsis thaliana]

Seq. No. 299606
Seq. ID LIB3156-004-Q1-K1-C7
Method BLASTX
NCBI GI g2695711
BLAST score 160
E value 7.0e-11
Match length 62
% identity 50
NCBI Description (AJ001370) cytochrome b5 [Olea europaea]

Seq. No. 299607
Seq. ID LIB3156-004-Q1-K1-C9
Method BLASTX
NCBI GI g3126965
BLAST score 206
E value 5.0e-17
Match length 118
% identity 45
NCBI Description (AF061806) basic chitinase [Elaeagnus umbellata]

Seq. No. 299608
Seq. ID LIB3156-004-Q1-K1-D6
Method BLASTX
NCBI GI g3913427
BLAST score 345
E value 1.0e-32
Match length 123
% identity 58
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767)

S-adenosylmethionine decarboxylase [Zea mays]

Seq. No. 299609
Seq. ID LIB3156-004-Q1-K1-G1
Method BLASTX
NCBI GI g99894
BLAST score 274
E value 3.0e-24
Match length 120
% identity 55
NCBI Description chlorophyll a/b-binding protein 5 - soybean

Seq. No. 299610
Seq. ID LIB3156-004-Q1-K1-H3
Method BLASTN
NCBI GI g22320
BLAST score 37
E value 2.0e-11
Match length 37
% identity 100
NCBI Description Maize H1 mRNA for H1 histone

Seq. No. 299611
Seq. ID LIB3156-005-Q1-K1-B3
Method BLASTX
NCBI GI g2832632
BLAST score 320
E value 1.0e-29
Match length 126
% identity 52
NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No. 299612
Seq. ID LIB3156-005-Q1-K1-B4
Method BLASTX
NCBI GI g266398
BLAST score 309
E value 2.0e-28
Match length 90
% identity 63
NCBI Description TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR INHIBITOR) (CHFI) >gi_68849_pir_TIZM1 trypsin/factor XIIa inhibitor precursor - maize >gi_22327_emb_CAA37998_(X54064) corn Hageman factor inhibitor [Zea mays]

Seq. No. 299613
Seq. ID LIB3156-005-Q1-K1-D2
Method BLASTX
NCBI GI g118104
BLAST score 439
E value 1.0e-43
Match length 110
% identity 78
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) - maize >gi_168461 (M55021) cyclophilin [Zea mays]

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>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 299614
Seq. ID LIB3156-005-Q1-K1-E1
Method BLASTX
NCBI GI g1184776
BLAST score 164
E value 6.0e-12
Match length 39
% identity 82
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]

Seq. No. 299615
Seq. ID LIB3156-005-Q1-K1-G3
Method BLASTX
NCBI GI g2832247
BLAST score 149
E value 3.0e-14
Match length 78
% identity 65
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 299616
Seq. ID LIB3156-005-Q1-K1-G9
Method BLASTX
NCBI GI g498040
BLAST score 212
E value 6.0e-17
Match length 65
% identity 66
NCBI Description (L33793) ORF [Senecio odorus]

Seq. No. 299617
Seq. ID LIB3156-006-Q1-K1-B10
Method BLASTX
NCBI GI g2894568
BLAST score 167
E value 7.0e-12
Match length 69
% identity 43
NCBI Description (AL021890) putative protein [Arabidopsis thaliana]

Seq. No. 299618
Seq. ID LIB3156-006-Q1-K1-E9
Method BLASTN
NCBI GI g452340
BLAST score 255
E value 1.0e-141
Match length 275
% identity 99
NCBI Description Z.mays mRNA for type II light-harvesting chlorophyll a/b-binding protein

Seq. No. 299619
Seq. ID LIB3156-007-Q1-K1-A7
Method BLASTN

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NCBI GI	g758352
BLAST score	79
E value	2.0e-36
Match length	182
% identity	86
NCBI Description	Z.mays mRNA for cysteine synthase
Seq. No.	299620
Seq. ID	LIB3156-007-Q1-K1-B5
Method	BLASTX
NCBI GI	g322752
BLAST score	311
E value	8.0e-29
Match length	97
% identity	58
NCBI Description	auxin-independent growth promoter - Nicotiana tabacum >gi_559921_emb_CAA56570_ (X80301) axi 1 [Nicotiana tabacum]
Seq. No.	299621
Seq. ID	LIB3156-007-Q1-K1-C4
Method	BLASTX
NCBI GI	g1170508
BLAST score	139
E value	8.0e-09
Match length	50
% identity	58
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8) >gi_2119931_pir_S60244 translation initiation factor eIF-4A.8, anther-specific - common tobacco >gi_475219_emb_CAA55639_ (X79004) translation initiation factor (eIF-4A) [Nicotiana tabacum] >gi_475221_emb_CAA55640_ (X79005) translation initiation factor (eIF-4A) [Nicotiana tabacum]
Seq. No.	299622
Seq. ID	LIB3156-007-Q1-K1-F10
Method	BLASTX
NCBI GI	g2440160
BLAST score	174
E value	2.0e-12
Match length	73
% identity	48
NCBI Description	(Y14836) beta-galactosidase [Phagemid cloning vector pTZ19U]
Seq. No.	299623
Seq. ID	LIB3156-007-Q1-K1-F8
Method	BLASTX
NCBI GI	g1709619
BLAST score	220
E value	6.0e-21
Match length	92
% identity	64
NCBI Description	PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) / DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP) >gi_2146814_pir_S69181 protein disulfide isomerase (EC

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5.3.4.1) precursor - maize >gi_625148 (L39014) protein disulfide isomerase [Zea mays]

Seq. No. 299624
Seq. ID LIB3156-007-Q1-K1-H10
Method BLASTX
NCBI GI g626042
BLAST score 178
E value 4.0e-13
Match length 51
% identity 65
NCBI Description beta-glucosidase, root meristem (EC 3.2.1.-) precursor - maize >gi_435313_emb_CAA52293_ (X74217) beta-glucosidase [Zea mays]

Seq. No. 299625
Seq. ID LIB3156-007-Q1-K1-H3
Method BLASTX
NCBI GI g3334222
BLAST score 164
E value 2.0e-12
Match length 61
% identity 69
NCBI Description 4-HYDROXYPHENYL PYRUVATE DIOXYGENASE (4HPPD) (HPD)
>gi_2695710_emb_CAA04245_ (AJ000693)
4-hydroxyphenylpyruvate dioxygenase [Hordeum vulgare]

Seq. No. 299626
Seq. ID LIB3156-008-Q1-K1-B3
Method BLASTX
NCBI GI g1346882
BLAST score 381
E value 1.0e-36
Match length 105
% identity 69
NCBI Description PHYTOENE SYNTHASE PRECURSOR (MEL5) >gi_2129505_pir_S56668
geranylgeranyl-diphosphate geranylgeranyltransferase (EC
2.5.1.32) precursor - muskmelon >gi_870985_emb_CAA85775_
(Z37543) phytoene synthase [Cucumis melo]

Seq. No. 299627
Seq. ID LIB3156-008-Q1-K1-C3
Method BLASTX
NCBI GI g1173347
BLAST score 272
E value 6.0e-24
Match length 61
% identity 89
NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
>gi_100803_pir_S23452 sedoheptulose-bisphosphatase (EC
3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
(X65540) sedoheptulose-1,7-bisphosphatase [Triticum
aestivum]

Seq. No. 299628
Seq. ID LIB3156-008-Q1-K1-D11

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Method	BLASTX
NCBI GI	g3451075
BLAST score	247
E value	5.0e-21
Match length	132
% identity	36
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]
Seq. No.	299629
Seq. ID	LIB3156-008-Q1-K1-H12
Method	BLASTX
NCBI GI	g3128177
BLAST score	218
E value	1.0e-17
Match length	107
% identity	47
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.	299630
Seq. ID	LIB3156-009-Q1-K1-B6
Method	BLASTX
NCBI GI	g133867
BLAST score	197
E value	3.0e-15
Match length	98
% identity	44
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]
Seq. No.	299631
Seq. ID	LIB3156-009-Q1-K1-B8
Method	BLASTX
NCBI GI	g133867
BLAST score	224
E value	2.0e-18
Match length	95
% identity	56
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]
Seq. No.	299632
Seq. ID	LIB3156-009-Q1-K1-C4
Method	BLASTN
NCBI GI	g236729
BLAST score	40
E value	4.0e-13
Match length	76
% identity	84
NCBI Description	metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
Seq. No.	299633
Seq. ID	LIB3156-009-Q1-K1-C9
Method	BLASTX
NCBI GI	g2384669
BLAST score	155

E value 3.0e-10
Match length 45
% identity 64
NCBI Description (AF012656) putative potassium transporter AtKT1p [Arabidopsis thaliana]

Seq. No. 299634
Seq. ID LIB3156-009-Q1-K1-E9
Method BLASTX
NCBI GI g2146732
BLAST score 458
E value 8.0e-46
Match length 118
% identity 39
NCBI Description FK506-binding protein - Arabidopsis thaliana >gi_1373396 (U57838) rof1 [Arabidopsis thaliana]

Seq. No. 299635
Seq. ID LIB3156-009-Q1-K1-H11
Method BLASTX
NCBI GI g115833
BLAST score 340
E value 2.0e-32
Match length 77
% identity 78
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi_100195_pir_SI1877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum]

Seq. No. 299636
Seq. ID LIB3156-010-Q1-K1-A1
Method BLASTX
NCBI GI g3036951
BLAST score 528
E value 6.0e-54
Match length 101
% identity 98
NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 299637
Seq. ID LIB3156-010-Q1-K1-B3
Method BLASTX
NCBI GI g531829
BLAST score 214
E value 3.0e-17
Match length 79
% identity 53
NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No. 299638
Seq. ID LIB3156-010-Q1-K1-B7
Method BLASTX
NCBI GI g134104
BLAST score 148

Seq. No. 299638
Seq. ID LIB3156-010-Q1-K1-C7
Method BLASTX
NCBI GI g730510
BLAST score 226
E value 1.0e-18
Match length 103
% identity 49
NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)
>gi_99800_pir_PW0007 chaperonin 62.5K beta chain - rape
plastid >gi_167117 (M35600) 60-kDa beta-polypeptide of
plastid chaperonin-60 precursor [Brassica napus]

Seq. No. 299639
Seq. ID LIB3156-010-Q1-K1-C8
Method BLASTX
NCBI GI g730510
BLAST score 226
E value 1.0e-18
Match length 103
% identity 49
NCBI Description RAS-RELATED PROTEIN RIC1 >gi_542150_pir_S38740 GTP-binding
protein - rice >gi_432607_gb_AAB28535_ (S66160) ras-related
GTP binding protein possessing GTPase activity=ric1 [Oryza
sativa=rice, var. Yamahoushi, callus, Peptide, 202 aa]
[Oryza sativa]

Seq. No. 299640
Seq. ID LIB3156-010-Q1-K1-D9
Method BLASTX
NCBI GI g1550814
BLAST score 301
E value 1.0e-27
Match length 89
% identity 71
NCBI Description (Y07959) 60S acidic ribosomal protein P0 [Zea mays]

Seq. No. 299641
Seq. ID LIB3156-010-Q1-K1-E2
Method BLASTN
NCBI GI g4079799
BLAST score 34
E value 2.0e-09
Match length 62
% identity 89
NCBI Description Oryza sativa S-phase-specific ribosomal protein (RSPSP94)
mRNA, complete cds

Seq. No. 299642
Seq. ID LIB3156-011-Q1-K1-A2
Method BLASTX
NCBI GI g2497492
BLAST score 362
E value 1.0e-34
Match length 113
% identity 64
NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
KINASE) >gi_1653646_dbj_BAA18558_ (D90915) uridine
monophosphate kinase [Synechocystis sp.]

Seq. No. 299643

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Seq. ID	LIB3156-011-Q1-K1-A5
Method	BLASTX
NCBI GI	g4539423
BLAST score	143
E value	4.0e-09
Match length	48
% identity	54
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]
Seq. No.	299644
Seq. ID	LIB3156-011-Q1-K1-B4
Method	BLASTN
NCBI GI	g2828011
BLAST score	84
E value	2.0e-39
Match length	116
% identity	93
NCBI Description	Zea mays starch synthase I precursor (Ss1) mRNA, nuclear gene encoding plastid protein, complete cds
Seq. No.	299645
Seq. ID	LIB3156-011-Q1-K1-B5
Method	BLASTN
NCBI GI	g3450841
BLAST score	47
E value	2.0e-17
Match length	59
% identity	95
NCBI Description	Oryza sativa mitogen activated protein kinase kinase (MEK1) mRNA, complete cds
Seq. No.	299646
Seq. ID	LIB3156-011-Q1-K1-C2
Method	BLASTX
NCBI GI	g2130105
BLAST score	266
E value	1.0e-23
Match length	78
% identity	74
NCBI Description	histone H2A type 2 (clone wch2A-4) - wheat >gi_536892_dbj_BAA07278_ (D38089) protein H2A [Triticum aestivum] >gi_536896_dbj_BAA07280_ (D38091) protein H2A [Triticum aestivum],
Seq. No.	299647
Seq. ID	LIB3156-011-Q1-K1-D1
Method	BLASTX
NCBI GI	g4151319
BLAST score	230
E value	4.0e-19
Match length	48
% identity	96
NCBI Description	(AF089084) putative auxin efflux carrier protein; AtPIN1 [Arabidopsis thaliana]
Seq. No.	299648

Seq. ID LIB3156-011-Q1-K1-D3
Method BLASTX
NCBI GI g1172811
BLAST score 242
E value 8.0e-21
Match length 65
% identity 71
NCBI Description 60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPPRESSOR SC34)
>gi_1076751_pir_S49575 ribosomal protein L10.e, cytosolic
- rice >gi_575355_emb_CAA57339_ (X81691) putative tumor
supresser [Oryza sativa]

Seq. No. 299649
Seq. ID LIB3156-011-Q1-K1-E2
Method BLASTX
NCBI GI g1173218
BLAST score 142
E value 2.0e-11
Match length 59
% identity 71
NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal
protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No. 299650
Seq. ID LIB3156-011-Q1-K1-G6
Method BLASTX
NCBI GI g3335365
BLAST score 170
E value 3.0e-12
Match length 91
% identity 43
NCBI Description (AC003028) high affinity calcium antiporter [Arabidopsis
thaliana]

Seq. No. 299651
Seq. ID LIB3156-012-Q1-K1-D11
Method BLASTN
NCBI GI g168514
BLAST score 46
E value 9.0e-17
Match length 66
% identity 92
NCBI Description Z.mays c1 locus myb homologue cDNA, exons 1-3

Seq. No. 299652
Seq. ID LIB3156-012-Q1-K1-E3
Method BLASTX
NCBI GI g2623300
BLAST score 297
E value 6.0e-27
Match length 98
% identity 57
NCBI Description (AC002409) putative protein phosphatase 2C [Arabidopsis
thaliana]

Seq. No. 299653

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Seq. ID	LIB3156-013-Q1-K1-A9
Method	BLASTX
NCBI GI	g2662310
BLAST score	208
E value	1.0e-16
Match length	39
% identity	97
NCBI Description	(AB009307) bpw1 [Hordeum vulgare]
Seq. No.	299654
Seq. ID	LIB3156-013-Q1-K1-C2
Method	BLASTX
NCBI GI	g3152607
BLAST score	152
E value	4.0e-10
Match length	45
% identity	60
NCBI Description	(AC004482) putative receptor kinase [Arabidopsis thaliana]
Seq. No.	299655
Seq. ID	LIB3156-013-Q1-K1-C4
Method	BLASTX
NCBI GI	g3746964
BLAST score	241
E value	9.0e-21
Match length	84
% identity	60
NCBI Description	(AF092168) signal recognition particle 54 kDa subunit precursor [Arabidopsis thaliana]
Seq. No.	299656
Seq. ID	LIB3156-013-Q1-K1-C9
Method	BLASTX
NCBI GI	g2668744
BLAST score	265
E value	2.0e-23
Match length	75
% identity	67
NCBI Description	(AF034946) ubiquitin conjugating enzyme [Zea mays]
Seq. No.	299657
Seq. ID	LIB3156-013-Q1-K1-D6
Method	BLASTN
NCBI GI	g2582640
BLAST score	37
E value	2.0e-11
Match length	65
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for arginine-serine-rich splicing factor, RSp40
Seq. No.	299658
Seq. ID	LIB3156-013-Q1-K1-E4
Method	BLASTN
NCBI GI	g236729
BLAST score	153
E value	1.0e-80

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Match length 231
% identity 91
NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]

Seq. No. 299659
Seq. ID LIB3156-013-Q1-K1-G12
Method BLASTX
NCBI GI g1076758
BLAST score 269
E value 1.0e-23
Match length 108
% identity 57
NCBI Description heat-shock protein precursor - rye >gi_2130093_pir_S65776
heat-shock protein, 82K, precursor - rye
>gi_556673_emb_CAA82945_ (Z30243) heat-shock protein
[Secale cereale]

Seq. No. 299660
Seq. ID LIB3156-013-Q1-K1-G6
Method BLASTN
NCBI GI g22292
BLAST score 37
E value 1.0e-11
Match length 77
% identity 87
NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 299661
Seq. ID LIB3156-014-Q1-K1-D4
Method BLASTX
NCBI GI g2499932
BLAST score 397
E value 1.0e-38
Match length 128
% identity 66
NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305
(U22442) adenine phosphoribosyltransferase form 1 [Triticum
aestivum]

Seq. No. 299662
Seq. ID LIB3156-014-Q1-K1-F3
Method BLASTN
NCBI GI g1532072
BLAST score 163
E value 2.0e-86
Match length 186
% identity 97
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No. 299663
Seq. ID LIB3156-015-Q1-K1-A5
Method BLASTX
NCBI GI g1419090
BLAST score 231
E value 2.0e-19
Match length 111
% identity 49

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NCBI Description (X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]

Seq. No. 299664
Seq. ID LIB3156-015-Q1-K1-B10
Method BLASTX
NCBI GI g1044940
BLAST score 387
E value 2.0e-37
Match length 102
% identity 74
NCBI Description (X92422) fusion gene [Zea mays]

Seq. No. 299665
Seq. ID LIB3156-015-Q1-K1-D11
Method BLASTX
NCBI GI g3212539
BLAST score 147
E value 1.0e-09
Match length 64
% identity 50
NCBI Description Chain A, Structure Of Human Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity >gi_3212540_pdb_1IVH_B Chain B, Structure Of Human Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity >gi_3212541_pdb_1IVH_C Chain C, Structure Of Human Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity >gi_3212542_pdb_1IVH_D Chain D, Structure Of Human Isovaleryl-Coa Dehydrogenase At 2.6 Angstroms Resolution: Structural Basis For Substrate Specificity

Seq. No. 299666
Seq. ID LIB3156-015-Q1-K1-E12
Method BLASTN
NCBI GI g4140643
BLAST score 68
E value 8.0e-30
Match length 120
% identity 89
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299667
Seq. ID LIB3156-015-Q1-K1-F6
Method BLASTX
NCBI GI g112994
BLAST score 322
E value 7.0e-30
Match length 71
% identity 92
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN >gi_82685_pir_S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564) ABA-inducible gene protein [Zea mays] >gi_226091_prf_1410284A abscisic acid inducible gene [Zea

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Seq. No. 299668
Seq. ID LIB3156-015-Q1-K1-G11
Method BLASTX
NCBI GI g4415916
BLAST score 447
E value 2.0e-44
Match length 149
% identity 58
NCBI Description (AC006282) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No. 299669
Seq. ID LIB3156-015-Q1-K1-G12
Method BLASTX
NCBI GI g554565
BLAST score 279
E value 6.0e-25
Match length 78
% identity 73
NCBI Description (M24889) glutathione S-transferase [Artificial gene]

Seq. No. 299670
Seq. ID LIB3156-015-Q1-K1-G6
Method BLASTX
NCBI GI g3860247
BLAST score 214
E value 1.0e-17
Match length 58
% identity 69
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 299671
Seq. ID LIB3156-015-Q1-K1-H7
Method BLASTN
NCBI GI g175854
BLAST score 36
E value 7.0e-11
Match length 60
% identity 90
NCBI Description O.sativa 28S large subunit rRNA, 5' end

Seq. No. 299672
Seq. ID LIB3156-016-Q1-K1-A7
Method BLASTX
NCBI GI g115782
BLAST score 163
E value 4.0e-18
Match length 63
% identity 64
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_72747_pir_CDWT chlorophyll a/b-binding protein precursor - wheat >gi_170674 (M10144) chlorophyll a/b-binding protein precursor [Triticum aestivum]

Seq. No. 299673

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Seq. ID	LIB3156-016-Q1-K1-B11
Method	BLASTX
NCBI GI	g1657621
BLAST score	148
E value	1.0e-13
Match length	96
% identity	50
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]
Seq. No.	299674
Seq. ID	LIB3156-016-Q1-K1-B8
Method	BLASTX
NCBI GI	g542179
BLAST score	494
E value	4.0e-50
Match length	115
% identity	83
NCBI Description	alpha tubulin - maize >gi_629837_pir_S39998 tubulin alpha chain - maize (fragment) >gi_393401_emb_CAA52158_ (X73980) alpha tubulin [Zea mays]
Seq. No.	299675
Seq. ID	LIB3156-016-Q1-K1-C9
Method	BLASTX
NCBI GI	g3914430
BLAST score	400
E value	4.0e-39
Match length	87
% identity	86
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta subunit [Spinacia oleracea]
Seq. No.	299676
Seq. ID	LIB3156-016-Q1-K1-D10
Method	BLASTX
NCBI GI	g1587206
BLAST score	237
E value	2.0e-26
Match length	122
% identity	60
NCBI Description	T complex protein [Cucumis sativus]
Seq. No.	299677
Seq. ID	LIB3156-016-Q1-K1-D4
Method	BLASTX
NCBI GI	g4512616
BLAST score	343
E value	2.0e-32
Match length	83
% identity	80
NCBI Description	(AC004793) Contains similarity to gi_1653332 extragenic suppressor (SuhB) from Synechocystis sp. gb_D90912 and is a member of the Inositol monophosphatase family PF_00459. EST gb_AA597395 comes from this gene. [Arabidopsis tha

Seq. No. 299678
Seq. ID LIB3156-016-Q1-K1-E11
Method BLASTX
NCBI GI g2208962
BLAST score 211
E value 4.0e-17
Match length 66
% identity 67
NCBI Description (Y10118) signal recognition particle subunit 14 [Oryza sativa]

Seq. No. 299679
Seq. ID LIB3156-016-Q1-K1-F11
Method BLASTX
NCBI GI g3355468
BLAST score 244
E value 5.0e-21
Match length 91
% identity 59
NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No. 299680
Seq. ID LIB3156-016-Q1-K1-H9
Method BLASTX
NCBI GI g1008904
BLAST score 264
E value 5.0e-44
Match length 109
% identity 80
NCBI Description (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]

Seq. No. 299681
Seq. ID LIB3156-017-Q1-K1-B12
Method BLASTX
NCBI GI g4457221
BLAST score 143
E value 2.0e-09
Match length 50
% identity 58
NCBI Description (AF127797) putative bZIP DNA-binding protein [Capsicum chinense]

Seq. No. 299682
Seq. ID LIB3156-017-Q1-K1-B2
Method BLASTX
NCBI GI g2766452
BLAST score 183
E value 1.0e-13
Match length 71
% identity 54
NCBI Description (AF029858) cytochrome P450 CYP71E1 [Sorghum bicolor]

Seq. No. 299683
Seq. ID LIB3156-017-Q1-K1-C10
Method BLASTX

NCBI GI g1931647
BLAST score 167
E value 1.0e-11
Match length 75
% identity 45
NCBI Description (U95973) endomembrane protein EMP70 precursor isolog [Arabidopsis thaliana]

Seq. No. 299684
Seq. ID LIB3156-017-Q1-K1-C5
Method BLASTN
NCBI GI g167086
BLAST score 34
E value 8.0e-10
Match length 94
% identity 84
NCBI Description Hordeum vulgare photosystem I protein (PSI-L) mRNA, complete cds

Seq. No. 299685
Seq. ID LIB3156-017-Q1-K1-D11
Method BLASTX
NCBI GI g3776005
BLAST score 154
E value 1.0e-10
Match length 45
% identity 67
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 299686
Seq. ID LIB3156-017-Q1-K1-D3
Method BLASTX
NCBI GI g113621
BLAST score 264
E value 2.0e-23
Match length 66
% identity 82
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A cytoplasmic aldolase [Zea mays]

Seq. No. 299687
Seq. ID LIB3156-017-Q1-K1-D6
Method BLASTX
NCBI GI g2764992
BLAST score 166
E value 3.0e-18
Match length 97
% identity 55
NCBI Description (Y08609) plasma membrane polypeptide [Nicotiana tabacum]

Seq. No. 299688
Seq. ID LIB3156-017-Q1-K1-E12
Method BLASTX

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NCBI GI	g2760334
BLAST score	259
E value	2.0e-22
Match length	83
% identity	57
NCBI Description	(AC002130) F1N21.5 [Arabidopsis thaliana]
Seq. No.	299689
Seq. ID	LIB3156-017-Q1-K1-G11
Method	BLASTN
NCBI GI	g21892
BLAST score	94
E value	1.0e-45
Match length	134
% identity	93
NCBI Description	T.aestivum (clone pTAU1.3) U1 snRNA
Seq. No.	299690
Seq. ID	LIB3156-017-Q1-K1-H9
Method	BLASTN
NCBI GI	g312178
BLAST score	181
E value	2.0e-97
Match length	219
% identity	96
NCBI Description	Z.mays GapC2 gene
Seq. No.	299691
Seq. ID	LIB3156-020-Q1-K1-A10
Method	BLASTX
NCBI GI	g4587549
BLAST score	225
E value	6.0e-19
Match length	61
% identity	69
NCBI Description	(AC006577) Similar to gb_U55861 RNA binding protein nucleolysin (TIAR) from Mus musculus and contains several PF_00076 RNA recognition motif domains. ESTs gb_T21032 and gb_T44127 come from this gene. [Arabidopsis t
Seq. No.	299692
Seq. ID	LIB3156-020-Q1-K1-A7
Method	BLASTX
NCBI GI	g3687240
BLAST score	323
E value	5.0e-30
Match length	121
% identity	50
NCBI Description	(AC005169) extensin-like protein [Arabidopsis thaliana]
Seq. No.	299693
Seq. ID	LIB3156-021-Q1-K1-D1
Method	BLASTX
NCBI GI	g2842698
BLAST score	194
E value	2.0e-15
Match length	48

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% identity 79
NCBI Description PROBABLE ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC)
>gi_1644319_emb_CAB03609.1_ (Z81317) arp 2-3 complex 20kd
subunit [Schizosaccharomyces pombe]

Seq. No. 299694
Seq. ID LIB3156-021-Q1-K1-D4
Method BLASTN
NCBI GI g18963
BLAST score 231
E value 1.0e-127
Match length 247
% identity 98
NCBI Description Z.mays mRNA for dehydrin (dhn3)

Seq. No. 299695
Seq. ID LIB3156-021-Q1-K1-F6
Method BLASTX
NCBI GI g3169182
BLAST score 191
E value 2.0e-14
Match length 40
% identity 78
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]

Seq. No. 299696
Seq. ID LIB3156-021-Q1-K1-G2
Method BLASTX
NCBI GI g4587550
BLAST score 267
E value 2.0e-23
Match length 70
% identity 73
NCBI Description (AC006577) EST gb_R64848 comes from this gene. [Arabidopsis thaliana]

Seq. No. 299697
Seq. ID LIB3156-021-Q1-K1-G3
Method BLASTX
NCBI GI g1076758
BLAST score 431
E value 7.0e-43
Match length 99
% identity 86
NCBI Description heat-shock protein precursor - rye >gi_2130093_pir_S65776
heat-shock protein, 82K, precursor - rye
>gi_556673_emb_CAA82945_ (Z30243) heat-shock protein
[Secale cereale]

Seq. No. 299698
Seq. ID LIB3156-021-Q1-K1-G8
Method BLASTX
NCBI GI g4587550
BLAST score 437
E value 2.0e-43
Match length 133
% identity 65

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NCBI Description (AC006577) EST gb_R64848 comes from this gene. [Arabidopsis thaliana]

Seq. No. 299699
Seq. ID LIB3157-002-Q1-K1-A8
Method BLASTN
NCBI GI g4140643
BLAST score 39
E value 1.0e-12
Match length 39
% identity 100
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299700
Seq. ID LIB3157-002-Q1-K1-E6
Method BLASTN
NCBI GI g22204
BLAST score 35
E value 2.0e-10
Match length 59
% identity 90
NCBI Description Maize Bz-McC gene for UDPglucose flavonoid glycosyl-transferase

Seq. No. 299701
Seq. ID LIB3157-002-Q1-K1-F3
Method BLASTX
NCBI GI g729470
BLAST score 517
E value 9.0e-53
Match length 123
% identity 77
NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
>gi_542089_pir_JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_(Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No. 299702
Seq. ID LIB3157-002-Q1-K1-F5
Method BLASTX
NCBI GI g4263517
BLAST score 153
E value 3.0e-10
Match length 80
% identity 39
NCBI Description (AC004044) similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis thaliana]

Seq. No. 299703
Seq. ID LIB3157-003-Q1-K1-A2
Method BLASTX
NCBI GI g2137490

BLAST score 205
E value 2.0e-16
Match length 98
% identity 48
NCBI Description lymphocyte specific helicase - mouse >gi_805296 (U25691)
lymphocyte specific helicase [Mus musculus]

Seq. No. 299704
Seq. ID LIB3157-003-Q1-K1-C2
Method BLASTN
NCBI GI g2668741
BLAST score 253
E value 1.0e-140
Match length 253
% identity 100
NCBI Description Zea mays glycine-rich RNA binding protein (GRP) mRNA,
complete cds

Seq. No. 299705
Seq. ID LIB3157-003-Q1-K1-H8
Method BLASTN
NCBI GI g22237
BLAST score 192
E value 1.0e-104
Match length 200
% identity 99
NCBI Description Maize mRNA for cytosolic GAPDH (GapC)
glyceraldehyde-3-phosphate dehydrogenase

Seq. No. 299706
Seq. ID LIB3157-004-Q1-K1-A11
Method BLASTN
NCBI GI g22292
BLAST score 53
E value 4.0e-21
Match length 61
% identity 97
NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 299707
Seq. ID LIB3157-004-Q1-K1-A2
Method BLASTX
NCBI GI g3894186
BLAST score 241
E value 2.0e-20
Match length 107
% identity 50
NCBI Description (AC005662) putative embryo-abundant protein [Arabidopsis
thaliana]

Seq. No. 299708
Seq. ID LIB3157-004-Q1-K1-A6
Method BLASTN
NCBI GI g2668747
BLAST score 119
E value 2.0e-60
Match length 123

% identity 99
NCBI Description Zea mays ribosomal protein L17 (rpl17) mRNA, complete cds

Seq. No. 299709
Seq. ID LIB3157-004-Q1-K1-A9
Method BLASTX
NCBI GI g2668742
BLAST score 211
E value 6.0e-17
Match length 71
% identity 63
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 299710
Seq. ID LIB3157-004-Q1-K1-E2
Method BLASTX
NCBI GI g3913430
BLAST score 223
E value 3.0e-18
Match length 94
% identity 48
NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13) >gi_2407195 (AF017153) putative RNA helicase and RNA dependent ATPase [Mus musculus]

Seq. No. 299711
Seq. ID LIB3157-005-Q1-K1-A10
Method BLASTN
NCBI GI g22161
BLAST score 110
E value 6.0e-55
Match length 154
% identity 93
NCBI Description Z.mays MANT1 mRNA for adenine nucleotide translocator (also called ADP/ATP translocase)

Seq. No. 299712
Seq. ID LIB3157-005-Q1-K1-C12
Method BLASTX
NCBI GI g730456
BLAST score 198
E value 1.0e-15
Match length 43
% identity 86
NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 299713
Seq. ID LIB3157-005-Q1-K1-G10
Method BLASTX
NCBI GI g4336747
BLAST score 166
E value 2.0e-11
Match length 66
% identity 52
NCBI Description (AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No. 299714

Seq. ID LIB3157-005-Q1-K1-G3
Method BLASTX
NCBI GI g531829
BLAST score 209
E value 1.0e-16
Match length 66
% identity 62
NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No. 299715
Seq. ID LIB3157-006-Q1-K1-F9
Method BLASTN
NCBI GI g2062691
BLAST score 37
E value 1.0e-11
Match length 37
% identity 100
NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete cds

Seq. No. 299716
Seq. ID LIB3157-007-Q1-K1-F1
Method BLASTN
NCBI GI g463151
BLAST score 45
E value 4.0e-16
Match length 65
% identity 92
NCBI Description Zea mays high sulfur zein gene, complete cds

Seq. No. 299717
Seq. ID LIB3157-007-Q1-K1-G12
Method BLASTN
NCBI GI g2921303
BLAST score 67
E value 2.0e-29
Match length 159
% identity 86
NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA, complete cds

Seq. No. 299718
Seq. ID LIB3157-007-Q1-K1-H4
Method BLASTX
NCBI GI g3128168
BLAST score 190
E value 2.0e-14
Match length 59
% identity 58
NCBI Description (AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No. 299719
Seq. ID LIB3157-007-Q1-K1-H7
Method BLASTN
NCBI GI g1870198

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BLAST score 62
E value 6.0e-27
Match length 62
% identity 100
NCBI Description Z.mays mRNA for acyl carrier protein

Seq. No. 299720
Seq. ID LIB3157-008-Q1-K1-B6
Method BLASTX
NCBI GI g2160174
BLAST score 221
E value 4.0e-18
Match length 58
% identity 74
NCBI Description (AC000132) Identical to A. thaliana PUR2 (gb_X74766). ESTs
gb_ATTS3927,gb_N96446 come from this gene. [Arabidopsis
thaliana]

Seq. No. 299721
Seq. ID LIB3157-008-Q1-K1-G6
Method BLASTN
NCBI GI g1063665
BLAST score 48
E value 2.0e-18
Match length 146
% identity 82
NCBI Description Zea mays unknown protein mRNA, complete cds

Seq. No. 299722
Seq. ID LIB3157-008-Q1-K1-H9
Method BLASTN
NCBI GI g3043528
BLAST score 147
E value 6.0e-77
Match length 171
% identity 97
NCBI Description Zea mays mRNA for flavin containing polyamine oxidase (PAO)

Seq. No. 299723
Seq. ID LIB3157-009-Q1-K1-B6
Method BLASTN
NCBI GI g949979
BLAST score 34
E value 9.0e-10
Match length 57
% identity 89
NCBI Description Z.mays Glossy2 locus DNA

Seq. No. 299724
Seq. ID LIB3157-009-Q1-K1-C11
Method BLASTX
NCBI GI g2511531
BLAST score 172
E value 2.0e-12
Match length 40
% identity 85
NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]

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>gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
[Eleusine indica]

Seq. No. 299725
Seq. ID LIB3157-009-Q1-K1-D9
Method BLASTN
NCBI GI g2773153
BLAST score 61
E value 9.0e-26
Match length 157
% identity 85
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein (Asrl1) mRNA, complete cds

Seq. No. 299726
Seq. ID LIB3157-009-Q1-K1-G10
Method BLASTN
NCBI GI g1177368
BLAST score 170
E value 1.0e-90
Match length 294
% identity 90
NCBI Description Z.mays mRNA for ribosomal protein L39

Seq. No. 299727
Seq. ID LIB3157-009-Q1-K1-G11
Method BLASTX
NCBI GI g3928093
BLAST score 191
E value 2.0e-14
Match length 48
% identity 77
NCBI Description (AC005770) IVR-like protein [Arabidopsis thaliana]

Seq. No. 299728
Seq. ID LIB3157-012-Q1-K1-A3
Method BLASTN
NCBI GI g531828
BLAST score 47
E value 2.0e-17
Match length 79
% identity 90
NCBI Description Cloning vector pSport1, complete cds

Seq. No. 299729
Seq. ID LIB3157-012-Q1-K1-G6
Method BLASTX
NCBI GI g531829
BLAST score 163
E value 2.0e-11
Match length 63
% identity 51
NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No. 299730
Seq. ID LIB3157-013-Q1-K1-A12

Method BLASTN
NCBI GI g1498052
BLAST score 105
E value 5.0e-52
Match length 197
% identity 88
NCBI Description Zea mays ribosomal protein S8 mRNA, complete cds

Seq. No. 299731
Seq. ID LIB3157-013-Q1-K1-E8
Method BLASTN
NCBI GI g168577
BLAST score 68
E value 6.0e-30
Match length 109
% identity 99
NCBI Description Maize phospholipid transfer protein mRNA, 3' end

Seq. No. 299732
Seq. ID LIB3157-014-Q1-K1-A8
Method BLASTN
NCBI GI g1532072
BLAST score 73
E value 7.0e-33
Match length 236
% identity 83
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No. 299733
Seq. ID LIB3157-014-Q1-K1-B6
Method BLASTX
NCBI GI g1706738
BLAST score 273
E value 4.0e-24
Match length 119
% identity 44
NCBI Description FLAVONOL 3-SULFOTRANSFERASE (F3-ST) >gi_498645 (U10275)
flavonol 3-sulfotransferase [Flaveria bidentis]

Seq. No. 299734
Seq. ID LIB3157-014-Q1-K1-C12
Method BLASTX
NCBI GI g531829
BLAST score 200
E value 1.0e-15
Match length 69
% identity 57
NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector
pSport1]

Seq. No. 299735
Seq. ID LIB3157-014-Q1-K1-G12
Method BLASTX
NCBI GI g3789942
BLAST score 144
E value 1.0e-14
Match length 68

% identity 14
NCBI Description (AF093505) polyubiquitin [Saccharum hybrid cultivar H32-8560]

Seq. No. 299736
Seq. ID LIB3157-015-Q1-K1-D5
Method BLASTX
NCBI GI g971137
BLAST score 145
E value 4.0e-09
Match length 58
% identity 48
NCBI Description (D63840) modified alpha peptide of E. coli beta-galactosidase [Cloning vector pKF296]
>gi_971149_dbj_BAA09905_(D63844) modified alpha peptide of E. coli beta-galactosidase [Cloning vector pKF16k]

Seq. No. 299737
Seq. ID LIB3157-015-Q1-K1-G5
Method BLASTN
NCBI GI g3821780
BLAST score 37
E value 2.0e-11
Match length 37
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 299738
Seq. ID LIB3157-016-Q1-K1-C12
Method BLASTN
NCBI GI g498774
BLAST score 77
E value 2.0e-35
Match length 263
% identity 82
NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein

Seq. No. 299739
Seq. ID LIB3157-016-Q1-K1-C3
Method BLASTN
NCBI GI g3420038
BLAST score 60
E value 1.0e-25
Match length 123
% identity 44
NCBI Description Zea mays gypsy/Ty3-type retrotransposon Tekay, complete sequence

Seq. No. 299740
Seq. ID LIB3157-016-Q1-K1-F7
Method BLASTN
NCBI GI g1870200
BLAST score 59
E value 6.0e-25
Match length 75
% identity 95
NCBI Description Z.mays cyp71c2 gene

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Seq. No.	299741
Seq. ID	LIB3157-016-Q1-K1-G2
Method	BLASTX
NCBI GI	g1079321
BLAST score	155
E value	2.0e-13
Match length	83
% identity	51
NCBI Description	XPMC2 protein - African clawed frog >gi_595380 (U10185) XPMC2 protein [Xenopus laevis]
Seq. No.	299742
Seq. ID	LIB3157-017-Q1-K1-A12
Method	BLASTX
NCBI GI	g1711381
BLAST score	137
E value	1.0e-08
Match length	53
% identity	57
NCBI Description	PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT) >gi_1256204_dbj_BAA12206 (D84061) phosphoserine aminotransferase [Spinacia oleracea]
Seq. No.	299743
Seq. ID	LIB3157-017-Q1-K1-C6
Method	BLASTX
NCBI GI	g567893
BLAST score	177
E value	8.0e-13
Match length	73
% identity	52
NCBI Description	(L37382) beta-galactosidase-complementation protein [Cloning vector]
Seq. No.	299744
Seq. ID	LIB3157-017-Q1-K1-D10
Method	BLASTN
NCBI GI	g342631
BLAST score	104
E value	2.0e-51
Match length	239
% identity	86
NCBI Description	Maize mitochondrial F-1-ATPase subunit-2 mRNA, complete cds
Seq. No.	299745
Seq. ID	LIB3157-017-Q1-K1-D5
Method	BLASTN
NCBI GI	g433038
BLAST score	95
E value	6.0e-46
Match length	202
% identity	88
NCBI Description	Zea mays W-22 clone cDNA7 retroelement PREM-1-containing mRNA
Seq. No.	299746

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Seq. ID	LIB3157-017-Q1-K1-D8
Method	BLASTN
NCBI GI	g22223
BLAST score	55
E value	3.0e-22
Match length	59
% identity	98
NCBI Description	Maize cab-1 gene for chlorophyll a/b-binding protein
Seq. No.	299747
Seq. ID	LIB3157-017-Q1-K1-E9
Method	BLASTN
NCBI GI	g22332
BLAST score	76
E value	7.0e-35
Match length	120
% identity	91
NCBI Description	Z.mays HRGP gene
Seq. No.	299748
Seq. ID	LIB3157-018-Q1-K1-B11
Method	BLASTN
NCBI GI	g1498052
BLAST score	160
E value	8.0e-85
Match length	229
% identity	92
NCBI Description	Zea mays ribosomal protein S8 mRNA, complete cds
Seq. No.	299749
Seq. ID	LIB3157-018-Q1-K1-C12
Method	BLASTX
NCBI GI	g2323410
BLAST score	186
E value	5.0e-14
Match length	56
% identity	61
NCBI Description	(AF015913) Skb1Hs [Homo sapiens]
Seq. No.	299750
Seq. ID	LIB3157-018-Q1-K1-E11
Method	BLASTN
NCBI GI	g531828
BLAST score	42
E value	1.0e-14
Match length	82
% identity	88
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	299751
Seq. ID	LIB3157-018-Q1-K1-G9
Method	BLASTX
NCBI GI	g168422
BLAST score	211
E value	5.0e-17
Match length	46
% identity	89

NCBI Description (J04550) auxin-binding protein precursor [Zea mays]
Seq. No. 299752
Seq. ID LIB3157-018-Q1-K1-H6
Method BLASTX
NCBI GI g2267597
BLAST score 259
E value 1.0e-24
Match length 83
% identity 70
NCBI Description (AF009413) 10 kDa chaperonin [Oryza sativa]
Seq. No. 299753
Seq. ID LIB3157-019-Q1-K1-A10
Method BLASTX
NCBI GI g3894187
BLAST score 218
E value 1.0e-17
Match length 83
% identity 63
NCBI Description (AC005662) hypothetical protein [Arabidopsis thaliana]
Seq. No. 299754
Seq. ID LIB3157-019-Q1-K1-A3
Method BLASTX
NCBI GI g2864618
BLAST score 149
E value 1.0e-09
Match length 67
% identity 46
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]
Seq. No. 299755
Seq. ID LIB3157-019-Q1-K1-C8
Method BLASTX
NCBI GI g2160180
BLAST score 261
E value 1.0e-22
Match length 76
% identity 63
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No. 299756
Seq. ID LIB3157-019-Q1-K1-G1
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No. 299757
Seq. ID LIB3157-019-Q1-K1-H1
Method BLASTX
NCBI GI g4235430
BLAST score 187

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E value 3.0e-14
Match length 50
% identity 72
NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No. 299758
Seq. ID LIB3157-020-Q1-K1-A4
Method BLASTN
NCBI GI g22091
BLAST score 108
E value 4.0e-54
Match length 173
% identity 91
NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. 299759
Seq. ID LIB3157-020-Q1-K1-A7
Method BLASTN
NCBI GI g444046
BLAST score 48
E value 4.0e-18
Match length 48
% identity 100
NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor

Seq. No. 299760
Seq. ID LIB3157-020-Q1-K1-C11
Method BLASTN
NCBI GI g22324
BLAST score 120
E value 5.0e-61
Match length 192
% identity 91
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No. 299761
Seq. ID LIB3157-020-Q1-K1-G1
Method BLASTN
NCBI GI g168500
BLAST score 86
E value 7.0e-41
Match length 110
% identity 95
NCBI Description Maize (Zea mays) histone H4 gene (H4C14), complete cds

Seq. No. 299762
Seq. ID LIB3157-021-Q1-K1-B10
Method BLASTN
NCBI GI g3822035
BLAST score 146
E value 2.0e-76
Match length 201
% identity 94
NCBI Description Zea mays endo-1,3-1,4-beta-D-glucanase mRNA, complete cds

Seq. No. 299763
Seq. ID LIB3157-021-Q1-K1-C4

Method BLASTX
NCBI GI g1001834
BLAST score 538
E value 4.0e-55
Match length 143
% identity 69
NCBI Description (D64005) hypothetical protein [Synechocystis sp.]

Seq. No. 299764
Seq. ID LIB3157-021-Q1-K1-D4
Method BLASTN
NCBI GI g168468
BLAST score 42
E value 3.0e-14
Match length 42
% identity 100
NCBI Description Maize ferredoxin I (Fd) isoprotein mRNA, pFD1

Seq. No. 299765
Seq. ID LIB3157-021-Q1-K1-E9
Method BLASTN
NCBI GI g22251
BLAST score 55
E value 5.0e-22
Match length 55
% identity 100
NCBI Description Z.mays mRNA that delineates a novel subset of cortical cells

Seq. No. 299766
Seq. ID LIB3157-021-Q1-K1-G1
Method BLASTN
NCBI GI g1244652
BLAST score 81
E value 1.0e-37
Match length 141
% identity 89
NCBI Description Zea mays copia-type retroelement PREM-2 gag gene, complete cds

Seq. No. 299767
Seq. ID LIB3158-001-Q1-K1-C6
Method BLASTX
NCBI GI g1170937
BLAST score 203
E value 4.0e-16
Match length 51
% identity 76
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No. 299768
Seq. ID LIB3158-001-Q1-K1-D2
Method BLASTX
NCBI GI g3024018

BLAST score	303
E value	1.0e-27
Match length	71
% identity	85
NCBI Description	INITIATION FACTOR 5A (EIF-5A) (EIF-4D) >gi_1546919_emb_CAA69225_(Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation initiation factor 5A [Zea mays]
Seq. No.	299769
Seq. ID	LIB3158-001-Q1-K1-E2
Method	BLASTX
NCBI GI	g1747294
BLAST score	184
E value	3.0e-14
Match length	47
% identity	79
NCBI Description	(D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
Seq. No.	299770
Seq. ID	LIB3158-001-Q1-K1-E5
Method	BLASTX
NCBI GI	g480669
BLAST score	289
E value	3.0e-26
Match length	103
% identity	62
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Jerusalem artichoke (fragment) >gi_1359894_emb_CAA81210_(Z26251) NADPH-ferrihemoprotein reductase [Helianthus tuberosus]
Seq. No.	299771
Seq. ID	LIB3158-001-Q1-K1-F6
Method	BLASTX
NCBI GI	g693916
BLAST score	372
E value	5.0e-36
Match length	85
% identity	85
NCBI Description	(U21111) chlorophyll a/b binding protein [Solanum tuberosum]
Seq. No.	299772
Seq. ID	LIB3158-003-Q1-K1-B2
Method	BLASTX
NCBI GI	g2662343
BLAST score	196
E value	2.0e-15
Match length	80
% identity	51
NCBI Description	(D63581) EF-1 alpha [Oryza sativa]
Seq. No.	299773
Seq. ID	LIB3158-003-Q1-K1-C11
Method	BLASTN
NCBI GI	g169818
BLAST score	76

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E value	1.0e-34
Match length	76
% identity	100
NCBI Description	Rice 25S ribosomal RNA gene
Seq. No.	299774
Seq. ID	LIB3158-003-Q1-K1-D2
Method	BLASTN
NCBI GI	g2921303
BLAST score	98
E value	4.0e-48
Match length	170
% identity	89
NCBI Description	Zea mays herbicide safener binding protein (SBP1) mRNA, complete cds
Seq. No.	299775
Seq. ID	LIB3158-003-Q1-K1-D9
Method	BLASTX
NCBI GI	g548604
BLAST score	164
E value	2.0e-11
Match length	34
% identity	88
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_1076728_pir_S51813 photosystem-I PSI-F chain precursor - barley >gi_469560 (U08135) photosystem-I PSI-F subunit precursor [Hordeum vulgare]
Seq. No.	299776
Seq. ID	LIB3158-003-Q1-K1-E11
Method	BLASTX
NCBI GI	g3068714
BLAST score	201
E value	2.0e-30
Match length	114
% identity	61
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]
Seq. No.	299777
Seq. ID	LIB3158-003-Q1-K1-G5
Method	BLASTN
NCBI GI	g1850902
BLAST score	93
E value	5.0e-45
Match length	121
% identity	95
NCBI Description	Z.mays cyp71c4 gene
Seq. No.	299778
Seq. ID	LIB3158-003-Q1-K1-G6
Method	BLASTX
NCBI GI	g3258575
BLAST score	320
E value	6.0e-30
Match length	93

% identity 70
NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 299779
Seq. ID LIB3158-003-Q1-K1-G8
Method BLASTX
NCBI GI g3603353
BLAST score 218
E value 8.0e-18
Match length 109
% identity 46
NCBI Description (AF074843) peroxisomal targeting signal type 1 receptor [Arabidopsis thaliana]

Seq. No. 299780
Seq. ID LIB3158-004-Q1-K1-A8
Method BLASTX
NCBI GI g4454799
BLAST score 158
E value 3.0e-11
Match length 38
% identity 87
NCBI Description (AF079782) translation initiation factor 4A2 [Zea mays]

Seq. No. 299781
Seq. ID LIB3158-004-Q1-K1-F4
Method BLASTN
NCBI GI g435312
BLAST score 73
E value 2.0e-33
Match length 81
% identity 98
NCBI Description Z.mays mRNA for beta-D-glucosidase

Seq. No. 299782
Seq. ID LIB3158-005-Q1-K1-A12
Method BLASTX
NCBI GI g4539459
BLAST score 152
E value 3.0e-10
Match length 59
% identity 54
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 299783
Seq. ID LIB3158-005-Q1-K1-A3
Method BLASTX
NCBI GI g82734
BLAST score 645
E value 9.0e-68
Match length 136
% identity 29
NCBI Description ubiquitin precursor - maize (fragment)
>gi_226763_prf_1604470A poly-ubiquitin [Zea mays]

Seq. No. 299784
Seq. ID LIB3158-005-Q1-K1-A5

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Method	BLASTN
NCBI GI	g1060934
BLAST score	55
E value	2.0e-22
Match length	63
% identity	97
NCBI Description	Maize mRNA for mLIP15 (DNA-binding factor), complete cds
Seq. No.	299785
Seq. ID	LIB3158-005-Q1-K1-H11
Method	BLASTX
NCBI GI	g3176669
BLAST score	162
E value	3.0e-11
Match length	57
% identity	42
NCBI Description	(AC004393) End is cut off. [Arabidopsis thaliana]
Seq. No.	299786
Seq. ID	LIB3158-005-Q1-K1-H12
Method	BLASTN
NCBI GI	g3108052
BLAST score	47
E value	2.0e-17
Match length	59
% identity	95
NCBI Description	Zea mays myo-inositol 1-phosphate synthase mRNA, complete cds
Seq. No.	299787
Seq. ID	LIB3158-006-Q1-K1-B9
Method	BLASTX
NCBI GI	g2285792
BLAST score	168
E value	9.0e-12
Match length	43
% identity	70
NCBI Description	(AB004568) cyanase [Arabidopsis thaliana] >gi_3287503_dbj_BAA31224_ (AB015748) cyanase [Arabidopsis thaliana]
Seq. No.	299788
Seq. ID	LIB3158-006-Q1-K1-D4
Method	BLASTX
NCBI GI	g531829
BLAST score	163
E value	2.0e-11
Match length	64
% identity	55
NCBI Description	(U12390) beta-galactosidase alpha peptide [cloning vector pSport1]
Seq. No.	299789
Seq. ID	LIB3158-006-Q1-K1-E5
Method	BLASTN
NCBI GI	g4140643
BLAST score	109

E value 2.0e-54
Match length 237
% identity 87
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 299790
Seq. ID LIB3158-006-Q1-K1-F5
Method BLASTX
NCBI GI g1666228
BLAST score 293
E value 2.0e-34
Match length 83
% identity 92
NCBI Description (U76190) actin [Pisum sativum] >gi_1666230 (U76191) actin [Pisum sativum] >gi_1724137 (U81046) actin [Pisum sativum] >gi_1724139 (U81047) actin [Pisum sativum]

Seq. No. 299791
Seq. ID LIB3158-008-Q1-K1-B6
Method BLASTX
NCBI GI g3450889
BLAST score 167
E value 4.0e-12
Match length 70
% identity 53
NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No. 299792
Seq. ID LIB3158-008-Q1-K1-B7
Method BLASTX
NCBI GI g1705678
BLAST score 258
E value 1.0e-22
Match length 84
% identity 68
NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213) valosin-containing protein [Glycine max]

Seq. No. 299793
Seq. ID LIB3158-008-Q1-K1-E4
Method BLASTN
NCBI GI g2921303
BLAST score 75
E value 2.0e-34
Match length 159
% identity 87
NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA, complete cds

Seq. No. 299794
Seq. ID LIB3158-008-Q1-K1-F4
Method BLASTX
NCBI GI g4585901
BLAST score 148
E value 4.0e-17

Match length 119
% identity 43
NCBI Description (AC007133) hypothetical protein [Arabidopsis thaliana]

Seq. No. 299795
Seq. ID LIB3158-008-Q1-K1-F7
Method BLASTX
NCBI GI g1362615
BLAST score 149
E value 1.0e-17
Match length 100
% identity 50
NCBI Description iswi protein - fruit fly (Drosophila melanogaster)
>gi_439197 (L27127) ISWI protein [Drosophila melanogaster]

Seq. No. 299796
Seq. ID LIB3158-008-Q1-K1-H11
Method BLASTX
NCBI GI g541800
BLAST score 238
E value 3.0e-20
Match length 78
% identity 64
NCBI Description protein kinase (EC 2.7.1.37) cdc2-Pa - Norway spruce
>gi_454980_emb_CAA54746_ (X77680) cdc2Pa [Picea abies]

Seq. No. 299797
Seq. ID LIB3158-010-Q1-K1-E10
Method BLASTX
NCBI GI g2129613
BLAST score 414
E value 1.0e-40
Match length 141
% identity 59
NCBI Description homeotic protein BELL - Arabidopsis thaliana >gi_1122533
(U39944) BELL1 [Arabidopsis thaliana]

Seq. No. 299798
Seq. ID LIB3158-010-Q1-K1-E2
Method BLASTX
NCBI GI g2370232
BLAST score 152
E value 3.0e-10
Match length 44
% identity 64
NCBI Description (AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]

Seq. No. 299799
Seq. ID LIB3158-010-Q1-K1-E4
Method BLASTN
NCBI GI g3043528
BLAST score 41
E value 1.0e-13
Match length 77
% identity 88
NCBI Description Zea mays mRNA for flavin containing polyamine oxidase (PAO)

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Seq. No.	299800
Seq. ID	LIB3158-010-Q1-K1-G11
Method	BLASTX
NCBI GI	g2245378
BLAST score	143
E value	3.0e-13
Match length	80
% identity	53
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]
Seq. No.	299801
Seq. ID	LIB3158-011-Q1-K1-B10
Method	BLASTX
NCBI GI	g4580394
BLAST score	214
E value	2.0e-17
Match length	62
% identity	60
NCBI Description	(AC007171) putative fatty acid elongase [Arabidopsis thaliana]
Seq. No.	299802
Seq. ID	LIB3158-011-Q1-K1-C4
Method	BLASTX
NCBI GI	g3688328
BLAST score	192
E value	3.0e-15
Match length	64
% identity	66
NCBI Description	(AJ228325) reverse transcriptase [Ginkgo biloba]
Seq. No.	299803
Seq. ID	LIB3158-012-Q1-K1-A6
Method	BLASTX
NCBI GI	g4090884
BLAST score	188
E value	3.0e-14
Match length	62
% identity	63
NCBI Description	(AF025333) vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana]
Seq. No.	299804
Seq. ID	LIB3158-012-Q1-K1-A7
Method	BLASTN
NCBI GI	g559535
BLAST score	46
E value	9.0e-17
Match length	146
% identity	83
NCBI Description	Z.mays mRNA for metallothionein
Seq. No.	299805
Seq. ID	LIB3158-012-Q1-K1-B3
Method	BLASTX
NCBI GI	g1498388
BLAST score	405

E value 1.0e-39
Match length 104
% identity 86
NCBI Description (U60510) actin [Zea mays]

Seq. No. 299806
Seq. ID LIB3158-012-Q1-K1-H10
Method BLASTX
NCBI GI g629843
BLAST score 353
E value 1.0e-33
Match length 99
% identity 74
NCBI Description heat shock protein hsp70-4 - maize (fragment)
>gi_498773_emb_CAA55183_ (X78414) heat shock protein 70 kDa
[Zea mays]

Seq. No. 299807
Seq. ID LIB3158-012-Q1-K1-H4
Method BLASTN
NCBI GI g22121
BLAST score 35
E value 2.0e-10
Match length 111
% identity 83
NCBI Description Maize alcohol dehydrogenase 1 gene (Adh1-1F)

Seq. No. 299808
Seq. ID LIB3158-014-Q1-K1-A11
Method BLASTX
NCBI GI g119355
BLAST score 158
E value 5.0e-11
Match length 59
% identity 58
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
>gi_100869_pir_S16257 phosphopyruvate hydratase (EC
4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
[Zea mays]

Seq. No. 299809
Seq. ID LIB3158-014-Q1-K1-A12
Method BLASTX
NCBI GI g3377797
BLAST score 175
E value 4.0e-14
Match length 71
% identity 65
NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara]

Seq. No. 299810
Seq. ID LIB3158-014-Q1-K1-A3

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Method	BLASTX
NCBI GI	g2880047
BLAST score	182
E value	3.0e-16
Match length	118
% identity	44
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]
Seq. No.	299811
Seq. ID	LIB3158-014-Q1-K1-B9
Method	BLASTX
NCBI GI	g531829
BLAST score	144
E value	4.0e-09
Match length	62
% identity	48
NCBI Description	(U12390) beta-galactosidase alpha peptide [cloning vector pSport1]
Seq. No.	299812
Seq. ID	LIB3158-014-Q1-K1-C8
Method	BLASTN
NCBI GI	g500854
BLAST score	36
E value	6.0e-11
Match length	96
% identity	84
NCBI Description	Maize dissociation element DNA
Seq. No.	299813
Seq. ID	LIB3158-014-Q1-K1-E8
Method	BLASTN
NCBI GI	g473602
BLAST score	71
E value	7.0e-32
Match length	151
% identity	87
NCBI Description	Zea mays W-22 histone H2A mRNA, complete cds
Seq. No.	299814
Seq. ID	LIB3158-014-Q1-K1-G5
Method	BLASTX
NCBI GI	g728630
BLAST score	170
E value	5.0e-12
Match length	59
% identity	61
NCBI Description	(X85103) orf [Oryza sativa]
Seq. No.	299815
Seq. ID	LIB3158-014-Q1-K1-G9
Method	BLASTX
NCBI GI	g1518540
BLAST score	268
E value	1.0e-23
Match length	103
% identity	56

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NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No. 299816
Seq. ID LIB3158-015-Q1-K1-A4
Method BLASTX
NCBI GI g2149640
BLAST score 230
E value 1.0e-19
Match length 63
% identity 65
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No. 299817
Seq. ID LIB3158-015-Q1-K1-C5
Method BLASTX
NCBI GI g2996096
BLAST score 545
E value 3.0e-56
Match length 107
% identity 98
NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]
Seq. No. 299818
Seq. ID LIB3158-015-Q1-K1-D1
Method BLASTX
NCBI GI g1173456
BLAST score 140
E value 4.0e-09
Match length 44
% identity 55
NCBI Description SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) >gi_600750 (U15009) Sm D3 [Homo sapiens]
Seq. No. 299819
Seq. ID LIB3158-016-Q1-K1-A7
Method BLASTX
NCBI GI g1710841
BLAST score 150
E value 5.0e-10
Match length 43
% identity 70
NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_758247 emb CAA56278_ (X79905) S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]
Seq. No. 299820
Seq. ID LIB3158-016-Q1-K1-D2
Method BLASTX
NCBI GI g2995953
BLAST score 266
E value 3.0e-23
Match length 72
% identity 69
NCBI Description (AF053565) glutaredoxin I [Mesembryanthemum crystallinum]
Seq. No. 299821

Seq. ID LIB3158-016-Q1-K1-E4
 Method BLASTX
 NCBI GI g2190992
 BLAST score 202
 E value 3.0e-16
 Match length 83
 % identity 51
 NCBI Description (AF004358) glutathione S-transferase TSI-1 [Aegilops tauschii]

Seq. No. 299822
 Seq. ID LIB3158-016-Q1-K1-F12
 Method BLASTX
 NCBI GI g417482
 BLAST score 139
 E value 8.0e-09
 Match length 41
 % identity 63
 NCBI Description PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir_JQ2254 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta chain - garden pea >gi_169049 (L08664) farnesyl-protein transferase beta-subunit [Pisum sativum]

Seq. No. 299823
 Seq. ID LIB3158-017-Q1-K1-A10
 Method BLASTX
 NCBI GI g1532168
 BLAST score 189
 E value 1.0e-14
 Match length 60
 % identity 75
 NCBI Description (U63815) localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initiation codon and stop codon could not be precisely determined [Arabidopsis thaliana]

Seq. No. 299824
 Seq. ID LIB3158-017-Q1-K1-B11
 Method BLASTX
 NCBI GI g1076644
 BLAST score 161
 E value 1.0e-11
 Match length 72
 % identity 49
 NCBI Description sucrose transport protein - common tobacco >gi_575351_emb_CAA57727_ (X82276) sucrose transporter [Nicotiana tabacum]

Seq. No. 299825
 Seq. ID LIB3158-017-Q1-K1-B12
 Method BLASTX
 NCBI GI g1061040
 BLAST score 350
 E value 1.0e-33

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Match length 76
% identity 84
NCBI Description (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]
>gi_1587694_prf_2207220A sterol C-methyltransferase
[Arabidopsis thaliana]

Seq. No. 299826
Seq. ID LIB3158-017-Q1-K1-B4
Method BLASTX
NCBI GI g1532165
BLAST score 264
E value 4.0e-23
Match length 80
% identity 60
NCBI Description (U63815) similar to dehydrogenase encoded by GenBank
Accession Number S39508; localized according to blastn
similarity to EST sequences; therefore, the coding span
corresponds only to an area of similarity since the
initiation codon and stop

Seq. No. 299827
Seq. ID LIB3158-017-Q1-K1-C10
Method BLASTX
NCBI GI g416758
BLAST score 247
E value 3.0e-21
Match length 86
% identity 58
NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130)
carboxypeptidase Y-like protein [Arabidopsis thaliana]
>gi_445120_prf_1908426A carboxypeptidase Y [Arabidopsis
thaliana]

Seq. No. 299828
Seq. ID LIB3158-017-Q1-K1-D12
Method BLASTX
NCBI GI g2827715
BLAST score 432
E value 6.0e-43
Match length 107
% identity 26
NCBI Description (AL021684) receptor protein kinase - like protein
[Arabidopsis thaliana]

Seq. No. 299829
Seq. ID LIB3158-017-Q1-K1-F11
Method BLASTX
NCBI GI g2829924
BLAST score 177
E value 2.0e-13
Match length 72
% identity 53
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 299830
Seq. ID LIB3158-017-Q1-K1-F3
Method BLASTN

NCBI GI g13923
BLAST score 60
E value 1.0e-25
Match length 100
% identity 91
NCBI Description Maize mitochondrial gene for 18S rRNA

Seq. No. 299831
Seq. ID LIB3158-017-Q1-K1-F9
Method BLASTX
NCBI GI g1150932
BLAST score 305
E value 3.0e-28
Match length 89
% identity 70
NCBI Description (X88864) cyclin [Medicago sativa]

Seq. No. 299832
Seq. ID LIB3158-017-Q1-K1-G12
Method BLASTX
NCBI GI g4206210
BLAST score 151
E value 2.0e-10
Match length 43
% identity 65
NCBI Description (AF071527) putative calcium channel [Arabidopsis thaliana]
>gi_4263043_gb_AAD15312_(AC005142) putative calcium
channel [Arabidopsis thaliana]

Seq. No. 299833
Seq. ID LIB3158-017-Q1-K1-G9
Method BLASTX
NCBI GI g1053047
BLAST score 416
E value 3.0e-41
Match length 83
% identity 100
NCBI Description (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
[Glycine max]

Seq. No. 299834
Seq. ID LIB3158-017-Q1-K1-H10
Method BLASTX
NCBI GI g3452497
BLAST score 442
E value 3.0e-44
Match length 87
% identity 97
NCBI Description (Y17796) ketol-acid reductoisomerase [Pisum sativum]

Seq. No. 299835
Seq. ID LIB3158-017-Q1-K1-H11
Method BLASTX
NCBI GI g4580460
BLAST score 396
E value 6.0e-39

Match length 84
% identity 93
NCBI Description (AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No. 299836
Seq. ID LIB3158-018-Q1-K1-D4
Method BLASTX
NCBI GI g3378652
BLAST score 602
E value 1.0e-62
Match length 119
% identity 99
NCBI Description (AJ005039) CaM-1 [Nicotiana plumbaginifolia]
>gi_3378654_emb_CAA06307_ (AJ005040) CaM-2 [Nicotiana plumbaginifolia]

Seq. No. 299837
Seq. ID LIB3158-018-Q1-K1-E4
Method BLASTX
NCBI GI g629858
BLAST score 219
E value 9.0e-18
Match length 38
% identity 100
NCBI Description protein kinase C inhibitor - maize

Seq. No. 299838
Seq. ID LIB3158-018-Q1-K1-F1
Method BLASTX
NCBI GI g4587614
BLAST score 256
E value 4.0e-22
Match length 82
% identity 52
NCBI Description (AC006951) hypothetical protein [Arabidopsis thaliana]

Seq. No. 299839
Seq. ID LIB3158-018-Q1-K1-F10
Method BLASTX
NCBI GI g4582445
BLAST score 175
E value 1.0e-12
Match length 49
% identity 65
NCBI Description (AC007071) unknown protein [Arabidopsis thaliana]
>gi_4589952_gb_AAD26470.1_AC007169_2 (AC007169) unknown protein [Arabidopsis thaliana]

Seq. No. 299840
Seq. ID LIB3158-018-Q1-K1-G5
Method BLASTN
NCBI GI g22435
BLAST score 71
E value 9.0e-32
Match length 133
% identity 87

NCBI Description Z.mays PK1 gene for receptor-like protein kinase

Seq. No. 299841
Seq. ID LIB3158-018-Q1-K1-H3
Method BLASTX
NCBI GI g119355
BLAST score 365
E value 6.0e-35
Match length 128
% identity 64
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
>gi_100869_pir_S16257 phosphopyruvate hydratase (EC
4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
[Zea mays]

Seq. No. 299842
Seq. ID LIB3159-001-Q1-K1-A9
Method BLASTN
NCBI GI g4140643
BLAST score 107
E value 2.0e-53
Match length 215
% identity 33
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
complete sequence

Seq. No. 299843
Seq. ID LIB3159-001-Q1-K1-C10
Method BLASTN
NCBI GI g16072
BLAST score 47
E value 2.0e-17
Match length 202
% identity 81
NCBI Description Acetabularia mediterranea zein gene

Seq. No. 299844
Seq. ID LIB3159-001-Q1-K1-C9
Method BLASTX
NCBI GI g141606
BLAST score 154
E value 2.0e-10
Match length 74
% identity 50
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
>gi_72309_pir_ZIZMD1 19K zein precursor (clone cZ19D1) -
maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]

Seq. No. 299845
Seq. ID LIB3159-001-Q1-K1-E9
Method BLASTN
NCBI GI g22514
BLAST score 87
E value 2.0e-41
Match length 262
% identity 84

NCBI Description Maize Zcl gene for Zein Zcl (14 kD zein-2)

Seq. No. 299846
Seq. ID LIB3159-001-Q1-K1-F11
Method BLASTX
NCBI GI g2832246
BLAST score 232
E value 2.0e-19
Match length 61
% identity 77
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 299847
Seq. ID LIB3159-001-Q1-K1-H10
Method BLASTN
NCBI GI g168687
BLAST score 35
E value 4.0e-10
Match length 51
% identity 92
NCBI Description Maize 22 kDa zein mRNA, clone cZ22C2, partial cds

Seq. No. 299848
Seq. ID LIB3159-002-Q1-K1-C4
Method BLASTX
NCBI GI g2501353
BLAST score 182
E value 6.0e-14
Match length 72
% identity 56
NCBI Description TRANSKETOLASE, CHLOROPLAST (TK) >gi_1084440_pir_S54300
transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum
(fragment) >gi_664901_emb_CAA86607_ (Z46646) transketolase
[Craterostigma plantagineum]

Seq. No. 299849
Seq. ID LIB3159-002-Q1-K1-D3
Method BLASTX
NCBI GI g2149640
BLAST score 159
E value 4.0e-11
Match length 66
% identity 61
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No. 299850
Seq. ID LIB3159-002-Q1-K1-D4
Method BLASTX
NCBI GI g3024018
BLAST score 374
E value 2.0e-36
Match length 77
% identity 95
NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
>gi_1546919_emb_CAA69225_ (Y07920) translation initiation
factor 5A [Zea mays] >gi_2668738 (AF034943) translation
initiation factor 5A [Zea mays]

Seq. No. 299851
Seq. ID LIB3159-002-Q1-K1-E7
Method BLASTX
NCBI GI g1903359
BLAST score 145
E value 4.0e-09
Match length 83
% identity 40
NCBI Description (AC000104) F19P19.21 [Arabidopsis thaliana]

Seq. No. 299852
Seq. ID LIB3159-002-Q1-K1-F10
Method BLASTX
NCBI GI g4567273
BLAST score 291
E value 4.0e-26
Match length 119
% identity 55
NCBI Description (AC006841) putative vacuolar proton ATPase subunit [Arabidopsis thaliana]

Seq. No. 299853
Seq. ID LIB3159-002-Q1-K1-F3
Method BLASTN
NCBI GI g22312
BLAST score 37
E value 2.0e-11
Match length 123
% identity 89
NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)

Seq. No. 299854
Seq. ID LIB3159-002-Q1-K1-F6
Method BLASTN
NCBI GI g22292
BLAST score 103
E value 9.0e-51
Match length 191
% identity 96
NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 299855
Seq. ID LIB3159-002-Q1-K1-H8
Method BLASTN
NCBI GI g168575
BLAST score 99
E value 1.0e-48
Match length 164
% identity 90
NCBI Description Maize phospholipid transfer protein mRNA, complete cds. of clone 9C2

Seq. No. 299856
Seq. ID LIB3159-003-Q1-K1-A6
Method BLASTX

NCBI GI g4096786
 BLAST score 188
 E value 2.0e-14
 Match length 60
 % identity 68
 NCBI Description (U39958) NADP-malic enzyme [Zea mays]

Seq. No. 299857
 Seq. ID LIB3159-003-Q1-K1-B12
 Method BLASTX
 NCBI GI g3885884
 BLAST score 424
 E value 8.0e-42
 Match length 97
 % identity 86
 NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 299858
 Seq. ID LIB3159-004-Q1-K1-D1
 Method BLASTX
 NCBI GI g464707
 BLAST score 450
 E value 7.0e-45
 Match length 111
 % identity 76
 NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir_S37496 ribosomal protein S18.A - Arabidopsis thaliana
 >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana]
 >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana]
 >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana]
 >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No. 299859
 Seq. ID LIB3159-005-Q1-K1-A4
 Method BLASTX
 NCBI GI g2288999
 BLAST score 320
 E value 5.0e-34
 Match length 90
 % identity 78
 NCBI Description (AC002335) electron transfer flavoprotein ubiquinone oxidoreductase isolog [Arabidopsis thaliana]

Seq. No. 299860
 Seq. ID LIB3159-005-Q1-K1-B1
 Method BLASTX
 NCBI GI g3033380
 BLAST score 206

E value 3.0e-16
Match length 66
% identity 65
NCBI Description (AC004238) putative coatomer epsilon subunit [Arabidopsis thaliana]

Seq. No. 299861
Seq. ID LIB3159-005-Q1-K1-F3
Method BLASTX
NCBI GI g4056480
BLAST score 159
E value 7.0e-11
Match length 41
% identity 73
NCBI Description (AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No. 299862
Seq. ID LIB3159-005-Q1-K1-F4
Method BLASTN
NCBI GI g22227
BLAST score 165
E value 7.0e-88
Match length 251
% identity 95
NCBI Description Z.mays CAB48 gene for chlorophyll a/b binding protein

Seq. No. 299863
Seq. ID LIB3159-007-Q1-K1-E12
Method BLASTN
NCBI GI g22646
BLAST score 66
E value 1.0e-28
Match length 158
% identity 94
NCBI Description Z.mays MFS18 mRNA

Seq. No. 299864
Seq. ID LIB3159-007-Q1-K1-E7
Method BLASTX
NCBI GI g2921512
BLAST score 215
E value 2.0e-17
Match length 92
% identity 54
NCBI Description (AF037460) GF14 protein [Fritillaria agrestis]

Seq. No. 299865
Seq. ID LIB3159-007-Q1-K1-F12
Method BLASTX
NCBI GI g2894379
BLAST score 206
E value 2.0e-16
Match length 85
% identity 53
NCBI Description (Y14573) ring finger protein [Hordeum vulgare]

Seq. No. 299866

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Seq. ID	LIB3159-007-Q1-K1-F6
Method	BLASTX
NCBI GI	g3096949
BLAST score	245
E value	5.0e-21
Match length	92
% identity	54
NCBI Description	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]
Seq. No.	299867
Seq. ID	LIB3159-007-Q1-K1-F8
Method	BLASTX
NCBI GI	g3096949
BLAST score	187
E value	1.0e-23
Match length	96
% identity	59
NCBI Description	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]
Seq. No.	299868
Seq. ID	LIB3159-007-Q1-K1-G12
Method	BLASTX
NCBI GI	g3885344
BLAST score	173
E value	2.0e-12
Match length	94
% identity	37
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana] >gi_4557057_gb_AAD22497.1_AC007154_1 (AC007154) unknown protein [Arabidopsis thaliana]
Seq. No.	299869
Seq. ID	LIB3159-007-Q1-K1-G9
Method	BLASTX
NCBI GI	g118104
BLAST score	187
E value	1.0e-14
Match length	45
% identity	84
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) - maize >gi_168461 (M55021) cyclophilin [Zea mays] >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
Seq. No.	299870
Seq. ID	LIB3159-007-Q1-K1-H2
Method	BLASTX
NCBI GI	g2511590
BLAST score	174
E value	1.0e-12
Match length	66
% identity	53

DRAFT Sequence

NCBI Description (Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] >gi_3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]

Seq. No. 299871
Seq. ID LIB3159-008-Q1-K1-A1
Method BLASTX
NCBI GI g3193303
BLAST score 168
E value 2.0e-12
Match length 64
% identity 55

NCBI Description (AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis thaliana]

Seq. No. 299872
Seq. ID LIB3159-008-Q1-K1-B2
Method BLASTX
NCBI GI g4206306
BLAST score 503
E value 3.0e-51
Match length 110
% identity 91

NCBI Description (AF049110) prpol [Zea mays]

Seq. No. 299873
Seq. ID LIB3159-008-Q1-K1-B4
Method BLASTX
NCBI GI g1129145
BLAST score 223
E value 4.0e-18
Match length 94
% identity 62

NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

Seq. No. 299874
Seq. ID LIB3159-008-Q1-K1-C5
Method BLASTX
NCBI GI g3914006
BLAST score 186
E value 1.0e-19
Match length 64
% identity 84

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi_1816588 (U85495) LON2 [Zea mays]

Seq. No. 299875
Seq. ID LIB3159-008-Q1-K1-C6
Method BLASTX
NCBI GI g1498053
BLAST score 203
E value 3.0e-16
Match length 66
% identity 67

Q309644444444444444

NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. 299876
Seq. ID LIB3159-008-Q1-K1-D3
Method BLASTX
NCBI GI g3021270
BLAST score 470
E value 3.0e-47
Match length 122
% identity 72
NCBI Description (AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]

Seq. No. 299877
Seq. ID LIB3159-008-Q1-K1-E10
Method BLASTX
NCBI GI g115771
BLAST score 364
E value 4.0e-35
Match length 67
% identity 99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll a/b-binding protein precursor - maize >gi_22224_emb_CAA32900 (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

Seq. No. 299878
Seq. ID LIB3159-008-Q1-K1-E7
Method BLASTX
NCBI GI g4104561
BLAST score 165
E value 1.0e-11
Match length 65
% identity 49
NCBI Description (AF036960) subtilisin-like protease [Glycine max]

Seq. No. 299879
Seq. ID LIB3159-008-Q1-K1-F1
Method BLASTX
NCBI GI g2541876
BLAST score 273
E value 5.0e-24
Match length 137
% identity 42
NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No. 299880
Seq. ID LIB3159-008-Q1-K1-G10
Method BLASTX
NCBI GI g100728
BLAST score 195
E value 4.0e-15
Match length 70
% identity 61
NCBI Description aspartate transaminase (EC 2.6.1.1) AAT3 precursor - proso

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millet >gi_1084464_pir_S53304 aspartate aminotransferase -
proso millet >gi_20601_emb_CAA45024 (X63430) aspartate
aminotransferase [Panicum miliaceum]
>gi_435459_dbj_BAA04993 (D25323) aspartate
aminotransferase [Panicum miliaceum]

Seq. No. 299881
Seq. ID LIB3159-008-Q1-K1-G7
Method BLASTX
NCBI GI g2842480
BLAST score 189
E value 2.0e-16
Match length 86
% identity 57
NCBI Description (AL021749) ADP, ATP carrier-like protein [Arabidopsis thaliana]

Seq. No. 299882
Seq. ID LIB3159-009-Q1-K1-D7
Method BLASTX
NCBI GI g135060
BLAST score 245
E value 2.0e-26
Match length 101
% identity 68
NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
(SHRUNKEN-1) >gi_66570_pir_YUZMS sucrose synthase (EC
2.4.1.13) - maize >gi_22486_emb_CAA26247 (X02400) sucrose
synthase [Zea mays] >gi_22488_emb_CAA26229 (X02382)
sucrose synthase [Zea mays]

Seq. No. 299883
Seq. ID LIB3159-009-Q1-K1-E8
Method BLASTX
NCBI GI g3914899
BLAST score 272
E value 1.0e-31
Match length 88
% identity 83
NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal
protein S4 type I [Zea mays]

Seq. No. 299884
Seq. ID LIB3159-009-Q1-K1-F6
Method BLASTX
NCBI GI g4160432
BLAST score 193
E value 9.0e-15
Match length 116
% identity 35
NCBI Description (AF071592) kinesin superfamily motor KIF4 [Homo sapiens]

Seq. No. 299885
Seq. ID LIB3159-009-Q1-K1-G3
Method BLASTX
NCBI GI g1514643
BLAST score 149

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E value 4.0e-11
Match length 81
% identity 53
NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No. 299886
Seq. ID LIB3159-009-Q1-K1-H11
Method BLASTX
NCBI GI g4096756
BLAST score 151
E value 5.0e-10
Match length 79
% identity 42
NCBI Description (U39394) alpha-1,3/4-fucosidase precursor [Streptomyces sp.]

Seq. No. 299887
Seq. ID LIB3159-009-Q1-K1-H2
Method BLASTX
NCBI GI g4406764
BLAST score 176
E value 3.0e-13
Match length 69
% identity 54
NCBI Description (AC006836) putative uridylyl transferase [Arabidopsis thaliana]

Seq. No. 299888
Seq. ID LIB3159-010-Q1-K1-B5
Method BLASTX
NCBI GI g1084481
BLAST score 332
E value 3.0e-31
Match length 103
% identity 71
NCBI Description heat shock protein 70 - Maize

Seq. No. 299889
Seq. ID LIB3159-010-Q1-K1-C2
Method BLASTX
NCBI GI g3850581
BLAST score 276
E value 2.0e-24
Match length 95
% identity 58
NCBI Description (AC005278) EST gb_N96383 comes from this gene. [Arabidopsis thaliana]

Seq. No. 299890
Seq. ID LIB3159-010-Q1-K1-D6
Method BLASTX
NCBI GI g4309734
BLAST score 273
E value 1.0e-25
Match length 101
% identity 61
NCBI Description (AC006439) putative 26S proteosome regulatory subunit 8

[Arabidopsis thaliana]

Seq. No. 299891
Seq. ID LIB3159-011-Q1-K1-A9
Method BLASTN
NCBI GI g22356
BLAST score 116
E value 1.0e-58
Match length 176
% identity 93
NCBI Description Maize mRNA for light-harvesting chlorophyll a/b binding protein LHCP

Seq. No. 299892
Seq. ID LIB3159-011-Q1-K1-B11
Method BLASTX
NCBI GI g3163946
BLAST score 604
E value 7.0e-63
Match length 112
% identity 99
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No. 299893
Seq. ID LIB3159-011-Q1-K1-B4
Method BLASTX
NCBI GI g2894568
BLAST score 333
E value 4.0e-31
Match length 85
% identity 69
NCBI Description (AL021890) putative protein [Arabidopsis thaliana]

Seq. No. 299894
Seq. ID LIB3159-011-Q1-K1-B7
Method BLASTX
NCBI GI g4586027
BLAST score 190
E value 1.0e-14
Match length 93
% identity 44
NCBI Description (AC007109) putative ribosomal protein L14 [Arabidopsis thaliana]

Seq. No. 299895
Seq. ID LIB3159-011-Q1-K1-F4
Method BLASTN
NCBI GI g473602
BLAST score 53
E value 5.0e-21
Match length 197
% identity 82
NCBI Description Zea mays W-22 histone H2A mRNA, complete cds

Seq. No. 299896
Seq. ID LIB3159-011-Q1-K1-F5
Method BLASTX

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NCBI GI	g544421
BLAST score	141
E value	7.0e-09
Match length	41
% identity	73
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 1 >gi_485420_pir_S12311 glycine-rich RNA-binding protein (clone S1) - sorghum (fragment) >gi_21623_emb_CAA40863_ (X57663) glycine-rich RNA-binding protein [Sorghum bicolor]
Seq. No.	299897
Seq. ID	LIB3159-011-Q1-K1-H11
Method	BLASTX
NCBI GI	g3914899
BLAST score	198
E value	2.0e-15
Match length	118
% identity	40
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal protein S4 type I [Zea mays]
Seq. No.	299898
Seq. ID	LIB3159-011-Q1-K1-H9
Method	BLASTX
NCBI GI	g115771
BLAST score	583
E value	2.0e-60
Match length	107
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll a/b-binding protein precursor - maize >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]
Seq. No.	299899
Seq. ID	LIB3159-012-Q1-K1-B3
Method	BLASTN
NCBI GI	g22091
BLAST score	171
E value	2.0e-91
Match length	255
% identity	92
NCBI Description	Z.diploperennis gene for hydroxyproline-rich glycoprotein
Seq. No.	299900
Seq. ID	LIB3159-012-Q1-K1-C12
Method	BLASTX
NCBI GI	g2529677
BLAST score	190
E value	2.0e-14
Match length	91
% identity	45
NCBI Description	(AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana]
Seq. No.	299901

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Seq. ID LIB3159-012-Q1-K1-E10
Method BLASTX
NCBI GI g2160177
BLAST score 402
E value 3.0e-39
Match length 120
% identity 62
NCBI Description (AC000132) EST gb_R64758 comes from this gene. [Arabidopsis thaliana]

Seq. No. 299902
Seq. ID LIB3159-012-Q1-K1-E8
Method BLASTX
NCBI GI g3236242
BLAST score 221
E value 6.0e-18
Match length 86
% identity 57
NCBI Description (AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No. 299903
Seq. ID LIB3159-012-Q1-K1-G1
Method BLASTX
NCBI GI g4454051
BLAST score 171
E value 3.0e-12
Match length 45
% identity 71
NCBI Description (AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No. 299904
Seq. ID LIB3159-012-Q1-K1-G12
Method BLASTN
NCBI GI g2589161
BLAST score 127
E value 5.0e-65
Match length 181
% identity 92
NCBI Description Zea mays mRNA for aldehyde oxidase, complete cds

Seq. No. 299905
Seq. ID LIB3159-013-Q1-K1-A5
Method BLASTX
NCBI GI g1206013
BLAST score 337
E value 1.0e-31
Match length 64
% identity 97
NCBI Description (U44087) beta-D-glucosidase precursor [Zea mays]

Seq. No. 299906
Seq. ID LIB3159-013-Q1-K1-C4
Method BLASTX
NCBI GI g4105269
BLAST score 153

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E value 4.0e-10
Match length 102
% identity 46
NCBI Description (AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]

Seq. No. 299907
Seq. ID LIB3159-013-Q1-K1-F10
Method BLASTX
NCBI GI g3252807
BLAST score 279
E value 8.0e-25
Match length 133
% identity 45
NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No. 299908
Seq. ID LIB3159-013-Q1-K1-G1
Method BLASTX
NCBI GI g1495804
BLAST score 390
E value 7.0e-38
Match length 125
% identity 59
NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No. 299909
Seq. ID LIB3159-013-Q1-K1-G11
Method BLASTX
NCBI GI g730526
BLAST score 195
E value 5.0e-15
Match length 95
% identity 46
NCBI Description 60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
>gi_480787_pir_S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No. 299910
Seq. ID LIB3159-013-Q1-K1-G3
Method BLASTX
NCBI GI g4210330
BLAST score 284
E value 1.0e-25
Match length 101
% identity 58
NCBI Description (AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No. 299911
Seq. ID LIB3159-013-Q1-K1-H3
Method BLASTN
NCBI GI g758352
BLAST score 92
E value 2.0e-44
Match length 234

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% identity 85
NCBI Description Z.mays mRNA for cysteine synthase

Seq. No. 299912
Seq. ID LIB3159-013-Q1-K1-H6
Method BLASTX
NCBI GI g2851508
BLAST score 410
E value 4.0e-40
Match length 81
% identity 86
NCBI Description 60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No. 299913
Seq. ID LIB3159-015-Q1-K1-A2
Method BLASTN
NCBI GI g3789953
BLAST score 42
E value 1.0e-14
Match length 54
% identity 94
NCBI Description Oryza sativa chlorophyll a/b-binding protein precursor (Cab26) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 299914
Seq. ID LIB3159-015-Q1-K1-B1
Method BLASTX
NCBI GI g4105798
BLAST score 172
E value 2.0e-12
Match length 96
% identity 34
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 299915
Seq. ID LIB3159-015-Q1-K1-E3
Method BLASTX
NCBI GI g2129668
BLAST score 161
E value 1.0e-11
Match length 63
% identity 57
NCBI Description phosphoglycerate kinase - Arabidopsis thaliana (fragment) >gi_1022803 (U37700) phosphoglycerate kinase [Arabidopsis thaliana]

Seq. No. 299916
Seq. ID LIB3159-015-Q1-K1-E4
Method BLASTX
NCBI GI g2827663
BLAST score 180
E value 4.0e-13

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Match length 125
% identity 12
NCBI Description (AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]

Seq. No. 299917
Seq. ID LIB3159-015-Q1-K1-F8
Method BLASTX
NCBI GI g4651204
BLAST score 267
E value 1.0e-23
Match length 92
% identity 49
NCBI Description (AB026262) ring finger protein [Cicer arietinum]

Seq. No. 299918
Seq. ID LIB3159-015-Q1-K1-H3
Method BLASTX
NCBI GI g3522956
BLAST score 141
E value 4.0e-09
Match length 67
% identity 48
NCBI Description (AC004411) putative pectinacetylesterase precursor [Arabidopsis thaliana]

Seq. No. 299919
Seq. ID LIB3159-015-Q1-K1-H5
Method BLASTX
NCBI GI g1170937
BLAST score 511
E value 5.0e-52
Match length 103
% identity 95
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No. 299920
Seq. ID LIB3159-016-Q1-K1-C11
Method BLASTX
NCBI GI g3775987
BLAST score 351
E value 4.0e-33
Match length 128
% identity 58
NCBI Description (AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No. 299921
Seq. ID LIB3159-016-Q1-K1-C12
Method BLASTX
NCBI GI g729135
BLAST score 386
E value 2.0e-37
Match length 106
% identity 76

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NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
(S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID
3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir_S28612
catechol O-methyltransferase (EC 2.1.1.6) - maize
>gi_168532 (M73235) O-methyltransferase [Zea mays]

Seq. No. 299922
Seq. ID LIB3159-016-Q1-K1-E8
Method BLASTX
NCBI GI g3294467
BLAST score 164
E value 6.0e-12
Match length 71
% identity 49
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]

Seq. No. 299923
Seq. ID LIB3159-016-Q1-K1-F4
Method BLASTX
NCBI GI g1661160
BLAST score 347
E value 6.0e-35
Match length 97
% identity 75
NCBI Description (U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 299924
Seq. ID LIB3159-016-Q1-K1-F8
Method BLASTN
NCBI GI g2326946
BLAST score 54
E value 2.0e-21
Match length 118
% identity 86
NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29

Seq. No. 299925
Seq. ID LIB3159-016-Q1-K1-G11
Method BLASTX
NCBI GI g120670
BLAST score 236
E value 1.0e-19
Match length 49
% identity 98
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi_100879_pir_S06879 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) C - maize
>gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]

Seq. No. 299926
Seq. ID LIB3159-016-Q1-K1-H8
Method BLASTX
NCBI GI g4505743
BLAST score 175
E value 1.0e-12
Match length 93
% identity 42

NCBI Description prefoldin 5 >gi_2498565_sp_Q99471_MM1_HUMAN C-MYC BINDING PROTEIN MM-1 >gi_1731809_dbj_BAA14006_ (D89667) c-myc binding protein [Homo sapiens]

Seq. No. 299927
Seq. ID LIB3159-017-Q1-K1-C3
Method BLASTX
NCBI GI g2827621
BLAST score 165
E value 2.0e-11
Match length 83
% identity 51
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 299928
Seq. ID LIB3159-017-Q1-K1-C4
Method BLASTX
NCBI GI g3877997
BLAST score 164
E value 1.0e-11
Match length 83
% identity 35
NCBI Description (Z92970) predicted using Genefinder; Similarity to Bovine protien disulphide isomerase ER-60 (SW:P38657); cDNA EST EMBL:D69661 comes from this gene; cDNA EST EMBL:T01819 comes from this gene; cDNA EST EMBL:T01942 comes from thi

Seq. No. 299929
Seq. ID LIB3159-017-Q1-K1-F5
Method BLASTX
NCBI GI g1658313
BLAST score 138
E value 3.0e-17
Match length 60
% identity 38
NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 299930
Seq. ID LIB3159-017-Q1-K1-G12
Method BLASTX
NCBI GI g226261
BLAST score 152
E value 2.0e-10
Match length 39
% identity 74
NCBI Description alpha1 tubulin [Arabidopsis thaliana]

Seq. No. 299931
Seq. ID LIB3159-017-Q1-K1-G8
Method BLASTX
NCBI GI g3393044
BLAST score 177
E value 2.0e-13
Match length 53
% identity 68
NCBI Description (AJ000153) sucrose synthase type 2 [Triticum aestivum]

Seq. No. 299932
Seq. ID LIB3159-018-Q1-K1-C10
Method BLASTX
NCBI GI g115771
BLAST score 264
E value 3.0e-23
Match length 69
% identity 78
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll a/b-binding protein precursor - maize >gi_22224_emb_CAA32900 (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

Seq. No. 299933
Seq. ID LIB3159-018-Q1-K1-C12
Method BLASTX
NCBI GI g729671
BLAST score 173
E value 1.0e-14
Match length 69
% identity 70
NCBI Description HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]

Seq. No. 299934
Seq. ID LIB3159-018-Q1-K1-C3
Method BLASTX
NCBI GI g4587585
BLAST score 240
E value 3.0e-20
Match length 105
% identity 51
NCBI Description (AC007232) hypothetical protein [Arabidopsis thaliana]

Seq. No. 299935
Seq. ID LIB3159-018-Q1-K1-D3
Method BLASTX
NCBI GI g595768
BLAST score 155
E value 3.0e-10
Match length 47
% identity 62
NCBI Description (U13866) non-functional lacZ alpha peptide [Cloning vector]

Seq. No. 299936
Seq. ID LIB3159-018-Q1-K1-F12
Method BLASTX
NCBI GI g4512649
BLAST score 173
E value 7.0e-15
Match length 85
% identity 58
NCBI Description (AC007048) hypothetical protein [Arabidopsis thaliana]

Seq. No. 299937
Seq. ID LIB3159-018-Q1-K1-F2
Method BLASTX

NCBI GI g2842648
BLAST score 171
E value 5.0e-21
Match length 119
% identity 43
NCBI Description U2 SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR 35 KD SUBUNIT RELATED-PROTEIN 2 >gi_2137782_pir_A57120 small nuclear ribonucleoprotein auxiliary factor U2 - mouse
>gi_927659_dbj_BAA08143_ (D45205) U2af1-rs2 [Mus musculus]

Seq. No. 299938
Seq. ID LIB3159-019-Q1-K1-A4
Method BLASTX
NCBI GI g3335359
BLAST score 175
E value 1.0e-12
Match length 115
% identity 35
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 299939
Seq. ID LIB3159-019-Q1-K1-C12
Method BLASTX
NCBI GI g641905
BLAST score 202
E value 6.0e-16
Match length 92
% identity 48
NCBI Description (U19267) cysteine proteinase [Zinnia elegans]

Seq. No. 299940
Seq. ID LIB3159-019-Q1-K1-C2
Method BLASTX
NCBI GI g1519251
BLAST score 248
E value 2.0e-30
Match length 109
% identity 70
NCBI Description (U65957) GF14-c protein [Oryza sativa]

Seq. No. 299941
Seq. ID LIB3159-019-Q1-K1-C6
Method BLASTN
NCBI GI g551482
BLAST score 134
E value 3.0e-69
Match length 306
% identity 90
NCBI Description Zea mays ABA- and ripening-inducible-like protein mRNA, complete cds

Seq. No. 299942
Seq. ID LIB3159-019-Q1-K1-D11
Method BLASTX
NCBI GI g3386617
BLAST score 186
E value 4.0e-14

Match length 63
% identity 59
NCBI Description (AC004665) putative cell division protein (ftsY)
[Arabidopsis thaliana]

Seq. No. 299943
Seq. ID LIB3159-019-Q1-K1-E2
Method BLASTX
NCBI GI g2344894
BLAST score 296
E value 7.0e-27
Match length 73
% identity 82
NCBI Description (AC002388) hypothetical protein [Arabidopsis thaliana]

Seq. No. 299944
Seq. ID LIB3159-019-Q1-K1-E5
Method BLASTX
NCBI GI g116317
BLAST score 149
E value 1.0e-09
Match length 55
% identity 55
NCBI Description BASIC ENDOCHITINASE 2 PRECURSOR >gi_100669_pir_S15997
chitinase (EC 3.2.1.14) - rice >gi_227845_prf_1712313A
basic chitinase [Oryza sativa]

Seq. No. 299945
Seq. ID LIB3159-019-Q1-K1-F3
Method BLASTN
NCBI GI g294844
BLAST score 68
E value 5.0e-30
Match length 156
% identity 86
NCBI Description Saccharum hybrid cultivar H65-7052 membrane protein mRNA,
complete cds

Seq. No. 299946
Seq. ID LIB3159-019-Q1-K1-F4
Method BLASTX
NCBI GI g2559012
BLAST score 233
E value 1.0e-19
Match length 78
% identity 62
NCBI Description (AF026293) chaperonin containing t-complex polypeptide 1,
beta subunit; CCT-beta [Homo sapiens] >gi_4090929
(AF026166) chaperonin-containing TCP-1 beta subunit homolog
[Homo sapiens]

Seq. No. 299947
Seq. ID LIB3159-019-Q1-K1-G1
Method BLASTX
NCBI GI g1370603
BLAST score 439
E value 1.0e-43

Match length : 108
% identity : 80
NCBI Description : (X98245) annexin p35 [Zea mays]

Seq. No. : 299948
Seq. ID : LIB3159-019-Q1-K1-H9
Method : BLASTX
NCBI GI : g1877026
BLAST score : 177
E value : 7.0e-13
Match length : 50
% identity : 74
NCBI Description : (D78336) ribosomal protein S19 [Oryza sativa]

Seq. No. : 299949
Seq. ID : LIB3159-020-Q1-K1-A4
Method : BLASTX
NCBI GI : g3059131
BLAST score : 162
E value : 3.0e-11
Match length : 105
% identity : 39
NCBI Description : (AJ000478) cytochrome P450 [Helianthus tuberosus]

Seq. No. : 299950
Seq. ID : LIB3159-020-Q1-K1-A5
Method : BLASTN
NCBI GI : g22274
BLAST score : 90
E value : 2.0e-43
Match length : 97
% identity : 99
NCBI Description : Maize 26S - 17S rDNA spacer region from Black Mexican Sweet (BMS) suspension cells

Seq. No. : 299951
Seq. ID : LIB3159-020-Q1-K1-B8
Method : BLASTX
NCBI GI : g1169782
BLAST score : 202
E value : 4.0e-16
Match length : 73
% identity : 53
NCBI Description : FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis thaliana]

Seq. No. : 299952
Seq. ID : LIB3159-020-Q1-K1-D1
Method : BLASTX
NCBI GI : g115786
BLAST score : 416
E value : 5.0e-41
Match length : 93
% identity : 87
NCBI Description : CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea

mays]

Seq. No. 299953
Seq. ID LIB3159-020-Q1-K1-E7
Method BLASTN
NCBI GI g1370602
BLAST score 121
E value 1.0e-61
Match length 225
% identity 88
NCBI Description Z.mays mRNA for annexin p35

Seq. No. 299954
Seq. ID LIB3159-021-Q1-K1-A11
Method BLASTN
NCBI GI g168704
BLAST score 60
E value 2.0e-25
Match length 92
% identity 91
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 299955
Seq. ID LIB3159-021-Q1-K1-B11
Method BLASTX
NCBI GI g310587
BLAST score 266
E value 1.0e-37
Match length 126
% identity 66
NCBI Description (L20864) ascorbate peroxidase [Spinacia oleracea]
>gi_1384110 dbj_BAA12890_ (D85864) cytosolic ascorbate peroxidase [Spinacia oleracea]

Seq. No. 299956
Seq. ID LIB3159-021-Q1-K1-D2
Method BLASTX
NCBI GI g115764
BLAST score 248
E value 4.0e-28
Match length 96
% identity 71
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE I PRECURSOR (CAB-6A) (LIGHT-HARVESTING COMPLEX I 26 KD PROTEIN)
>gi_170494 (J03558) chlorophyll a/b binding protein precursor [Lycopersicon esculentum]

Seq. No. 299957
Seq. ID LIB3159-021-Q1-K1-D6
Method BLASTX
NCBI GI g3024018
BLAST score 467
E value 7.0e-47
Match length 115
% identity 78
NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
>gi_1546919_emb_CAA69225_ (Y07920) translation initiation

factor 5A [Zea mays] >gi_2668738 (AF034943) translation
initiation factor 5A [Zea mays]

Seq. No. 299958
Seq. ID LIB3159-021-Q1-K1-E3
Method BLASTX
NCBI GI g4006913
BLAST score 235
E value 8.0e-20
Match length 77
% identity 60
NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 299959
Seq. ID LIB3159-021-Q1-K1-E6
Method BLASTX
NCBI GI g1706082
BLAST score 215
E value 1.0e-17
Match length 85
% identity 52
NCBI Description SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)
>gi_629787_pir_S44191 serine-type carboxypeptidase (EC
3.4.16.1) II-3 - barley >gi_619350_bbs_153536
CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,
cv. Alexis, aleurone, Peptide, 516 aa]
>gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3
[Hordeum vulgare]

Seq. No. 299960
Seq. ID LIB3159-021-Q1-K1-F11
Method BLASTX
NCBI GI g2190552
BLAST score 389
E value 1.0e-37
Match length 114
% identity 64
NCBI Description (AC001229) Similar to Holcus major pollen allergen
(gb_Z27084). [Arabidopsis thaliana]

Seq. No. 299961
Seq. ID LIB3159-021-Q1-K1-F5
Method BLASTX
NCBI GI g3702338
BLAST score 272
E value 4.0e-24
Match length 101
% identity 50
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 299962
Seq. ID LIB3159-021-Q1-K1-H3
Method BLASTX
NCBI GI g118104
BLAST score 144
E value 2.0e-10
Match length 83

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% identity 44
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 299963
Seq. ID LIB3179-001-P1-K2-E11
Method BLASTX
NCBI GI g2687358
BLAST score 336
E value 1.0e-35
Match length 124
% identity 70
NCBI Description (AF033263) nonphototropic hypocotyl 1 [Zea mays]

Seq. No. 299964
Seq. ID LIB3179-001-P2-K1-A3
Method BLASTX
NCBI GI g1172861
BLAST score 286
E value 8.0e-26
Match length 90
% identity 63
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR
(RUBISCO LARGE SUBUNIT) >gi_1363613_pir_S58560
ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain
- maize chloroplast >gi_18036_emb_CAA78027_ (Z11973)
Ribulose bisphosphate carboxylase [Zea mays]
>gi_902230_emb_CAA60294_ (X86563) rubisco large subunit
[Zea mays]

Seq. No. 299965
Seq. ID LIB3179-001-P2-K1-C10
Method BLASTX
NCBI GI g4539677
BLAST score 147
E value 1.0e-09
Match length 88
% identity 43
NCBI Description (AF061282) patatin-like protein [Sorghum bicolor]

Seq. No. 299966
Seq. ID LIB3179-001-P2-K1-D12
Method BLASTX
NCBI GI g2944088
BLAST score 179
E value 3.0e-13
Match length 68
% identity 53
NCBI Description (AF050102) glutathione s-transferase [Oryza sativa]

Seq. No. 299967
Seq. ID LIB3179-001-P2-K1-D4
Method BLASTX
NCBI GI g131225

BLAST score 367
E value 4.0e-35
Match length 130
% identity 57
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 299968
Seq. ID LIB3179-001-P2-K1-D6
Method BLASTX
NCBI GI g2879811
BLAST score 238
E value 4.0e-20
Match length 89
% identity 54
NCBI Description (AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No. 299969
Seq. ID LIB3179-001-P2-K1-E11
Method BLASTX
NCBI GI g531829
BLAST score 189
E value 2.0e-14
Match length 78
% identity 53
NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No. 299970
Seq. ID LIB3179-001-P2-K1-E6
Method BLASTX
NCBI GI g531829
BLAST score 138
E value 1.0e-08
Match length 75
% identity 49
NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No. 299971
Seq. ID LIB3179-001-P2-K1-F11
Method BLASTX
NCBI GI g2687358
BLAST score 220
E value 5.0e-18
Match length 109
% identity 50
NCBI Description (AF033263) nonphototropic hypocotyl 1 [Zea mays]

Seq. No. 299972
Seq. ID LIB3179-001-P2-K1-F9
Method BLASTX
NCBI GI g3599491
BLAST score 285
E value 1.0e-25

Match length 118
% identity 48
NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]

Seq. No. 299973
Seq. ID LIB3179-001-P2-K1-G1
Method BLASTX
NCBI GI g1362086
BLAST score 388
E value 1.0e-37
Match length 99
% identity 76
NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir_S65957
5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No. 299974
Seq. ID LIB3179-001-P2-K1-G11
Method BLASTX
NCBI GI g445612
BLAST score 171
E value 3.0e-12
Match length 52
% identity 65
NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No. 299975
Seq. ID LIB3179-001-P2-K1-H12
Method BLASTN
NCBI GI g475252
BLAST score 44
E value 9.0e-16
Match length 131
% identity 85
NCBI Description Z.mays MPI gene

Seq. No. 299976
Seq. ID LIB3179-001-P2-K1-H4
Method BLASTX
NCBI GI g2494261
BLAST score 222
E value 7.0e-32
Match length 116
% identity 61
NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_99903_pir_S21567 translation elongation factor Tu precursor - soybean chloroplast >gi_18776_emb_CAA46864_ (X66062) EF-Tu [Glycine max] >gi_448921_prf_1918220A elongation factor Tu [Glycine max]

Seq. No. 299977
Seq. ID LIB3179-001-P2-K1-H7
Method BLASTX

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NCBI GI	g2501189
BLAST score	227
E value	8.0e-19
Match length	114
% identity	48
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir_S61419 thiamine biosynthetic enzyme thil-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme [Zea mays]
Seq. No.	299978
Seq. ID	LIB3179-002-P1-K1-C1
Method	BLASTX
NCBI GI	g461550
BLAST score	241
E value	2.0e-20
Match length	59
% identity	80
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir_B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]
Seq. No.	299979
Seq. ID	LIB3179-002-P1-K1-D4
Method	BLASTN
NCBI GI	g559535
BLAST score	64
E value	1.0e-27
Match length	136
% identity	87
NCBI Description	Z.mays mRNA for metallothionein
Seq. No.	299980
Seq. ID	LIB3179-002-P1-K1-D7
Method	BLASTX
NCBI GI	g994736
BLAST score	147
E value	9.0e-10
Match length	46
% identity	65
NCBI Description	(M18327) LacOPZ-alpha peptide from pUC9; putative [cloning vectors] >gi_994738 (M18328) LacOPZ-alpha peptide from pUC9; putative [cloning vectors] >gi_994740 (M18329) LacOPZ-alpha peptide from pUC9; putative [cloning vectors]
Seq. No.	299981
Seq. ID	LIB3179-002-P1-K1-G4
Method	BLASTN
NCBI GI	g342630
BLAST score	39
E value	9.0e-13
Match length	148
% identity	82
NCBI Description	Maize chloroplast His-tRNA gene on Ecol fragment

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Seq. No.	299982
Seq. ID	LIB3179-002-P1-K2-F4
Method	BLASTN
NCBI GI	g405634
BLAST score	294
E value	1.0e-164
Match length	334
% identity	97
NCBI Description	Z.mays zmcpt mRNA triose phosphate/phosphate translocator
Seq. No.	299983
Seq. ID	LIB3179-002-P2-K1-A3
Method	BLASTX
NCBI GI	g1174613
BLAST score	423
E value	1.0e-41
Match length	144
% identity	63
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_ (D17788) rice homologue of Tat binding protein [Oryza sativa]
Seq. No.	299984
Seq. ID	LIB3179-002-P2-K1-A5
Method	BLASTX
NCBI GI	g567893
BLAST score	223
E value	4.0e-18
Match length	95
% identity	45
NCBI Description	(L37382) beta-galactosidase-complementation protein [Cloning vector]
Seq. No.	299985
Seq. ID	LIB3179-002-P2-K1-B10
Method	BLASTN
NCBI GI	g475252
BLAST score	37
E value	3.0e-11
Match length	296
% identity	78
NCBI Description	Z.mays MPI gene
Seq. No.	299986
Seq. ID	LIB3179-002-P2-K1-C1
Method	BLASTX
NCBI GI	g461550
BLAST score	180
E value	3.0e-13
Match length	65
% identity	63
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir_B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast - Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]

SEQUENCE DRAFT

Seq. No.	299987
Seq. ID	LIB3179-002-P2-K1-C10
Method	BLASTX
NCBI GI	g1853970
BLAST score	262
E value	9.0e-23
Match length	136
% identity	44
NCBI Description	(D88122) CPRD46 protein [Vigna unguiculata]
Seq. No.	299988
Seq. ID	LIB3179-002-P2-K1-D1
Method	BLASTN
NCBI GI	g3264597
BLAST score	75
E value	5.0e-34
Match length	242
% identity	84
NCBI Description	Zea mays trypsin inhibitor mRNA, complete cds
Seq. No.	299989
Seq. ID	LIB3179-002-P2-K1-D10
Method	BLASTX
NCBI GI	g2501578
BLAST score	400
E value	5.0e-39
Match length	124
% identity	59
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN NEVER >gi_2129913_pir_S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]
Seq. No.	299990
Seq. ID	LIB3179-002-P2-K1-D3
Method	BLASTX
NCBI GI	g3287494
BLAST score	289
E value	7.0e-26
Match length	129
% identity	53
NCBI Description	(D78504) similar to yeast SRP1 [Oryza sativa]
Seq. No.	299991
Seq. ID	LIB3179-002-P2-K1-D5
Method	BLASTX
NCBI GI	g3287494
BLAST score	236
E value	8.0e-20
Match length	100
% identity	57
NCBI Description	(D78504) similar to yeast SRP1 [Oryza sativa]
Seq. No.	299992
Seq. ID	LIB3179-002-P2-K1-D6
Method	BLASTX

NCBI GI g4544419
BLAST score 149
E value 2.0e-09
Match length 79
% identity 48
NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]

Seq. No. 299993
Seq. ID LIB3179-002-P2-K1-E2
Method BLASTX
NCBI GI g131134
BLAST score 384
E value 4.0e-37
Match length 117
% identity 64
NCBI Description PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1
>gi_1363576_pir_S58552 photosystem I protein A1 - maize
chloroplast >gi_342595 (M11203) P700 chlorophyll a-protein
PSI-A1 [Zea mays] >gi_902222_emb_CAA60286_ (X86563) PSI
P700 apoprotein A1 [Zea mays]

Seq. No. 299994
Seq. ID LIB3179-002-P2-K1-F1
Method BLASTX
NCBI GI g1657851
BLAST score 172
E value 2.0e-12
Match length 51
% identity 35
NCBI Description (U73214) cold acclimation protein WCOR518 [Triticum
aestivum]

Seq. No. 299995
Seq. ID LIB3179-002-P2-K1-F10
Method BLASTX
NCBI GI g1698670
BLAST score 383
E value 5.0e-37
Match length 128
% identity 58
NCBI Description (U66241) S-like RNase [Zea mays]

Seq. No. 299996
Seq. ID LIB3179-002-P2-K1-G3
Method BLASTX
NCBI GI g133852
BLAST score 221
E value 6.0e-18
Match length 74
% identity 64
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S19 >gi_71030_pir_R3ZM19
ribosomal protein S19 - maize chloroplast
>gi_1208517_emb_CAA60374_ (X86563) ribosomal protein S19
[Zea mays] >gi_2654314_emb_CAA60326_ (X86563) ribosomal
protein S19 [Zea mays]

Seq. No. 299997

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Seq. ID	LIB3179-002-P2-K1-G7
Method	BLASTX
NCBI GI	g1550814
BLAST score	281
E value	6.0e-25
Match length	119
% identity	52
NCBI Description	(Y07959) 60S acidic ribosomal protein P0 [Zea mays]
Seq. No.	299998
Seq. ID	LIB3179-002-P2-K1-H1
Method	BLASTX
NCBI GI	g135535
BLAST score	297
E value	5.0e-27
Match length	95
% identity	67
NCBI Description	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) >gi_322602_pir_JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955 (D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana]
Seq. No.	299999
Seq. ID	LIB3179-002-P2-K1-H3
Method	BLASTN
NCBI GI	g1698669
BLAST score	121
E value	2.0e-61
Match length	385
% identity	83
NCBI Description	Zea mays S-like RNase (kin1) mRNA, complete cds
Seq. No.	300000
Seq. ID	LIB3179-002-P2-K1-H5
Method	BLASTX
NCBI GI	g1351271
BLAST score	192
E value	1.0e-14
Match length	55
% identity	67
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir_S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]
Seq. No.	300001
Seq. ID	LIB3179-019-P1-K1-D11
Method	BLASTX
NCBI GI	g1778147
BLAST score	270
E value	1.0e-23
Match length	58
% identity	95
NCBI Description	(U66403) phosphate/phosphoenolpyruvate translocator

SCIENCE SOURCE

precursor [Zea mays]

Seq. No.	300002
Seq. ID	LIB3179-019-P1-K1-E8
Method	BLASTN
NCBI GI	g474945
BLAST score	118
E value	1.0e-59
Match length	258
% identity	86
NCBI Description	Z.mays mRNA for subtilisin-chymotrypsin inhibitor
Seq. No.	300003
Seq. ID	LIB3179-020-P1-K1-A5
Method	BLASTX
NCBI GI	g266578
BLAST score	205
E value	3.0e-16
Match length	56
% identity	68
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir_S17560 metallothionein-like protein - maize >gi_236730_bbs_57629 (S57628) metallothionein homologue [Zea mays, Peptide, 76 aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186) metallothionein- like protein [Zea mays] >gi_228095_prf_1717215A metallothionein-like protein [Zea mays]
Seq. No.	300004
Seq. ID	LIB3179-020-P1-K1-A9
Method	BLASTN
NCBI GI	g559535
BLAST score	71
E value	7.0e-32
Match length	107
% identity	92
NCBI Description	Z.mays mRNA for metallothionein
Seq. No.	300005
Seq. ID	LIB3179-020-P1-K1-C2
Method	BLASTN
NCBI GI	g596079
BLAST score	108
E value	8.0e-54
Match length	287
% identity	85
NCBI Description	Zea mays thiamine biosynthetic enzyme (thil-2) mRNA, complete cds
Seq. No.	300006
Seq. ID	LIB3179-020-P1-K1-E9
Method	BLASTX
NCBI GI	g2980793
BLAST score	221
E value	6.0e-18
Match length	67
% identity	58

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NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 300007
Seq. ID LIB3179-020-P1-K1-F12
Method BLASTX
NCBI GI g115770
BLAST score 226
E value 1.0e-18
Match length 48
% identity 85
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_100533_pir_S07448 chlorophyll a/b-binding protein - swollen duckweed >gi_168290 (M12152) chlorophyll a/b apoprotein [Lemna gibba]

Seq. No. 300008
Seq. ID LIB3179-020-P1-K1-G2
Method BLASTX
NCBI GI g3522946
BLAST score 267
E value 1.0e-23
Match length 93
% identity 52
NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 300009
Seq. ID LIB3179-021-P1-K1-E5
Method BLASTX
NCBI GI g114599
BLAST score 347
E value 9.0e-33
Match length 99
% identity 71
NCBI Description ATP SYNTHASE EPSILON CHAIN >gi_67867_pir_PWZME H+-transporting ATP synthase (EC 3.6.1.34) epsilon chain - maize chloroplast >gi_342578 (J01421) coupling factor epsilon subunit [Zea mays] >gi_902228_emb_CAA60292_(X86563) ATPase epsilon subunit [Zea mays]

Seq. No. 300010
Seq. ID LIB3179-021-P1-K1-F1
Method BLASTX
NCBI GI g4581163
BLAST score 335
E value 3.0e-31
Match length 104
% identity 66
NCBI Description (AC006220) unknown protein [Arabidopsis thaliana]

Seq. No. 300011
Seq. ID LIB3179-022-P1-K1-F1
Method BLASTN
NCBI GI g12455
BLAST score 90
E value 6.0e-43
Match length 302
% identity 83

NCBI Description Maize chloroplast rp116 gene for ribosomal protein L16 exon

Seq. No. 300012
 Seq. ID LIB3179-023-P1-K1-C3
 Method BLASTX
 NCBI GI g2118425
 BLAST score 221
 E value 5.0e-18
 Match length 63
 % identity 71
 NCBI Description subtilisin/chymotrypsin inhibitor - maize
 >gi_475253_emb_CAA55588_(X78988) proteinase inhibitor [Zea mays]
 >gi_475922_emb_CAA49593_(X69972) proteinase inhibitor [Zea mays]
 >gi_559538_emb_CAA57677_(X82187) subtilisin /chymotrypsin-like inhibitor [Zea mays]

Seq. No. 300013
 Seq. ID LIB3179-023-P1-K1-E1
 Method BLASTX
 NCBI GI g132147
 BLAST score 296
 E value 5.0e-27
 Match length 99
 % identity 63
 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_68089_pir_RKZMS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - maize >gi_22474_emb_CAA29784_(X06535) ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi_217964_dbj_BAA00120_(D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi_359512_prf_1312317A ribulosebisphosphate carboxylase [Zea mays]

Seq. No. 300014
 Seq. ID LIB3179-023-P1-K1-H1
 Method BLASTX
 NCBI GI g115789
 BLAST score 245
 E value 4.0e-21
 Match length 60
 % identity 78
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-22L) (LHCP) >gi_20475_emb_CAA26212_(X02359) cab 22L precursor polypeptide (aa -34 to 233) [Petunia sp.]

Seq. No. 300015
 Seq. ID LIB3180-001-P1-M1-B6
 Method BLASTX
 NCBI GI g553073
 BLAST score 197
 E value 1.0e-21
 Match length 128
 % identity 52
 NCBI Description (M94481) reverse transcriptase [Zea mays]

Seq. No. 300016

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Seq. ID	LIB3180-001-P1-M1-D8
Method	BLASTX
NCBI GI	g3337356
BLAST score	248
E value	2.0e-21
Match length	54
% identity	89
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]
Seq. No.	300017
Seq. ID	LIB3180-001-P1-M1-G11
Method	BLASTX
NCBI GI	g3176712
BLAST score	180
E value	3.0e-13
Match length	91
% identity	37
NCBI Description	(AC002392) putative zinc-finger protein [Arabidopsis thaliana]
Seq. No.	300018
Seq. ID	LIB3180-002-P1-M1-C2
Method	BLASTN
NCBI GI	g4165327
BLAST score	42
E value	1.0e-14
Match length	54
% identity	96
NCBI Description	Oryza sativa 3-hydroxy-3-methylglutaryl-CoA reductase gene, promoter region and complete cds
Seq. No.	300019
Seq. ID	LIB3180-002-P1-M1-E11
Method	BLASTX
NCBI GI	g3021513
BLAST score	232
E value	2.0e-19
Match length	65
% identity	69
NCBI Description	(X96728) isocitrate dehydrogenase (NADP+) [Nicotiana tabacum]
Seq. No.	300020
Seq. ID	LIB3180-002-P1-M1-G10
Method	BLASTX
NCBI GI	g133961
BLAST score	199
E value	2.0e-15
Match length	63
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN S4 (OMNIPOTENT SUPPRESSOR PROTEIN SUP44) (RP12) (S2E) >gi_70888_pir_R3BYS2 ribosomal protein S2.e - yeast (Saccharomyces cerevisiae) >gi_172793 (M59375) ribosomal protein S4 [Saccharomyces cerevisiae] >gi_1322683_emb_CAA96831_ (Z72645) ORF YGL123w [Saccharomyces cerevisiae] >gi_1628451_emb_CAA63835_

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(X94106) SUP44 [Saccharomyces cerevisiae]

Seq. No.	300021
Seq. ID	LIB3180-003-P2-M1-C1
Method	BLASTX
NCBI GI	g1184774
BLAST score	152
E value	2.0e-10
Match length	48
% identity	67
NCBI Description	(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]
Seq. No.	300022
Seq. ID	LIB3180-003-P2-M1-C9
Method	BLASTX
NCBI GI	g3193284
BLAST score	379
E value	1.0e-36
Match length	102
% identity	69
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]
Seq. No.	300023
Seq. ID	LIB3180-003-P2-M1-D12
Method	BLASTX
NCBI GI	g3834321
BLAST score	412
E value	2.0e-40
Match length	127
% identity	65
NCBI Description	(AC005679) Strong similarity to F13P17.9 gi_3337356 transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]
Seq. No.	300024
Seq. ID	LIB3180-003-P2-M1-F3
Method	BLASTX
NCBI GI	g3122071
BLAST score	499
E value	8.0e-51
Match length	104
% identity	93
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2130148_pir_S66339 translation elongation factor eEF-1 alpha chain - maize >gi_1321656_dbj_BAA08249_ (D45408) alpha subunit of tlation elongation factor 1 [Zea mays]
Seq. No.	300025
Seq. ID	LIB3180-003-P2-M1-F9
Method	BLASTX
NCBI GI	g553125
BLAST score	268
E value	6.0e-24
Match length	79
% identity	70

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NCBI Description (L13975) dihydroxyacid dehydratase [Saccharomyces cerevisiae]

Seq. No. 300026
Seq. ID LIB3180-003-P2-M1-G12
Method BLASTX
NCBI GI g121631
BLAST score 263
E value 5.0e-23
Match length 76
% identity 68
NCBI Description GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR
>gi_72323_pir_KNNT2S glycine-rich protein 2 - wood tobacco
>gi_19743_emb_CAA42622_ (X60007) nsGRP-2 [Nicotiana sylvestris]

Seq. No. 300027
Seq. ID LIB3180-003-P2-M1-G9
Method BLASTX
NCBI GI g168691
BLAST score 311
E value 1.0e-28
Match length 95
% identity 69
NCBI Description (M29628) zein [Zea mays]

Seq. No. 300028
Seq. ID LIB3180-004-P2-M1-A11
Method BLASTN
NCBI GI g22292
BLAST score 36
E value 3.0e-11
Match length 80
% identity 86
NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 300029
Seq. ID LIB3180-004-P2-M1-B6
Method BLASTN
NCBI GI g22516
BLAST score 115
E value 6.0e-58
Match length 323
% identity 84
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 300030
Seq. ID LIB3180-004-P2-M1-B8
Method BLASTN
NCBI GI g168665
BLAST score 124
E value 2.0e-63
Match length 192
% identity 91
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 300031

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Seq. ID	LIB3180-004-P2-M1-C6
Method	BLASTX
NCBI GI	g113217
BLAST score	166
E value	8.0e-12
Match length	31
% identity	100
NCBI Description	ACTIN 1 >gi_100149_pir_S07002 actin 1 - carrot
Seq. No.	300032
Seq. ID	LIB3180-004-P2-M1-E4
Method	BLASTX
NCBI GI	g3551838
BLAST score	164
E value	2.0e-11
Match length	59
% identity	54
NCBI Description	(AF070967) SKP1-like protein [Nicotiana clevelandii]
Seq. No.	300033
Seq. ID	LIB3180-004-P2-M1-F5
Method	BLASTN
NCBI GI	g928931
BLAST score	43
E value	5.0e-15
Match length	79
% identity	89
NCBI Description	A.thaliana mRNA for putative dTDP-glucose 4-6-dehydratases
Seq. No.	300034
Seq. ID	LIB3180-004-P2-M1-G1
Method	BLASTX
NCBI GI	g1184774
BLAST score	215
E value	1.0e-17
Match length	68
% identity	65
NCBI Description	(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]
Seq. No.	300035
Seq. ID	LIB3180-005-P2-M1-A1
Method	BLASTX
NCBI GI	g141608
BLAST score	250
E value	2.0e-21
Match length	106
% identity	55
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa zein [Zea mays]
Seq. No.	300036
Seq. ID	LIB3180-005-P2-M1-A10
Method	BLASTN
NCBI GI	g168696
BLAST score	40

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E value	3.0e-13
Match length	72
% identity	89
NCBI Description	Z.mays zein mRNA, 3' end
Seq. No.	300037
Seq. ID	LIB3180-005-P2-M1-A2
Method	BLASTX
NCBI GI	g135060
BLAST score	221
E value	4.0e-18
Match length	94
% identity	52
NCBI Description	SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1) (SHRUNKEN-1) >gi_66570_pir_YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382) sucrose synthase [Zea mays]
Seq. No.	300038
Seq. ID	LIB3180-005-P2-M1-A3
Method	BLASTX
NCBI GI	g3142302
BLAST score	299
E value	3.0e-27
Match length	98
% identity	63
NCBI Description	(AC002411) Strong similarity to myosin heavy chain gb_Z34293 from A. thaliana. [Arabidopsis thaliana]
Seq. No.	300039
Seq. ID	LIB3180-005-P2-M1-A7
Method	BLASTX
NCBI GI	g16073
BLAST score	180
E value	2.0e-15
Match length	55
% identity	87
NCBI Description	(X59526) zein protein [Acetabularia mediterranea]
Seq. No.	300040
Seq. ID	LIB3180-005-P2-M1-B9
Method	BLASTX
NCBI GI	g141603
BLAST score	220
E value	3.0e-18
Match length	69
% identity	71
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20) >gi_72311_pir_ZIZM2 19K zein precursor (clone A20) - maize >gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]
Seq. No.	300041
Seq. ID	LIB3180-005-P2-M1-C12
Method	BLASTX
NCBI GI	g2668742
BLAST score	256

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E value 3.0e-22
Match length 73
% identity 68
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 300042
Seq. ID LIB3180-005-P2-M1-C3
Method BLASTN
NCBI GI g168652
BLAST score 97
E value 3.0e-47
Match length 153
% identity 91
NCBI Description Maize amyloplast-specific transit protein (waxy; wx+ locus), complete cds

Seq. No. 300043
Seq. ID LIB3180-005-P2-M1-C6
Method BLASTX
NCBI GI g1076678
BLAST score 388
E value 1.0e-37
Match length 78
% identity 100
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No. 300044
Seq. ID LIB3180-005-P2-M1-C8
Method BLASTN
NCBI GI g22509
BLAST score 179
E value 4.0e-96
Match length 283
% identity 91
NCBI Description Zea mays waxy (wx+) locus for UDP-glucose starch glycosyl transferase

Seq. No. 300045
Seq. ID LIB3180-005-P2-M1-D8
Method BLASTX
NCBI GI g2109293
BLAST score 216
E value 2.0e-17
Match length 121
% identity 40
NCBI Description (U97568) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 300046
Seq. ID LIB3180-005-P2-M1-F6
Method BLASTX
NCBI GI g1172833
BLAST score 331
E value 3.0e-31
Match length 68
% identity 91
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-1 >gi_495729 (L16789) small

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ras-related protein [Arabidopsis thaliana]
>gi_2058278_emb_CAA66047_ (X97379) atran1 [Arabidopsis thaliana]

Seq. No. 300047
Seq. ID LIB3180-005-P2-M1-G2
Method BLASTX
NCBI GI g2511531
BLAST score 330
E value 5.0e-31
Match length 66
% identity 94
NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]
>gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1 [Eleusine indica]

Seq. No. 300048
Seq. ID LIB3180-005-P2-M1-H4
Method BLASTX
NCBI GI g141599
BLAST score 184
E value 5.0e-14
Match length 55
% identity 69
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)
>gi_72316_pir_ZIZMA2 19K zein precursor (clone cZ19A2) - maize (fragment). >gi_168670 (M12142) 19 kDa zein protein [Zea mays]

Seq. No. 300049
Seq. ID LIB3180-007-P2-M1-A12
Method BLASTX
NCBI GI g1169528
BLAST score 206
E value 7.0e-17
Match length 53
% identity 81
NCBI Description ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi_602253 (U17973)
enolase [Zea mays]

Seq. No. 300050
Seq. ID LIB3180-007-P2-M1-B10
Method BLASTN
NCBI GI g22549
BLAST score 51
E value 5.0e-20
Match length 67
% identity 94
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 300051
Seq. ID LIB3180-007-P2-M1-B3
Method BLASTX
NCBI GI g113220
BLAST score 253
E value 7.0e-22

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Match length 63
% identity 78
NCBI Description ACTIN 1 >gi_71640_pir_ATZM1 actin - maize

Seq. No. 300052
Seq. ID LIB3180-007-P2-M1-B6
Method BLASTN
NCBI GI g786131
BLAST score 34
E value 2.0e-09
Match length 70
% identity 87
NCBI Description Oryza sativa root-specific RCc3 mRNA, complete cds

Seq. No. 300053
Seq. ID LIB3180-007-P2-M1-C10
Method BLASTX
NCBI GI g4510348
BLAST score 194
E value 2.0e-15
Match length 60
% identity 55
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 300054
Seq. ID LIB3180-007-P2-M1-C3
Method BLASTX
NCBI GI g2369714
BLAST score 218
E value 1.0e-17
Match length 122
% identity 49
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 300055
Seq. ID LIB3180-007-P2-M1-D1
Method BLASTN
NCBI GI g22272
BLAST score 95
E value 3.0e-46
Match length 159
% identity 90
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 300056
Seq. ID LIB3180-007-P2-M1-D11
Method BLASTX
NCBI GI g4519539
BLAST score 158
E value 1.0e-10
Match length 67
% identity 48
NCBI Description (AB016256) NAD-dependent sorbitol dehydrogenase [Malus domestica]

Seq. No. 300057
Seq. ID LIB3180-007-P2-M1-E10

Method BLASTX
NCBI GI g168691
BLAST score 360
E value 2.0e-34
Match length 104
% identity 73
NCBI Description (M29628) zein [Zea mays]

Seq. No. 300058
Seq. ID LIB3180-007-P2-M1-E6
Method BLASTX
NCBI GI g419803
BLAST score 290
E value 2.0e-26
Match length 79
% identity 73
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 300059
Seq. ID LIB3180-007-P2-M1-F11
Method BLASTX
NCBI GI g4165488
BLAST score 408
E value 4.0e-40
Match length 101
% identity 77
NCBI Description (AJ132399) alpha-tubulin 3 [Hordeum vulgare]

Seq. No. 300060
Seq. ID LIB3180-007-P2-M1-F4
Method BLASTX
NCBI GI g224509
BLAST score 303
E value 1.0e-27
Match length 114
% identity 61
NCBI Description zein E19 [Zea mays]

Seq. No. 300061
Seq. ID LIB3180-007-P2-M1-F5
Method BLASTX
NCBI GI g141597
BLAST score 223
E value 3.0e-18
Match length 114
% identity 52
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 300062
Seq. ID LIB3180-007-P2-M1-G5
Method BLASTX
NCBI GI g2316016
BLAST score 361

E value 2.0e-34
 Match length 138
 % identity 53
 NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]

 Seq. No. 300063
 Seq. ID LIB3180-007-P2-M1-H1
 Method BLASTN
 NCBI GI g1519252
 BLAST score 38
 E value 3.0e-12
 Match length 78
 % identity 87
 NCBI Description Oryza sativa GF14-d protein mRNA, complete cds

 Seq. No. 300064
 Seq. ID LIB3180-007-P2-M1-H11
 Method BLASTX
 NCBI GI g136757
 BLAST score 374
 E value 4.0e-36
 Match length 103
 % identity 71
 NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
>gi_100881_pir_S07314 UDPglucose--starch
glucosyltransferase (EC 2.4.1.11) precursor - maize
>gi_168653 (M24258) amyloplast-specific transit protein
[Zea mays] >gi_1644339_emb_CAA27574_ (X03935) glucosyl
transferase [Zea mays]

 Seq. No. 300065
 Seq. ID LIB3180-007-P2-M1-H5
 Method BLASTX
 NCBI GI g136063
 BLAST score 258
 E value 1.0e-22
 Match length 75
 % identity 71
 NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
>gi_68426_pir_ISZMT triose-phosphate isomerase (EC
5.3.1.1) - maize >gi_168647 (L00371) triosephosphate
isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)
triosephosphate isomerase [Zea mays]

 Seq. No. 300066
 Seq. ID LIB3180-007-P2-M1-H6
 Method BLASTX
 NCBI GI g551288
 BLAST score 396
 E value 1.0e-38
 Match length 95
 % identity 80
 NCBI Description (Z33611) phosphoglycerate mutase [Zea mays]

 Seq. No. 300067
 Seq. ID LIB3180-008-P2-M1-A2
 Method BLASTN

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NCBI GI	g3342032
BLAST score	141
E value	2.0e-73
Match length	141
% identity	100
NCBI Description	Elegia sp. Hahn 6994 18S small subunit ribosomal RNA gene, complete sequence
Seq. No.	300068
Seq. ID	LIB3180-008-P2-M1-C1
Method	BLASTN
NCBI GI	g168661
BLAST score	52
E value	2.0e-20
Match length	68
% identity	94
NCBI Description	Maize 15 kDa zein mRNA, clone cZ15A3, complete cds
Seq. No.	300069
Seq. ID	LIB3180-008-P2-M1-C9
Method	BLASTX
NCBI GI	g4210330
BLAST score	220
E value	2.0e-18
Match length	78
% identity	56
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]
Seq. No.	300070
Seq. ID	LIB3180-008-P2-M1-D12
Method	BLASTX
NCBI GI	g72307
BLAST score	326
E value	3.0e-30
Match length	110
% identity	65
NCBI Description	22K zein precursor (clone pZ22.3) - maize >gi_168686 (J01246) 26.99 kd zein protein [Zea mays]
Seq. No.	300071
Seq. ID	LIB3180-008-P2-M1-E2
Method	BLASTX
NCBI GI	g419803
BLAST score	376
E value	3.0e-36
Match length	124
% identity	60
NCBI Description	zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]
Seq. No.	300072
Seq. ID	LIB3180-008-P2-M1-E9
Method	BLASTX
NCBI GI	g4325342
BLAST score	141
E value	4.0e-09

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Match length 41
% identity 71
NCBI Description (AF128393) No definition line found [Arabidopsis thaliana]

Seq. No. 300073
Seq. ID LIB3180-008-P2-M1-F3
Method BLASTX
NCBI GI g22216
BLAST score 251
E value 1.0e-21
Match length 103
% identity 58
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 300074
Seq. ID LIB3180-008-P2-M1-F5
Method BLASTX
NCBI GI g4586246
BLAST score 176
E value 7.0e-13
Match length 83
% identity 46
NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 300075
Seq. ID LIB3180-008-P2-M1-G11
Method BLASTN
NCBI GI g22272
BLAST score 36
E value 5.0e-11
Match length 108
% identity 83
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 300076
Seq. ID LIB3180-008-P2-M1-G2
Method BLASTN
NCBI GI g4416300
BLAST score 90
E value 5.0e-43
Match length 222
% identity 43
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No. 300077
Seq. ID LIB3180-009-P2-M1-A1
Method BLASTX
NCBI GI g2911052
BLAST score 165
E value 9.0e-12
Match length 34
% identity 85
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 300078
Seq. ID LIB3180-009-P2-M1-A2

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Method BLASTX
NCBI GI g3023816
BLAST score 187
E value 2.0e-14
Match length 39
% identity 97
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi_968996 (U31676) glyceraldehyde-3-phosphate
dehydrogenase [Oryza sativa]

Seq. No. 300079
Seq. ID LIB3180-009-P2-M1-B3
Method BLASTN
NCBI GI g3511235
BLAST score 46
E value 9.0e-17
Match length 90
% identity 88
NCBI Description Zea mays starch branching enzyme IIb (ae) gene, complete
cds

Seq. No. 300080
Seq. ID LIB3180-009-P2-M1-B6
Method BLASTN
NCBI GI g22237
BLAST score 61
E value 5.0e-26
Match length 109
% identity 90
NCBI Description Maize mRNA for cytosolic GAPDH (GapC)
glyceraldehyde-3-phosphate dehydrogenase

Seq. No. 300081
Seq. ID LIB3180-009-P2-M1-B7
Method BLASTN
NCBI GI g22312
BLAST score 72
E value 9.0e-33
Match length 112
% identity 91
NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA =
abscisic acid)

Seq. No. 300082
Seq. ID LIB3180-009-P2-M1-C11
Method BLASTX
NCBI GI g2199566
BLAST score 293
E value 7.0e-27
Match length 76
% identity 75
NCBI Description (AF004210) cytochrome P-450 [Zea mays]

Seq. No. 300083
Seq. ID LIB3180-009-P2-M1-D8
Method BLASTX
NCBI GI g118390

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BLAST score	185
E value	3.0e-14
Match length	45
% identity	84
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi_2144526_pir_DCZMP pyruvate decarboxylase (EC 4.1.1.1) - maize >gi_22395_emb_CAA42120_ (X59546) pyruvate decarboxylase [Zea mays]
Seq. No.	300084
Seq. ID	LIB3180-009-P2-M1-E4
Method	BLASTX
NCBI GI	g3355311
BLAST score	158
E value	6.0e-11
Match length	33
% identity	88
NCBI Description	(AJ009737) eukaryotic translation initiation factor 6 [Beta vulgaris]
Seq. No.	300085
Seq. ID	LIB3180-009-P2-M1-E7
Method	BLASTX
NCBI GI	g461498
BLAST score	224
E value	1.0e-18
Match length	63
% identity	73
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir_S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]
Seq. No.	300086
Seq. ID	LIB3180-009-P2-M1-F11
Method	BLASTX
NCBI GI	g3043612
BLAST score	178
E value	4.0e-13
Match length	74
% identity	46
NCBI Description	(AB011116) KIAA0544 protein [Homo sapiens]
Seq. No.	300087
Seq. ID	LIB3180-009-P2-M1-H11
Method	BLASTX
NCBI GI	g3176714
BLAST score	164
E value	1.0e-11
Match length	77
% identity	40
NCBI Description	(AC002392) putative tRNA-splicing endonuclease positive effector [Arabidopsis thaliana]
Seq. No.	300088
Seq. ID	LIB3180-009-P2-M1-H4

Method BLASTX
NCBI GI g1169228
BLAST score 179
E value 2.0e-13
Match length 55
% identity 58
NCBI Description RNA HELICASE-LIKE PROTEIN DB10 >gi_1084413_pir_S42639
helicase-like protein - Wood tobacco
>gi_563986_dbj_BAA03763_ (D16247) RNA helicase like protein
DB10 [Nicotiana sylvestris]

Seq. No. 300089
Seq. ID LIB3180-009-P2-M1-H8
Method BLASTX
NCBI GI g1706958
BLAST score 195
E value 5.0e-15
Match length 91
% identity 49
NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 300090
Seq. ID LIB3180-010-P2-M1-A10
Method BLASTX
NCBI GI g1495251
BLAST score 198
E value 2.0e-15
Match length 76
% identity 55
NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No. 300091
Seq. ID LIB3180-010-P2-M1-B5
Method BLASTN
NCBI GI g22516
BLAST score 102
E value 4.0e-50
Match length 178
% identity 89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 300092
Seq. ID LIB3180-010-P2-M1-D12
Method BLASTX
NCBI GI g419803
BLAST score 294
E value 9.0e-27
Match length 82
% identity 74
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 300093
Seq. ID LIB3180-010-P2-M1-D4
Method BLASTN
NCBI GI g168484
BLAST score 203

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E value 1.0e-110
Match length 382
% identity 88
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 300094
Seq. ID LIB3180-010-P2-M1-E5
Method BLASTX
NCBI GI g4539292
BLAST score 249
E value 3.0e-21
Match length 114
% identity 50
NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No. 300095
Seq. ID LIB3180-010-P2-M1-F1
Method BLASTX
NCBI GI g119152
BLAST score 153
E value 2.0e-17
Match length 109
% identity 50
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
>gi_345384_pir_A45618 translation elongation factor eEF-1 alpha chain - nematode (Onchocerca volvulus) >gi_159885 (M64333) elongation factor [Onchocerca volvulus]

Seq. No. 300096
Seq. ID LIB3180-010-P2-M1-F2
Method BLASTX
NCBI GI g3176662
BLAST score 232
E value 2.0e-19
Match length 104
% identity 42
NCBI Description (AC004393) Similar to mannosyl-oligosaccharide glucosidase gb_X87237 from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 300097
Seq. ID LIB3180-010-P2-M1-F6
Method BLASTX
NCBI GI g548770
BLAST score 233
E value 9.0e-20
Match length 75
% identity 61
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]

Seq. No. 300098
Seq. ID LIB3180-010-P2-M1-F9
Method BLASTX
NCBI GI g3269288
BLAST score 139

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E value	5.0e-09
Match length	44
% identity	61
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]
Seq. No.	300099
Seq. ID	LIB3180-011-P2-M1-A6
Method	BLASTX
NCBI GI	g3786011
BLAST score	406
E value	6.0e-40
Match length	101
% identity	72
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]
Seq. No.	300100
Seq. ID	LIB3180-011-P2-M1-B11
Method	BLASTX
NCBI GI	g113621
BLAST score	288
E value	5.0e-50
Match length	110
% identity	96
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_(X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A cytoplasmic aldolase [Zea mays]
Seq. No.	300101
Seq. ID	LIB3180-011-P2-M1-B3
Method	BLASTX
NCBI GI	g3138799
BLAST score	267
E value	1.0e-23
Match length	60
% identity	85
NCBI Description	(AB014058) beta 6 subunit of 20S proteasome [Oryza sativa]
Seq. No.	300102
Seq. ID	LIB3180-011-P2-M1-C3
Method	BLASTN
NCBI GI	g602252
BLAST score	179
E value	4.0e-96
Match length	187
% identity	99
NCBI Description	Zea mays enolase (eno2) mRNA, complete cds
Seq. No.	300103
Seq. ID	LIB3180-011-P2-M1-F4
Method	BLASTX
NCBI GI	g129881
BLAST score	316
E value	3.0e-29

Match length 111
% identity 63
NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_482294_pir_A36094
pyrophosphate--fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) alpha chain - potato (cv. Kennebec) >gi_169538 (M55190) pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha-subunit [Solanum tuberosum]

Seq. No. 300104
Seq. ID LIB3180-011-P2-M1-H7
Method BLASTX
NCBI GI g4415916
BLAST score 146
E value 2.0e-09
Match length 52
% identity 56
NCBI Description (AC006282) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No. 300105
Seq. ID LIB3180-012-P2-M1-A8
Method BLASTN
NCBI GI g22172
BLAST score 61
E value 7.0e-26
Match length 101
% identity 91
NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit

Seq. No. 300106
Seq. ID LIB3180-012-P2-M1-B4
Method BLASTN
NCBI GI g22542
BLAST score 54
E value 1.0e-21
Match length 66
% identity 95
NCBI Description Maize gene for Mr 19000 alpha zein and 5'-flanking region

Seq. No. 300107
Seq. ID LIB3180-012-P2-M1-C12
Method BLASTN
NCBI GI g1519248
BLAST score 39
E value 9.0e-13
Match length 67
% identity 90
NCBI Description Oryza sativa GF14-b protein mRNA, complete cds

Seq. No. 300108
Seq. ID LIB3180-012-P2-M1-C4
Method BLASTN
NCBI GI g22272
BLAST score 94

E value 1.0e-45
Match length 138
% identity 93
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

Seq. No. 300109
Seq. ID LIB3180-012-P2-M1-D2
Method BLASTN
NCBI GI g2264311
BLAST score 37
E value 3.0e-11
Match length 65
% identity 89
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No. 300110
Seq. ID LIB3180-012-P2-M1-E3
Method BLASTN
NCBI GI g416150
BLAST score 64
E value 9.0e-28
Match length 116
% identity 89
NCBI Description Zea mays beta-8 tubulin (tub8) mRNA, complete cds

Seq. No. 300111
Seq. ID LIB3180-012-P2-M1-E5
Method BLASTN
NCBI GI g168704
BLAST score 127
E value 2.0e-65
Match length 175
% identity 93
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 300112
Seq. ID LIB3180-012-P2-M1-G6
Method BLASTN
NCBI GI g22549
BLAST score 151
E value 1.0e-79
Match length 231
% identity 91
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 300113
Seq. ID LIB3180-013-P2-M1-A4
Method BLASTX
NCBI GI g2789660
BLAST score 156
E value 2.0e-10
Match length 51
% identity 63
NCBI Description (AF040102) p105 [Arabidopsis thaliana]

Seq. No. 300114

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Seq. ID	LIB3180-013-P2-M1-B1
Method	BLASTX
NCBI GI	g82718
BLAST score	291
E value	2.0e-26
Match length	68
% identity	84
NCBI Description	pyruvate,orthophosphate dikinase (EC 2.7.9.1) 2, cytosolic - maize (fragment) >gi_257810_bbs_117087 (S46967) orthophosphate dikinase, PPDK {N-terminal} [maize, Peptide Partial, 90 aa] [Zea mays]
Seq. No.	300115
Seq. ID	LIB3180-013-P2-M1-B9
Method	BLASTX
NCBI GI	g548770
BLAST score	346
E value	8.0e-46
Match length	133
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]
Seq. No.	300116
Seq. ID	LIB3180-013-P2-M1-D2
Method	BLASTX
NCBI GI	g121631
BLAST score	200
E value	1.0e-15
Match length	83
% identity	54
NCBI Description	GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR >gi_72323_pir_KNNT2S glycine-rich protein 2 - wood tobacco >gi_19743_emb_CAA42622_ (X60007) nsGRP-2 [Nicotiana sylvestris]
Seq. No.	300117
Seq. ID	LIB3180-013-P2-M1-D3
Method	BLASTX
NCBI GI	g3914557
BLAST score	442
E value	4.0e-46
Match length	111
% identity	92
NCBI Description	RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED PROTEIN) >gi_1155265 (U40219) possible apospory-associated protein [Pennisetum ciliare]
Seq. No.	300118
Seq. ID	LIB3180-013-P2-M1-F2
Method	BLASTN
NCBI GI	g342659
BLAST score	319
E value	1.0e-179
Match length	327
% identity	100

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NCBI Description Maize (Black Mexican Sweet) mitochondrial 1.9 kb plasmid, complete

Seq. No. 300119
Seq. ID LIB3180-013-P2-M1-H5
Method BLASTN
NCBI GI g22524
BLAST score 50
E value 3.0e-19
Match length 81
% identity 93
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)

Seq. No. 300120
Seq. ID LIB3180-014-P2-M1-A5
Method BLASTX
NCBI GI g4033330
BLAST score 215
E value 2.0e-17
Match length 119
% identity 39
NCBI Description (Y18523) dTDP-glucose 4,6-dehydratase [Actinoplanes sp.]

Seq. No. 300121
Seq. ID LIB3180-014-P2-M1-C2
Method BLASTX
NCBI GI g3599491
BLAST score 302
E value 1.0e-27
Match length 119
% identity 51
NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]

Seq. No. 300122
Seq. ID LIB3180-014-P2-M1-D8
Method BLASTX
NCBI GI g168699
BLAST score 365
E value 7.0e-35
Match length 118
% identity 71
NCBI Description (M60836) zein [Zea mays]

Seq. No. 300123
Seq. ID LIB3180-014-P2-M1-E1
Method BLASTX
NCBI GI g114420
BLAST score 142
E value 7.0e-09
Match length 57
% identity 53
NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
>gi_100882_pir_S11491 H+-transporting ATP synthase (EC
3.6.1.34) beta chain, mitochondrial - maize
>gi_22173_emb_CAA38140_ (X54233) ATPase F1 subunit protein
[Zea mays] >gi_897618 (M36087) F-1-ATPase subunit 2 [Zea
mays]

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Seq. No.	300124
Seq. ID	LIB3180-014-P2-M1-E3
Method	BLASTN
NCBI GI	g2687433
BLAST score	43
E value	7.0e-15
Match length	95
% identity	86
NCBI Description	Tragopogon dubius large subunit 26S ribosomal RNA gene, partial sequence
Seq. No.	300125
Seq. ID	LIB3180-014-P2-M1-F3
Method	BLASTX
NCBI GI	g114420
BLAST score	498
E value	2.0e-50
Match length	110
% identity	91
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_100882_pir_S11491 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - maize >gi_22173_emb_CAA38140 (X54233) ATPase F1 subunit protein [Zea mays] >gi_897618 (M36087) F-1-ATPase subunit 2 [Zea mays]
Seq. No.	300126
Seq. ID	LIB3180-014-P2-M1-H10
Method	BLASTN
NCBI GI	g22549
BLAST score	42
E value	8.0e-15
Match length	70
% identity	90
NCBI Description	Maize gene for a 27kDa storage protein, zein
Seq. No.	300127
Seq. ID	LIB3180-015-P2-M1-D1
Method	BLASTX
NCBI GI	g3402679
BLAST score	161
E value	4.0e-11
Match length	68
% identity	59
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]
Seq. No.	300128
Seq. ID	LIB3180-015-P2-M1-E7
Method	BLASTX
NCBI GI	g4512685
BLAST score	148
E value	2.0e-09
Match length	38
% identity	66
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087)

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hypothetical protein [Arabidopsis thaliana]

Seq. No. 300129
Seq. ID LIB3180-015-P2-M1-G3
Method BLASTX
NCBI GI g3360293
BLAST score 263
E value 7.0e-28
Match length 99
% identity 70
NCBI Description (AF023166) leucine-rich repeat transmembrane protein kinase 3 [Zea mays]

Seq. No. 300130
Seq. ID LIB3180-015-P2-M1-G4
Method BLASTX
NCBI GI g2760345
BLAST score 441
E value 7.0e-44
Match length 90
% identity 26
NCBI Description (U84967) ubiquitin [Arabidopsis thaliana]

Seq. No. 300131
Seq. ID LIB3180-015-P2-M1-H5
Method BLASTX
NCBI GI g872116
BLAST score 242
E value 2.0e-20
Match length 125
% identity 22
NCBI Description (X79770) sti (stress inducible protein) [Glycine max]

Seq. No. 300132
Seq. ID LIB3180-015-P2-M1-H7
Method BLASTX
NCBI GI g2688619
BLAST score 398
E value 9.0e-39
Match length 135
% identity 49
NCBI Description (AE001169) conserved hypothetical protein [Borrelia burgdorferi]

Seq. No. 300133
Seq. ID LIB3180-016-P2-M1-A12
Method BLASTX
NCBI GI g3915826
BLAST score 302
E value 8.0e-28
Match length 71
% identity 80
NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 300134
Seq. ID LIB3180-016-P2-M1-B3
Method BLASTX

NCBI GI g1709619
BLAST score 274
E value 3.0e-24
Match length 80
% identity 68
NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
(GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
>gi_2146814_pir_S69181 protein disulfide isomerase (EC
5.3.4.1) precursor - maize >gi_625148 (L39014) protein
disulfide isomerase [Zea mays]

Seq. No. 300135
Seq. ID LIB3180-016-P2-M1-B5
Method BLASTN
NCBI GI g168425
BLAST score 61
E value 3.0e-26
Match length 61
% identity 100
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 300136
Seq. ID LIB3180-016-P2-M1-F12
Method BLASTN
NCBI GI g413792
BLAST score 35
E value 3.0e-10
Match length 139
% identity 81
NCBI Description Cloning vector lambda EMBL3 SP6/T7, left arm

Seq. No. 300137
Seq. ID LIB3180-016-P2-M1-G6
Method BLASTX
NCBI GI g4210330
BLAST score 209
E value 3.0e-17
Match length 49
% identity 80
NCBI Description (AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit
[Arabidopsis thaliana]

Seq. No. 300138
Seq. ID LIB3180-016-P2-M1-G9
Method BLASTX
NCBI GI g4322327
BLAST score 234
E value 6.0e-20
Match length 71
% identity 61
NCBI Description (AF080545) peptide transporter [Nepenthes alata]

Seq. No. 300139
Seq. ID LIB3180-017-P2-M1-A12
Method BLASTX
NCBI GI g4432841

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BLAST score	220
E value	7.0e-18
Match length	82
% identity	54
NCBI Description	(AC006283) hypothetical protein [Arabidopsis thaliana]
Seq. No.	300140
Seq. ID	LIB3180-017-P2-M1-B12
Method	BLASTX
NCBI GI	g168691
BLAST score	246
E value	6.0e-21
Match length	121
% identity	49
NCBI Description	(M29628) zein [Zea mays]
Seq. No.	300141
Seq. ID	LIB3180-017-P2-M1-B5
Method	BLASTN
NCBI GI	g984755
BLAST score	43
E value	6.0e-15
Match length	111
% identity	85
NCBI Description	O.sativa mRNA for chilling-inducible protein
Seq. No.	300142
Seq. ID	LIB3180-017-P2-M1-B7
Method	BLASTX
NCBI GI	g1658313
BLAST score	276
E value	2.0e-29
Match length	93
% identity	39
NCBI Description	(Y08987) osr40g2 [Oryza sativa]
Seq. No.	300143
Seq. ID	LIB3180-017-P2-M1-C1
Method	BLASTX
NCBI GI	g2832247
BLAST score	210
E value	5.0e-17
Match length	82
% identity	56
NCBI Description	(AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.	300144
Seq. ID	LIB3180-017-P2-M1-D2
Method	BLASTX
NCBI GI	g3914424
BLAST score	258
E value	2.0e-22
Match length	70
% identity	74
NCBI Description	PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi_2511592_emb_CAA74027.1_ (Y13693) multicatalytic

endopeptidase complex, proteasome component, alpha subunit
[Arabidopsis thaliana]

Seq. No. 300145
Seq. ID LIB3180-017-P2-M1-D7
Method BLASTN
NCBI GI g3747049
BLAST score 79
E value 2.0e-36
Match length 111
% identity 94
NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds

Seq. No. 300146
Seq. ID LIB3180-017-P2-M1-E1
Method BLASTX
NCBI GI g2506139
BLAST score 295
E value 1.0e-26
Match length 76
% identity 84
NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
(ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)
archain/delta-COP [Oryza sativa]

Seq. No. 300147
Seq. ID LIB3180-017-P2-M1-E9
Method BLASTX
NCBI GI g3372518
BLAST score 205
E value 3.0e-16
Match length 76
% identity 55
NCBI Description (AF050631) invertase [Zea mays]

Seq. No. 300148
Seq. ID LIB3180-017-P2-M1-F3
Method BLASTX
NCBI GI g1345587
BLAST score 175
E value 5.0e-13
Match length 64
% identity 62
NCBI Description 14-3-3-LIKE PROTEIN GF14-6 >gi_998430_bbs_164522 (S77133)
GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261
aa] [Zea mays]

Seq. No. 300149
Seq. ID LIB3180-017-P2-M1-F4
Method BLASTX
NCBI GI g67155
BLAST score 228
E value 4.0e-19
Match length 91
% identity 53
NCBI Description pyruvate,orthophosphate dikinase (EC 2.7.9.1) precursor -
maize

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Seq. No. 300150
Seq. ID LIB3180-017-P2-M1-G11
Method BLASTN
NCBI GI g168514
BLAST score 140
E value 8.0e-73
Match length 304
% identity 87
NCBI Description Z.mays c1 locus myb homologue cDNA, exons 1-3

Seq. No. 300151
Seq. ID LIB3180-017-P2-M1-G5
Method BLASTX
NCBI GI g119150
BLAST score 160
E value 2.0e-11
Match length 49
% identity 69
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
>gi_82081_pir_S10507 translation elongation factor eEF-1
alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF
1-alpha (AA 1-448) [Lycopersicon esculentum]
>gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha
[Lycopersicon esculentum]

Seq. No. 300152
Seq. ID LIB3180-017-P2-M1-H3
Method BLASTX
NCBI GI g2921209
BLAST score 268
E value 2.0e-23
Match length 72
% identity 78
NCBI Description (AF026148) beta-ketoacyl-ACP synthase I [Perilla
frutescens]

Seq. No. 300153
Seq. ID LIB3180-018-P2-M1-A11
Method BLASTX
NCBI GI g3236238
BLAST score 172
E value 2.0e-12
Match length 59
% identity 59
NCBI Description (AC004684) putative ARF1 GTPase activating protein
[Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_
(AB017876) Asp1 [Arabidopsis thaliana]

Seq. No. 300154
Seq. ID LIB3180-018-P2-M1-E1
Method BLASTN
NCBI GI g22549
BLAST score 178
E value 2.0e-95
Match length 270
% identity 92

NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 300155
Seq. ID LIB3180-018-P2-M1-E5
Method BLASTX
NCBI GI g3334474
BLAST score 190
E value 1.0e-14
Match length 71
% identity 59

NCBI Description OLEOSIN ZM-I (OLEOSIN 16 KD) (LIPID BODY-ASSOCIATED MAJOR PROTEIN) (LIPID BODY-ASSOCIATED PROTEIN L3)
>gi_1076817_pir_S52029 oleosin 16 - maize >gi_687245
(U13701) 16 kDa oleosin [Zea mays]

Seq. No. 300156
Seq. ID LIB3180-018-P2-M1-E8
Method BLASTX
NCBI GI g578545
BLAST score 179
E value 3.0e-13
Match length 112
% identity 10

NCBI Description (Z35759) ubiquitin [Tetrahymena pyriformis]

Seq. No. 300157
Seq. ID LIB3180-018-P2-M1-G10
Method BLASTX
NCBI GI g2369714
BLAST score 177
E value 3.0e-13
Match length 76
% identity 51

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 300158
Seq. ID LIB3180-018-P2-M1-G9
Method BLASTN
NCBI GI g556672
BLAST score 46
E value 5.0e-17
Match length 66
% identity 92

NCBI Description S.cereale (Halo) chloroplast mRNA for heat-shock protein

Seq. No. 300159
Seq. ID LIB3180-018-P2-M1-H3
Method BLASTX
NCBI GI g548770
BLAST score 440
E value 1.0e-43
Match length 101
% identity 83

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
ribosomal protein L3 [Oryza sativa]

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Seq. No. 300160
Seq. ID LIB3180-019-P2-M1-A11
Method BLASTX
NCBI GI g2117937
BLAST score 240
E value 2.0e-20
Match length 65
% identity 75
NCBI Description UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare]

Seq. No. 300161
Seq. ID LIB3180-019-P2-M1-A2
Method BLASTX
NCBI GI g1181673
BLAST score 234
E value 1.0e-19
Match length 73
% identity 66
NCBI Description (U41652) heat shock protein cognate 70 [Sorghum bicolor]

Seq. No. 300162
Seq. ID LIB3180-019-P2-M1-D11
Method BLASTX
NCBI GI g4510423
BLAST score 163
E value 1.0e-11
Match length 52
% identity 65
NCBI Description (AC006929) unknown protein [Arabidopsis thaliana]

Seq. No. 300163
Seq. ID LIB3180-019-P2-M1-D12
Method BLASTN
NCBI GI g22524
BLAST score 121
E value 7.0e-62
Match length 125
% identity 99
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)

Seq. No. 300164
Seq. ID LIB3180-019-P2-M1-G6
Method BLASTX
NCBI GI g1762945
BLAST score 158
E value 1.0e-10
Match length 50
% identity 60
NCBI Description (U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

Seq. No. 300165
Seq. ID LIB3180-019-P2-M1-H6
Method BLASTX
NCBI GI g3599491

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BLAST score 250
E value 1.0e-21
Match length 76
% identity 62
NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]

Seq. No. 300166
Seq. ID LIB3180-020-P2-M1-B7
Method BLASTN
NCBI GI g1532072
BLAST score 85
E value 3.0e-40
Match length 137
% identity 91
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No. 300167
Seq. ID LIB3180-020-P2-M1-C1
Method BLASTX
NCBI GI g1076809
BLAST score 156
E value 7.0e-11
Match length 71
% identity 51
NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize
>gi_758355_emb_CAA59800_ (X85805) H(+) -transporting ATPase
[Zea mays]

Seq. No. 300168
Seq. ID LIB3180-020-P2-M1-D3
Method BLASTX
NCBI GI g2959732
BLAST score 256
E value 2.0e-22
Match length 52
% identity 83
NCBI Description (Y13649) homologous to GATA-binding transcription factors
[Arabidopsis thaliana]

Seq. No. 300169
Seq. ID LIB3180-020-P2-M1-H4
Method BLASTX
NCBI GI g3152587
BLAST score 258
E value 2.0e-22
Match length 87
% identity 68
NCBI Description (AC002986) Similar to CREB-binding protein homolog
gb_U88570 from D. melanogaster and contains similarity to
callus-associated protein gb_U01961 from Nicotiana tabacum.
EST gb_W43427 comes from this gene. [Arabidopsis thaliana]

Seq. No. 300170
Seq. ID LIB3180-021-P2-M1-A12
Method BLASTX
NCBI GI g3608171
BLAST score 398

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E value 6.0e-39
Match length 103
% identity 80
NCBI Description (D86306) proton-translocating inorganic pyrophosphatase [Cucurbita moschata]

Seq. No. 300171
Seq. ID LIB3180-021-P2-M1-A6
Method BLASTX
NCBI GI g141597
BLAST score 363
E value 1.0e-34
Match length 130
% identity 64
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3_19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 300172
Seq. ID LIB3180-021-P2-M1-B11
Method BLASTN
NCBI GI g22549
BLAST score 106
E value 7.0e-53
Match length 158
% identity 92
NCBI Description Maize gene for a 27kDa storage protein, zein

Seq. No. 300173
Seq. ID LIB3180-021-P2-M1-C8
Method BLASTN
NCBI GI g2668743
BLAST score 64
E value 2.0e-27
Match length 80
% identity 95
NCBI Description Zea mays ubiquitin conjugating enzyme (UBC) mRNA, complete cds

Seq. No. 300174
Seq. ID LIB3180-021-P2-M1-D1
Method BLASTN
NCBI GI g22516
BLAST score 123
E value 8.0e-63
Match length 213
% identity 89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 300175
Seq. ID LIB3180-021-P2-M1-E9
Method BLASTN
NCBI GI g311238
BLAST score 84
E value 7.0e-40
Match length 136

% identity 91
NCBI Description Z.mays cat1 gene for catalase

Seq. No. 300176
Seq. ID LIB3180-021-P2-M1-F5
Method BLASTN
NCBI GI g1184771
BLAST score 95
E value 3.0e-46
Match length 185
% identity 89
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC2 (gpc2) mRNA, complete cds

Seq. No. 300177
Seq. ID LIB3180-021-P2-M1-G4
Method BLASTN
NCBI GI g168425
BLAST score 165
E value 7.0e-88
Match length 205
% identity 95
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 300178
Seq. ID LIB3180-022-P2-M1-C11
Method BLASTX
NCBI GI g119355
BLAST score 216
E value 2.0e-17
Match length 55
% identity 82
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
>gi_100869_pir_S16257 phosphopyruvate hydratase (EC
4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
[Zea mays]

Seq. No. 300179
Seq. ID LIB3180-022-P2-M1-C4
Method BLASTX
NCBI GI g113621
BLAST score 211
E value 2.0e-17
Match length 44
% identity 95
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
>gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A
cytoplasmic aldolase [Zea mays]

Seq. No. 300180
Seq. ID LIB3180-022-P2-M1-C7
Method BLASTN
NCBI GI g260041

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BLAST score	38
E value	3.0e-12
Match length	66
% identity	89
NCBI Description	Sh2=shrunken-2 locus [maize, mRNA Partial, 1867 nt]
Seq. No.	300181
Seq. ID	LIB3180-022-P2-M1-E6
Method	BLASTX
NCBI GI	g232172
BLAST score	239
E value	1.0e-20
Match length	77
% identity	66
NCBI Description	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi_481816_pir_S39504 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) - wheat >gi_21687_emb CAA46879_ (X66080) ADP-glucose pyrophosphorylase [Triticum aestivum]
Seq. No.	300182
Seq. ID	LIB3180-022-P2-M1-E7
Method	BLASTX
NCBI GI	g421929
BLAST score	215
E value	2.0e-17
Match length	60
% identity	11
NCBI Description	ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]
Seq. No.	300183
Seq. ID	LIB3180-022-P2-M1-F6
Method	BLASTX
NCBI GI	g3641839
BLAST score	197
E value	3.0e-15
Match length	52
% identity	67
NCBI Description	(AL023094) isoflavone reductase - like protein [Arabidopsis thaliana]
Seq. No.	300184
Seq. ID	LIB3180-023-P2-M1-A12
Method	BLASTX
NCBI GI	g168586
BLAST score	428
E value	2.0e-46
Match length	112
% identity	91
NCBI Description	(M58656) pyruvate,orthophosphate dikinase [Zea mays]
Seq. No.	300185
Seq. ID	LIB3180-023-P2-M1-D6
Method	BLASTX

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NCBI GI g3121867
BLAST score 186
E value 2.0e-14
Match length 71
% identity 54
NCBI Description COP1 REGULATORY PROTEIN >gi_1694900_emb_CAA70768_ (Y09579)
Cop1 protein [Pisum sativum]

Seq. No. 300186
Seq. ID LIB3180-023-P2-M1-D7
Method BLASTX
NCBI GI g4105719
BLAST score 286
E value 3.0e-26
Match length 54
% identity 93
NCBI Description (AF050128) cell wall invertase Incw2; beta-fructosidase
[Zea mays]

Seq. No. 300187
Seq. ID LIB3180-023-P2-M1-G9
Method BLASTX
NCBI GI g2507281
BLAST score 238
E value 3.0e-20
Match length 50
% identity 92
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_
(X97380) atran2 [Arabidopsis thaliana]

Seq. No. 300188
Seq. ID LIB3180-024-P2-M1-A12
Method BLASTX
NCBI GI g3135543
BLAST score 182
E value 5.0e-14
Match length 52
% identity 67
NCBI Description (AF062393) aquaporin [Oryza sativa]

Seq. No. 300189
Seq. ID LIB3180-024-P2-M1-A8
Method BLASTN
NCBI GI g602252
BLAST score 36
E value 6.0e-11
Match length 40
% identity 97
NCBI Description Zea mays enolase (eno2) mRNA, complete cds

Seq. No. 300190
Seq. ID LIB3180-024-P2-M1-B3
Method BLASTX
NCBI GI g3212871
BLAST score 195
E value 2.0e-15
Match length 76

% identity 51
NCBI Description (AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No. 300191
Seq. ID LIB3180-024-P2-M1-B9
Method BLASTX
NCBI GI g2655291
BLAST score 144
E value 1.0e-09
Match length 43
% identity 67
NCBI Description (AF032974) germin-like protein 4 [Oryza sativa]

Seq. No. 300192
Seq. ID LIB3180-024-P2-M1-C1
Method BLASTX
NCBI GI g22216
BLAST score 296
E value 8.0e-27
Match length 94
% identity 66
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 300193
Seq. ID LIB3180-024-P2-M1-C2
Method BLASTN
NCBI GI g602252
BLAST score 60
E value 2.0e-25
Match length 128
% identity 87
NCBI Description Zea mays enolase (eno2) mRNA, complete cds

Seq. No. 300194
Seq. ID LIB3180-024-P2-M1-D12
Method BLASTN
NCBI GI g168654
BLAST score 107
E value 4.0e-53
Match length 162
% identity 92
NCBI Description Zea mays ADP glucose pyrophosphorylase (shrunken-2) gene, complete cds

Seq. No. 300195
Seq. ID LIB3180-024-P2-M1-D8
Method BLASTX
NCBI GI g141605
BLAST score 455
E value 2.0e-45
Match length 124
% identity 73
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cz19C2) - maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

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Seq. No. 300196
Seq. ID LIB3180-024-P2-M1-E8
Method BLASTX
NCBI GI g4115371
BLAST score 265
E value 3.0e-23
Match length 113
% identity 52
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 300197
Seq. ID LIB3180-024-P2-M1-F2
Method BLASTX
NCBI GI g4104056
BLAST score 245
E value 3.0e-21
Match length 54
% identity 83
NCBI Description (AF031194) S276 [Triticum aestivum]

Seq. No. 300198
Seq. ID LIB3180-024-P2-M1-H3
Method BLASTX
NCBI GI g3043415
BLAST score 331
E value 4.0e-31
Match length 70
% identity 91
NCBI Description (Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No. 300199
Seq. ID LIB3180-024-P2-M1-H5
Method BLASTX
NCBI GI g3319882
BLAST score 152
E value 4.0e-10
Match length 86
% identity 45
NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer arietinum]

Seq. No. 300200
Seq. ID LIB3180-024-P2-M1-H7
Method BLASTX
NCBI GI g2275211
BLAST score 165
E value 2.0e-11
Match length 87
% identity 68
NCBI Description (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 300201
Seq. ID LIB3180-027-P2-M2-B8
Method BLASTX
NCBI GI g119150
BLAST score 387
E value 7.0e-38

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Match length	87
% identity	86
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_82081_pir_S10507 translation elongation factor eEF-1 alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF 1-alpha (AA 1-448) [Lycopersicon esculentum] >gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha [Lycopersicon esculentum]
Seq. No.	300202
Seq. ID	LIB3180-027-P2-M2-F11
Method	BLASTX
NCBI GI	g2498329
BLAST score	172
E value	8.0e-13
Match length	53
% identity	60
NCBI Description	PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir_S65571 pattern-formation protein GNOM - Arabidopsis thaliana >gi_1209633 (U36433) GNOM gene product [Arabidopsis thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]
Seq. No.	300203
Seq. ID	LIB3180-028-P2-M2-A6
Method	BLASTN
NCBI GI	g1491773
BLAST score	53
E value	3.0e-21
Match length	105
% identity	88
NCBI Description	Z.mays mRNA for cysteine proteinase, Seel
Seq. No.	300204
Seq. ID	LIB3180-028-P2-M2-C3
Method	BLASTX
NCBI GI	g3549667
BLAST score	188
E value	1.0e-14
Match length	68
% identity	60
NCBI Description	(AL031394) Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana]
Seq. No.	300205
Seq. ID	LIB3180-028-P2-M2-D11
Method	BLASTX
NCBI GI	g2760349
BLAST score	362
E value	1.0e-34
Match length	87
% identity	17
NCBI Description	(U84969) ubiquitin [Arabidopsis thaliana]

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Seq. No. 300206
Seq. ID LIB3180-028-P2-M2-F10
Method BLASTX
NCBI GI g417745
BLAST score 219
E value 6.0e-18
Match length 83
% identity 57
NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_170773 (L11872)
S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

Seq. No. 300207
Seq. ID LIB3180-028-P2-M2-F9
Method BLASTN
NCBI GI g168425
BLAST score 82
E value 1.0e-38
Match length 106
% identity 94
NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 300208
Seq. ID LIB3180-028-P2-M2-H8
Method BLASTX
NCBI GI g4138179
BLAST score 268
E value 4.0e-24
Match length 64
% identity 81
NCBI Description (AJ223969) elongation factor 1 alpha subunit [Malus domestica]

Seq. No. 300209
Seq. ID LIB3180-029-P2-M2-C4
Method BLASTN
NCBI GI g168482
BLAST score 80
E value 3.0e-37
Match length 184
% identity 86
NCBI Description Corn starch branching enzyme II mRNA, complete cds

Seq. No. 300210
Seq. ID LIB3180-029-P2-M2-F10
Method BLASTN
NCBI GI g3318612
BLAST score 53
E value 3.0e-21
Match length 69
% identity 94
NCBI Description Zea mays mRNA for mitochondrial phosphate transporter, complete cds

Seq. No. 300211
Seq. ID LIB3180-030-P2-M2-A2
Method BLASTX

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NCBI GI	g2642159
BLAST score	159
E value	1.0e-10
Match length	53
% identity	58
NCBI Description	(AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]
Seq. No.	300212
Seq. ID	LIB3180-030-P2-M2-B11
Method	BLASTX
NCBI GI	g129171
BLAST score	221
E value	6.0e-18
Match length	81
% identity	65
NCBI Description	OPAQUE-2 REGULATORY PROTEIN >gi_22388_emb_CAA33550_(X15544) opaque-2 protein [Zea mays]
Seq. No.	300213
Seq. ID	LIB3180-030-P2-M2-B4
Method	BLASTX
NCBI GI	g2104712
BLAST score	486
E value	3.0e-49
Match length	115
% identity	89
NCBI Description	(U95180) endosperm specific protein [Zea mays]
Seq. No.	300214
Seq. ID	LIB3180-030-P2-M2-F4
Method	BLASTX
NCBI GI	g1076748
BLAST score	209
E value	6.0e-17
Match length	65
% identity	62
NCBI Description	major intrinsic protein - rice >gi_440869_dbj_BAA04257_(D17443) major intrinsic protein [Oryza sativa]
Seq. No.	300215
Seq. ID	LIB3180-030-P2-M2-G3
Method	BLASTX
NCBI GI	g3281846
BLAST score	267
E value	1.0e-23
Match length	70
% identity	76
NCBI Description	(AJ006404) late elongated hypocotyl [Arabidopsis thaliana]
Seq. No.	300216
Seq. ID	LIB3180-031-P2-M2-A11
Method	BLASTX
NCBI GI	g2435522
BLAST score	192

E value 9.0e-15
Match length 70
% identity 54
NCBI Description (AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]

Seq. No. 300217
Seq. ID LIB3180-031-P2-M2-C1
Method BLASTN
NCBI GI g340933
BLAST score 35
E value 1.0e-10
Match length 87
% identity 85
NCBI Description Zea mays 10-kDa zein gene, complete cds

Seq. No. 300218
Seq. ID LIB3180-031-P2-M2-C5
Method BLASTN
NCBI GI g2282583
BLAST score 65
E value 2.0e-28
Match length 113
% identity 89
NCBI Description Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete cds

Seq. No. 300219
Seq. ID LIB3180-031-P2-M2-D12
Method BLASTN
NCBI GI g257040
BLAST score 167
E value 3.0e-89
Match length 187
% identity 97
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 300220
Seq. ID LIB3180-031-P2-M2-F2
Method BLASTN
NCBI GI g2286152
BLAST score 72
E value 2.0e-32
Match length 88
% identity 95
NCBI Description Zea mays cytoplasmic malate dehydrogenase mRNA, complete cds

Seq. No. 300221
Seq. ID LIB3180-031-P2-M2-F3
Method BLASTN
NCBI GI g2909845
BLAST score 92
E value 2.0e-44
Match length 122
% identity 93
NCBI Description Zea mays (S)-adenosyl-L-methionine:delta 24-sterol

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methyltransferase mRNA, complete cds

Seq. No. 300222
Seq. ID LIB3180-031-P2-M2-F7
Method BLASTX
NCBI GI g282994
BLAST score 212
E value 1.0e-17
Match length 45
% identity 82
NCBI Description Sip1 protein - barley >gi_167100 (M77475) seed imbibition protein [Hordeum vulgare]

Seq. No. 300223
Seq. ID LIB3180-031-P2-M2-G8
Method BLASTN
NCBI GI g2257755
BLAST score 51
E value 4.0e-20
Match length 95
% identity 88
NCBI Description Zea mays nucleolar histone deacetylase HD2-p39 mRNA, complete cds

Seq. No. 300224
Seq. ID LIB3180-032-P2-M2-C11
Method BLASTX
NCBI GI g1710551
BLAST score 281
E value 3.0e-25
Match length 51
% identity 100
NCBI Description 60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728_(X95458) ribosomal protein L39 [Zea mays]

Seq. No. 300225
Seq. ID LIB3180-033-P2-M2-B2
Method BLASTN
NCBI GI g435456
BLAST score 34
E value 4.0e-10
Match length 85
% identity 85
NCBI Description Proso millet gene for aspartate aminotransferase, complete cds

Seq. No. 300226
Seq. ID LIB3180-033-P2-M2-B5
Method BLASTX
NCBI GI g3132825
BLAST score 212
E value 2.0e-17
Match length 45
% identity 93
NCBI Description (AF063403) putative cytosine-5 DNA methyltransferase [Zea mays]

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Seq. No. 300227
Seq. ID LIB3180-033-P2-M2-C7
Method BLASTX
NCBI GI g2967456
BLAST score 182
E value 5.0e-14
Match length 50
% identity 74
NCBI Description (AB012048) sulfate transporter [Arabidopsis thaliana]

Seq. No. 300228
Seq. ID LIB3180-033-P2-M2-D1
Method BLASTN
NCBI GI g257807
BLAST score 57
E value 1.0e-23
Match length 61
% identity 98
NCBI Description cyppdkZml=orthophosphate dikinase {5'region} [maize, Genomic, 895 nt]

Seq. No. 300229
Seq. ID LIB3180-033-P2-M2-G10
Method BLASTX
NCBI GI g3334349
BLAST score 174
E value 6.0e-13
Match length 79
% identity 49
NCBI Description GLYCYL-tRNA SYNTHETASE (GLYCINE--tRNA LIGASE) (GLYRS)
>gi_2564215_emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 300230
Seq. ID LIB3180-033-P2-M2-G6
Method BLASTX
NCBI GI g3334349
BLAST score 193
E value 1.0e-19
Match length 85
% identity 59
NCBI Description GLYCYL-tRNA SYNTHETASE (GLYCINE--tRNA LIGASE) (GLYRS)
>gi_2564215_emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 300231
Seq. ID LIB3180-034-P2-M2-A3
Method BLASTN
NCBI GI g13918
BLAST score 75
E value 1.0e-34
Match length 115
% identity 91
NCBI Description Maize mitochondrial DNA for 5kB alpha-R1 repeat

Seq. No. 300232
Seq. ID LIB3180-034-P2-M2-B9

Method BLASTN
NCBI GI g1495231
BLAST score 41
E value 2.0e-14
Match length 79
% identity 87
NCBI Description Z.mays mRNA for 22kD zein protein

Seq. No. 300233
Seq. ID LIB3180-034-P2-M2-E3
Method BLASTX
NCBI GI g4581164
BLAST score 261
E value 3.0e-23
Match length 74
% identity 65
NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No. 300234
Seq. ID LIB3180-034-P2-M2-E7
Method BLASTN
NCBI GI g1184775
BLAST score 47
E value 8.0e-18
Match length 83
% identity 89
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4 (gpc4). mRNA, complete cds

Seq. No. 300235
Seq. ID LIB3180-034-P2-M2-F1
Method BLASTX
NCBI GI g136063
BLAST score 159
E value 2.0e-11
Match length 50
% identity 66
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
>gi_68426_pir_ISZMT triose-phosphate isomerase (EC
5.3.1.1) - maize >gi_168647 (L00371) triosephosphate
isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)
triosephosphate isomerase [Zea mays]

Seq. No. 300236
Seq. ID LIB3180-034-P2-M2-H12
Method BLASTN
NCBI GI g22544
BLAST score 144
E value 2.0e-75
Match length 176
% identity 95
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 300237
Seq. ID LIB3180-035-P2-M2-A2
Method BLASTX
NCBI GI g2511535

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BLAST score	298
E value	4.0e-44
Match length	106
% identity	86
NCBI Description	(AF008122) alpha-tubulin 3 [Eleusine indica]
Seq. No.	300238
Seq. ID	LIB3180-035-P2-M2-D10
Method	BLASTX
NCBI GI	g82720
BLAST score	252
E value	6.0e-45
Match length	115
% identity	87
NCBI Description	regulatory protein O2 - maize >gi_22384_emb_CAA34614_(X16618) O2 protein (AA 1-460) [Zea mays]
Seq. No.	300239
Seq. ID	LIB3180-035-P2-M2-F1
Method	BLASTX
NCBI GI	g1532210
BLAST score	269
E value	7.0e-43
Match length	136
% identity	67
NCBI Description	(U68268) cyclophilin A [Trypanosoma congolense]
Seq. No.	300240
Seq. ID	LIB3180-035-P2-M2-G1
Method	BLASTN
NCBI GI	g902524
BLAST score	37
E value	2.0e-11
Match length	121
% identity	83
NCBI Description	Zea mays clone MubG10 ubiquitin fusion protein gene, complete cds
Seq. No.	300241
Seq. ID	LIB3180-035-P2-M2-G12
Method	BLASTN
NCBI GI	g575730
BLAST score	45
E value	3.0e-16
Match length	65
% identity	92
NCBI Description	Z.mays mRNA for transmembrane protein
Seq. No.	300242
Seq. ID	LIB3180-035-P2-M2-H1
Method	BLASTN
NCBI GI	g22516
BLAST score	235
E value	1.0e-129
Match length	318
% identity	94
NCBI Description	Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 300243
Seq. ID LIB3180-036-P2-M2-A11
Method BLASTX
NCBI GI g3924596
BLAST score 265
E value 2.0e-23
Match length 78
% identity 71
NCBI Description (AF069442) putative phospho-ser/thr phosphatase [Arabidopsis thaliana]

Seq. No. 300244
Seq. ID LIB3180-036-P2-M2-A6
Method BLASTX
NCBI GI g300265
BLAST score 316
E value 4.0e-29
Match length 89
% identity 73
NCBI Description HSP68=68 kda heat-stress DnaK homolog [Lycopersicon peruvianum=tomatoes, Peptide Mitochondrial Partial, 580 aa]

Seq. No. 300245
Seq. ID LIB3180-036-P2-M2-C1
Method BLASTN
NCBI GI g169818
BLAST score 43
E value 5.0e-15
Match length 171
% identity 81
NCBI Description Rice 25S ribosomal RNA gene

Seq. No. 300246
Seq. ID LIB3180-036-P2-M2-E2
Method BLASTX
NCBI GI g3559805
BLAST score 614
E value 4.0e-64
Match length 134
% identity 78
NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No. 300247
Seq. ID LIB3180-036-P2-M2-E8
Method BLASTX
NCBI GI g1762130
BLAST score 235
E value 1.0e-19
Match length 66
% identity 77
NCBI Description (U46136) chaperonin-60 beta subunit [Solanum tuberosum]

Seq. No. 300248
Seq. ID LIB3180-036-P2-M2-F1
Method BLASTX

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NCBI GI	g584706
BLAST score	211
E value	8.0e-17
Match length	58
% identity	78
NCBI Description	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A) >gi_2130066_pir_JC5124 aspartate transaminase (EC 2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_ (D14673) aspartate aminotransferase [Oryza sativa]
Seq. No.	300249
Seq. ID	LIB3180-036-P2-M2-F10
Method	BLASTN
NCBI GI	g14395
BLAST score	177
E value	7.0e-95
Match length	302
% identity	94
NCBI Description	T.aestivum mitochondrion fMet, 18S, 5S repeat unit DNA
Seq. No.	300250
Seq. ID	LIB3180-036-P2-M2-F8
Method	BLASTX
NCBI GI	g4490330
BLAST score	377
E value	1.0e-36
Match length	75
% identity	92
NCBI Description	(AL035656) splicing factor-like protein [Arabidopsis thaliana]
Seq. No.	300251
Seq. ID	LIB3180-036-P2-M2-F9
Method	BLASTX
NCBI GI	g585084
BLAST score	170
E value	4.0e-12
Match length	43
% identity	77
NCBI Description	ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G) >gi_543383_pir_S40780 translation elongation factor G, mitochondrial - rat >gi_310102 (L14684) elongation factor G [Rattus norvegicus]
Seq. No.	300252
Seq. ID	LIB3180-036-P2-M2-G10
Method	BLASTX
NCBI GI	g3789911
BLAST score	194
E value	8.0e-15
Match length	81
% identity	48
NCBI Description	(AF081802) developmental protein DG1118 [Dictyostelium discoideum]
Seq. No.	300253
Seq. ID	LIB3180-036-P2-M2-G6

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Method BLASTX
NCBI GI g16073
BLAST score 422
E value 1.0e-41
Match length 134
% identity 68
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 300254
Seq. ID LIB3180-036-P2-M2-H3
Method BLASTN
NCBI GI g625147
BLAST score 153
E value 1.0e-80
Match length 296
% identity 94
NCBI Description Zea mays protein disulfide isomerase (pdi) mRNA, complete cds

Seq. No. 300255
Seq. ID LIB3180-037-P2-M2-A10
Method BLASTX
NCBI GI g168691
BLAST score 325
E value 3.0e-30
Match length 101
% identity 63
NCBI Description (M29628) zein [Zea mays]

Seq. No. 300256
Seq. ID LIB3180-037-P2-M2-A9
Method BLASTX
NCBI GI g2494073
BLAST score 139
E value 9.0e-09
Match length 46
% identity 54
NCBI Description BETAINE-ALDEHYDE DEHYDROGENASE (BADH)
>gi_2144333_pir_S71413 betaine-aldehyde dehydrogenase (EC
1.2.1.8) precursor - barley >gi_927643_dbj_BAA05466
(D26448) betaine aldehyde dehydrogenase [Hordeum vulgare]

Seq. No. 300257
Seq. ID LIB3180-037-P2-M2-D9
Method BLASTX
NCBI GI g168691
BLAST score 302
E value 1.0e-27
Match length 110
% identity 59
NCBI Description (M29628) zein [Zea mays]

Seq. No. 300258
Seq. ID LIB3180-037-P2-M2-F6
Method BLASTX
NCBI GI g1174448
BLAST score 145

E value 4.0e-09
Match length 42
% identity 71
NCBI Description TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]

Seq. No. 300259
Seq. ID LIB3180-037-P2-M2-G1
Method BLASTX
NCBI GI g4220523
BLAST score 312
E value 1.0e-28
Match length 98
% identity 58
NCBI Description (AL035356) putative alliin lyase [Arabidopsis thaliana]

Seq. No. 300260
Seq. ID LIB3180-038-P2-M2-A3
Method BLASTX
NCBI GI g4558460
BLAST score 419
E value 3.0e-41
Match length 81
% identity 100
NCBI Description (AF073775) replication origin activator ROA2 [Zea mays]

Seq. No. 300261
Seq. ID LIB3180-038-P2-M2-E2
Method BLASTX
NCBI GI g417154
BLAST score 350
E value 3.0e-33
Match length 113
% identity 63
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir_S25541 heat shock protein 82 - rice (strain Taichung Native One)
>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No. 300262
Seq. ID LIB3180-038-P2-M2-F10
Method BLASTX
NCBI GI g1658313
BLAST score 442
E value 4.0e-44
Match length 97
% identity 46
NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 300263
Seq. ID LIB3180-038-P2-M2-G12
Method BLASTX
NCBI GI g168586
BLAST score 484
E value 7.0e-49

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Match length 113
% identity 85
NCBI Description (M58656) pyruvate,orthophosphate dikinase [Zea mays]

Seq. No. 300264
Seq. ID LIB3180-038-P2-M2-G2
Method BLASTX
NCBI GI g4033424
BLAST score 295
E value 9.0e-27
Match length 89
% identity 72
NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic pyrophosphatase [Zea mays]

Seq. No. 300265
Seq. ID LIB3180-039-P2-M2-A10
Method BLASTX
NCBI GI g419803
BLAST score 211
E value 4.0e-17
Match length 80
% identity 50
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 300266
Seq. ID LIB3180-039-P2-M2-A7
Method BLASTX
NCBI GI g4321782
BLAST score 291
E value 2.0e-26
Match length 85
% identity 62
NCBI Description (AF061178) arsenical resistance ATPase [Mus musculus]

Seq. No. 300267
Seq. ID LIB3180-039-P2-M2-F3
Method BLASTN
NCBI GI g22514
BLAST score 121
E value 7.0e-62
Match length 153
% identity 95
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 300268
Seq. ID LIB3180-039-P2-M2-G2
Method BLASTX
NCBI GI g3420239
BLAST score 267
E value 2.0e-23
Match length 50
% identity 100
NCBI Description (AF059484) actin [Gossypium hirsutum]

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Seq. No.	300269
Seq. ID	LIB3180-039-P2-M2-G5
Method	BLASTX
NCBI GI	g1174613
BLAST score	344
E value	2.0e-32
Match length	80
% identity	84
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614 (D17788) rice homologue of Tat binding protein [Oryza sativa]
Seq. No.	300270
Seq. ID	LIB3180-039-P2-M2-H4
Method	BLASTX
NCBI GI	g113621
BLAST score	190
E value	2.0e-14
Match length	60
% identity	68
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf_1307278A cytoplasmic aldolase [Zea mays]
Seq. No.	300271
Seq. ID	LIB3180-040-P2-M2-A12
Method	BLASTN
NCBI GI	g625147
BLAST score	49
E value	1.0e-18
Match length	69
% identity	93
NCBI Description	Zea mays protein disulfide isomerase (pdi) mRNA, complete cds
Seq. No.	300272
Seq. ID	LIB3180-040-P2-M2-C12
Method	BLASTN
NCBI GI	g2832242
BLAST score	42
E value	2.0e-14
Match length	78
% identity	88
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	300273
Seq. ID	LIB3180-040-P2-M2-D8
Method	BLASTX
NCBI GI	g1184776
BLAST score	233
E value	1.0e-37
Match length	91
% identity	91

NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC4 [Zea mays]

Seq. No. 300274
Seq. ID LIB3180-040-P2-M2-E5
Method BLASTX
NCBI GI g4115936
BLAST score 258
E value 2.0e-22
Match length 83
% identity 65
NCBI Description (AF118223) No definition line found [Arabidopsis thaliana]

Seq. No. 300275
Seq. ID LIB3180-040-P2-M2-H10
Method BLASTX
NCBI GI g3935152
BLAST score 258
E value 2.0e-22
Match length 84
% identity 58
NCBI Description (AC005106) T25N20.16 [Arabidopsis thaliana]

Seq. No. 300276
Seq. ID LIB3180-040-P2-M2-H11
Method BLASTX
NCBI GI g2833378
BLAST score 187
E value 2.0e-14
Match length 87
% identity 43
NCBI Description HEXOKINASE >gi_619928 (U18754) hexokinase [Arabidopsis thaliana] >gi_1582383_prf_2118367A hexokinase [Arabidopsis thaliana]

Seq. No. 300277
Seq. ID LIB3180-041-P2-M2-C11
Method BLASTN
NCBI GI g22516
BLAST score 279
E value 1.0e-156
Match length 370
% identity 95
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 300278
Seq. ID LIB3180-041-P2-M2-D3
Method BLASTX
NCBI GI g1771780
BLAST score 444
E value 3.0e-44
Match length 96
% identity 93
NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 300279
Seq. ID LIB3180-041-P2-M2-E11

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Method BLASTN
NCBI GI g168704
BLAST score 102
E value 1.0e-50
Match length 122
% identity 96
NCBI Description Zea mays zein protein gene, complete cds

Seq. No. 300280
Seq. ID LIB3180-041-P2-M2-G5
Method BLASTX
NCBI GI g543867
BLAST score 163
E value 2.0e-11
Match length 76
% identity 57
NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
>gi_1076684_pir_A47493 H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor - sweet potato
>gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gamma subunit
[Ipomoea batatas]

Seq. No. 300281
Seq. ID LIB3180-042-P2-M2-A6
Method BLASTN
NCBI GI g22516
BLAST score 152
E value 4.0e-80
Match length 268
% identity 89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 300282
Seq. ID LIB3180-042-P2-M2-A7
Method BLASTX
NCBI GI g141615
BLAST score 266
E value 2.0e-23
Match length 72
% identity 78
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
>gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 300283
Seq. ID LIB3180-042-P2-M2-B3
Method BLASTN
NCBI GI g168484
BLAST score 183
E value 1.0e-98
Match length 243
% identity 94
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 300284
Seq. ID LIB3180-042-P2-M2-C12
Method BLASTN
NCBI GI g22292

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BLAST score	35
E value	1.0e-10
Match length	59
% identity	90
NCBI Description	Z.mays mRNA for glycine-rich protein
Seq. No.	300285
Seq. ID	LIB3180-042-P2-M2-D10
Method	BLASTX
NCBI GI	g141608
BLAST score	225
E value	9.0e-20
Match length	119
% identity	52
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir_S15655 zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa zein [Zea mays]
Seq. No.	300286
Seq. ID	LIB3180-042-P2-M2-E1
Method	BLASTN
NCBI GI	g1495231
BLAST score	89
E value	2.0e-42
Match length	154
% identity	88
NCBI Description	Z.mays mRNA for 22kD zein protein
Seq. No.	300287
Seq. ID	LIB3180-042-P2-M2-F2
Method	BLASTX
NCBI GI	g1169911
BLAST score	279
E value	5.0e-25
Match length	65
% identity	85
NCBI Description	1,4-ALPHA-GLUCAN BRANCHING ENZYME IIB PRECURSOR (STARCH BRANCHING ENZYME IIB) (Q-ENZYME) >gi_168483 (L08065) starch branching enzyme II [Zea mays]
Seq. No.	300288
Seq. ID	LIB3180-042-P2-M2-H2
Method	BLASTX
NCBI GI	g72307
BLAST score	267
E value	3.0e-23
Match length	91
% identity	65
NCBI Description	22K zein precursor (clone pZ22.3) - maize >gi_168686 (J01246) 26.99 kd zein protein [Zea mays]
Seq. No.	300289
Seq. ID	LIB3180-042-P2-M2-H5
Method	BLASTX
NCBI GI	g2257756
BLAST score	247
E value	5.0e-21

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Match length 96
& identity 56
NCBI Description (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]
>gi_3650466 (AF026917) histone deacetylase HD2-p39 [Zea mays]

Seq. No. 300290
Seq. ID LIB3180-042-P2-M2-H7
Method BLASTX
NCBI GI g3850583
BLAST score 262
E value 8.0e-23
Match length 106
& identity 53
NCBI Description (AC005278) Contains similarity to transcription initiation factor IIE, alpha subunit gb_X63468 from Homo sapiens.
[Arabidopsis thaliana]

Seq. No. 300291
Seq. ID LIB3180-042-P2-M2-H8
Method BLASTX
NCBI GI g2653558
BLAST score 344
E value 1.0e-32
Match length 102
& identity 69
NCBI Description (D50679) ferredoxin-sulfite reductase precursor [Zea mays]

Seq. No. 300292
Seq. ID LIB3180-043-P2-M2-B6
Method BLASTX
NCBI GI g1184774
BLAST score 211
E value 2.0e-17
Match length 47
& identity 89
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 300293
Seq. ID LIB3180-043-P2-M2-B7
Method BLASTX
NCBI GI g141597
BLAST score 248
E value 2.0e-28
Match length 100
& identity 75
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 300294
Seq. ID LIB3180-043-P2-M2-C10
Method BLASTX
NCBI GI g2507349
BLAST score 193

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E value	8.0e-15
Match length	113
% identity	37
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE (B150) (RNA POLYMERASE II SUBUNIT 2) >gi_82997_pir_A25884 DNA-directed RNA polymerase (EC 2.7.7.6) II 140K chain - yeast (Saccharomyces cerevisiae) >gi_1293711 (U55020) Rpb2p polymerase [Saccharomyces cerevisiae] >gi_1420379_emb_CAA99357_ (Z75059) ORF YOR151c [Saccharomyces cerevisiae]
Seq. No.	300295
Seq. ID	LIB3180-043-P2-M2-C7
Method	BLASTN
NCBI GI	g1184773
BLAST score	67
E value	2.0e-29
Match length	191
% identity	85
NCBI Description	Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3 (gpc3) mRNA, complete cds
Seq. No.	300296
Seq. ID	LIB3180-043-P2-M2-D10
Method	BLASTX
NCBI GI	g730450
BLAST score	341
E value	3.0e-32
Match length	99
% identity	68
NCBI Description	60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B) >gi_480649_pir_S37134 cold-induced protein BnC24B - rape >gi_398922_emb_CAA80343_ (Z22620) cold induced protein (BnC24B) [Brassica napus]
Seq. No.	300297
Seq. ID	LIB3180-043-P2-M2-D3
Method	BLASTX
NCBI GI	g141602
BLAST score	239
E value	2.0e-20
Match length	61
% identity	84
NCBI Description	ZEIN-ALPHA PRECURSOR (19 KD) (CLONE M6) >gi_82658_pir_A22831 19K zein precursor (clone M6) - maize >gi_22538_emb_CAA26294_ (X02450) zein precursor [Zea mays]
Seq. No.	300298
Seq. ID	LIB3180-043-P2-M2-G6
Method	BLASTX
NCBI GI	g2369714
BLAST score	272
E value	2.0e-24
Match length	79
% identity	67
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

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Seq. No.	300299
Seq. ID	LIB3180-043-P2-M2-H10
Method	BLASTX
NCBI GI	g2244772
BLAST score	259
E value	8.0e-23
Match length	77
% identity	60
NCBI Description	(Z97335) transport protein [Arabidopsis thaliana]
Seq. No.	300300
Seq. ID	LIB3180-044-P2-M2-A1
Method	BLASTX
NCBI GI	g1313907
BLAST score	140
E value	8.0e-09
Match length	82
% identity	46
NCBI Description	(D84507) CDPK-related protein kinase [Zea mays]
Seq. No.	300301
Seq. ID	LIB3180-044-P2-M2-C3
Method	BLASTX
NCBI GI	g1184776
BLAST score	215
E value	9.0e-18
Match length	59
% identity	75
NCBI Description	(U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]
Seq. No.	300302
Seq. ID	LIB3180-044-P2-M2-C5
Method	BLASTX
NCBI GI	g1545871
BLAST score	427
E value	2.0e-42
Match length	91
% identity	91
NCBI Description	(U66607) cyclin type B-like [Zea mays] >gi_1545873 (U66608) cyclin type B-like [Zea mays]
Seq. No.	300303
Seq. ID	LIB3180-044-P2-M2-D2
Method	BLASTN
NCBI GI	g1737491
BLAST score	35
E value	2.0e-10
Match length	63
% identity	89
NCBI Description	Triticum aestivum poly(A)-binding protein (wheatpab) mRNA, complete cds
Seq. No.	300304
Seq. ID	LIB3180-044-P2-M2-E11
Method	BLASTX
NCBI GI	g1184776

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BLAST score 419
E value 2.0e-41
Match length 90
% identity 91
NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC4 [Zea mays]

Seq. No. 300305
Seq. ID LIB3180-044-P2-M2-E6
Method BLASTX
NCBI GI g141616
BLAST score 208
E value 9.0e-17
Match length 61
% identity 62
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 300306
Seq. ID LIB3180-044-P2-M2-F12
Method BLASTX
NCBI GI g118104
BLAST score 362
E value 1.0e-34
Match length 79
% identity 91
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 300307
Seq. ID LIB3180-044-P2-M2-G7
Method BLASTN
NCBI GI g3694806
BLAST score 38
E value 3.0e-12
Match length 78
% identity 87
NCBI Description Zea mays alanine aminotransferase (alt) gene, complete cds

Seq. No. 300308
Seq. ID LIB3180-045-P2-M2-A6
Method BLASTX
NCBI GI g118104
BLAST score 376
E value 3.0e-36
Match length 102
% identity 73
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 300309

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Seq. ID	LIB3180-045-P2-M2-B9
Method	BLASTX
NCBI GI	g4204859
BLAST score	415
E value	8.0e-41
Match length	104
% identity	80
NCBI Description	(U55859) heat shock protein 80 [Triticum aestivum]
Seq. No.	300310
Seq. ID	LIB3180-045-P2-M2-F7
Method	BLASTX
NCBI GI	g3063473
BLAST score	315
E value	3.0e-29
Match length	105
% identity	63
NCBI Description	(AC003981) F22013.35 [Arabidopsis thaliana]
Seq. No.	300311
Seq. ID	LIB3180-045-P2-M2-G8
Method	BLASTX
NCBI GI	g547683
BLAST score	141
E value	5.0e-09
Match length	41
% identity	71
NCBI Description	HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] >gi_445601_prf_1909348A heat shock protein hsp80 [Lycopersicon esculentum]
Seq. No.	300312
Seq. ID	LIB3180-046-P2-M2-B4
Method	BLASTX
NCBI GI	g2224641
BLAST score	237
E value	7.0e-20
Match length	109
% identity	40
NCBI Description	(AB002348) KIAA0350 [Homo sapiens]
Seq. No.	300313
Seq. ID	LIB3180-046-P2-M2-D11
Method	BLASTN
NCBI GI	g4733890
BLAST score	46
E value	4.0e-17
Match length	106
% identity	86
NCBI Description	Zea mays unconventional myosin heavy chain (MYO1) mRNA, partial cds
Seq. No.	300314
Seq. ID	LIB3180-046-P2-M2-D3
Method	BLASTX
NCBI GI	g2827711

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BLAST score	335
E value	2.0e-31
Match length	107
% identity	65
NCBI Description	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]
Seq. No.	300315
Seq. ID	LIB3180-046-P2-M2-D5
Method	BLASTX
NCBI GI	g1184776
BLAST score	270
E value	7.0e-24
Match length	80
% identity	70
NCBI Description	(U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]
Seq. No.	300316
Seq. ID	LIB3180-046-P2-M2-G11
Method	BLASTX
NCBI GI	g1346432
BLAST score	210
E value	6.0e-17
Match length	72
% identity	58
NCBI Description	LEGUMAIN PRECURSOR (ASPARAGINYL ENDOPEPTIDASE) >gi_1076483_pir_JX0344 legumain (EC 3.4.22.34) precursor - jack bean >gi_499294_dbj_BAA06596 (D31787) asparaginyl endopeptidase (Legumain) [Canavalia ensiformis]
Seq. No.	300317
Seq. ID	LIB3180-047-P2-A6
Method	BLASTN
NCBI GI	g22326
BLAST score	56
E value	8.0e-23
Match length	92
% identity	90
NCBI Description	Z.mays gene for Hageman factor inhibitor
Seq. No.	300318
Seq. ID	LIB3180-047-P2-C2
Method	BLASTN
NCBI GI	g1532162
BLAST score	34
E value	9.0e-10
Match length	50
% identity	31
NCBI Description	Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14 genes, partial cds, AT.I.24-7, ascorbate peroxidase (ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.I
Seq. No.	300319
Seq. ID	LIB3180-047-P2-D5
Method	BLASTN

NCBI GI g22344
BLAST score 42
E value 2.0e-14
Match length 82
% identity 89
NCBI Description Maize gene for heat shock protein 70 exon 1 (clone 9508)

Seq. No. 300320
Seq. ID LIB3180-047-P2-D8
Method BLASTX
NCBI GI g4581111
BLAST score 152
E value 7.0e-10
Match length 140
% identity 29
NCBI Description (AC005825) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No. 300321
Seq. ID LIB3180-047-P2-G10
Method BLASTX
NCBI GI g3757521
BLAST score 153
E value 3.0e-10
Match length 67
% identity 48
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 300322
Seq. ID LIB3180-047-P2-G2
Method BLASTN
NCBI GI g22099
BLAST score 39
E value 4.0e-13
Match length 67
% identity 90
NCBI Description Z.mays 27kDa zein locus DNA

Seq. No. 300323
Seq. ID LIB3180-048-P2-A2
Method BLASTX
NCBI GI g4249382
BLAST score 234
E value 8.0e-20
Match length 64
% identity 67
NCBI Description (AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No. 300324
Seq. ID LIB3180-048-P2-B11
Method BLASTN
NCBI GI g4096785
BLAST score 52
E value 2.0e-20
Match length 88

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% identity 91
NCBI Description Zea mays NADP-malic enzyme root isoform mRNA, complete cds

Seq. No. 300325
Seq. ID LIB3180-048-P2-C10
Method BLASTX
NCBI GI g118104
BLAST score 237
E value 2.0e-33
Match length 88
% identity 77
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
maize >gi_168461 (M55021) cyclophilin [Zea mays]
>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 300326
Seq. ID LIB3180-048-P2-C5
Method BLASTN
NCBI GI g6598604
BLAST score 37
E value 2.0e-11
Match length 65
% identity 89
NCBI Description Arabidopsis thaliana chromosome II BAC F11A3 genomic
sequence, complete sequence

Seq. No. 300327
Seq. ID LIB3180-048-P2-D8
Method BLASTX
NCBI GI g2738248
BLAST score 304
E value 4.0e-28
Match length 88
% identity 66
NCBI Description (U97200) cobalamin-independent methionine synthase
[Arabidopsis thaliana]

Seq. No. 300328
Seq. ID LIB3180-048-P2-E10
Method BLASTN
NCBI GI g168652
BLAST score 124
E value 3.0e-63
Match length 128
% identity 99
NCBI Description Maize amyloplast-specific transit protein (waxy; wx+
locus), complete cds

Seq. No. 300329
Seq. ID LIB3180-048-P2-E6
Method BLASTX
NCBI GI g625509
BLAST score 443
E value 3.0e-44
Match length 94

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% identity	25
NCBI Description	ubiquitin precursor - Arabidopsis thaliana (fragment)
Seq. No.	300330
Seq. ID	LIB3180-048-P2-E7
Method	BLASTN
NCBI GI	g556685
BLAST score	114
E value	3.0e-57
Match length	129
% identity	98
NCBI Description	Z.mays mRNA for ADP-ribosylation factor
Seq. No.	300331
Seq. ID	LIB3180-048-P2-F1
Method	BLASTX
NCBI GI	g2282584
BLAST score	148
E value	6.0e-10
Match length	40
% identity	78
NCBI Description	(U76259) elongation factor 1-alpha [Zea mays]
Seq. No.	300332
Seq. ID	LIB3180-048-P2-F3
Method	BLASTX
NCBI GI	g542125
BLAST score	212
E value	2.0e-17
Match length	55
% identity	76
NCBI Description	translation elongation factor eEF-1 alpha chain - barley >gi_396134_emb_CAA80666 (Z23130) protein synthesis elongation factor-1 alpha [Hordeum vulgare]
Seq. No.	300333
Seq. ID	LIB3180-048-P2-G3
Method	BLASTX
NCBI GI	g1903034
BLAST score	201
E value	6.0e-16
Match length	68
% identity	50
NCBI Description	(X94625) amp-binding protein [Brassica napus]
Seq. No.	300334
Seq. ID	LIB3180-048-P2-G7
Method	BLASTX
NCBI GI	g168586
BLAST score	302
E value	5.0e-28
Match length	74
% identity	81
NCBI Description	(M58656) pyruvate,orthophosphate dikinase [Zea mays]
Seq. No.	300335
Seq. ID	LIB3180-048-P2-H6

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Method BLASTX
NCBI GI g3057120
BLAST score 492
E value 4.0e-50
Match length 90
% identity 98
NCBI Description (AF023159) starch synthase DULL1 [Zea mays]

Seq. No. 300336
Seq. ID LIB3180-049-P2-M1-A4
Method BLASTX
NCBI GI g20559
BLAST score 602
E value 1.0e-62
Match length 127
% identity 94
NCBI Description (X13301) hsp70 (AA 6 - 651) [Petunia x hybrida]

Seq. No. 300337
Seq. ID LIB3180-049-P2-M1-B2
Method BLASTX
NCBI GI g3914006
BLAST score 313
E value 5.0e-29
Match length 65
% identity 97
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi_1816588 (U85495) LON2 [Zea mays]

Seq. No. 300338
Seq. ID LIB3180-049-P2-M1-B9
Method BLASTX
NCBI GI g551288
BLAST score 345
E value 2.0e-32
Match length 82
% identity 82
NCBI Description (Z33611) phosphoglycerate mutase [Zea mays]

Seq. No. 300339
Seq. ID LIB3180-049-P2-M1-D12
Method BLASTN
NCBI GI g940880
BLAST score 54
E value 2.0e-21
Match length 146
% identity 85
NCBI Description Z.mays zag2 gene

Seq. No. 300340
Seq. ID LIB3180-049-P2-M1-D2
Method BLASTX
NCBI GI g4467124
BLAST score 241
E value 2.0e-20
Match length 136
% identity 37

NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 300341
Seq. ID LIB3180-049-P2-M1-D5
Method BLASTX
NCBI GI g3608171
BLAST score 475
E value 7.0e-60
Match length 139
% identity 86

NCBI Description (D86306) proton-translocating inorganic pyrophosphatase [Cucurbita moschata]

Seq. No. 300342
Seq. ID LIB3180-049-P2-M1-E1
Method BLASTX
NCBI GI g67155
BLAST score 240
E value 2.0e-20
Match length 119
% identity 56

NCBI Description pyruvate,orthophosphate dikinase (EC 2.7.9.1) precursor - maize

Seq. No. 300343
Seq. ID LIB3180-049-P2-M1-H11
Method BLASTX
NCBI GI g2288999
BLAST score 194
E value 9.0e-23
Match length 82
% identity 65

NCBI Description (AC002335) electron transfer flavoprotein ubiquinone oxidoreductase isolog [Arabidopsis thaliana]

Seq. No. 300344
Seq. ID LIB3180-049-P2-M1-H2
Method BLASTX
NCBI GI g1184776
BLAST score 442
E value 6.0e-44
Match length 88
% identity 95

NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]

Seq. No. 300345
Seq. ID LIB3180-049-P2-M1-H4
Method BLASTX
NCBI GI g4512667
BLAST score 572
E value 4.0e-66
Match length 137
% identity 86

NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 300346

DOCUMENT NUMBER

Seq. ID LIB3180-049-P2-M1-H9
Method BLASTX
NCBI GI g1184774
BLAST score 155
E value 2.0e-10
Match length 43
% identity 65
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC3 [Zea mays]

Seq. No. 300347
Seq. ID LIB3180-050-P2-M1-A9
Method BLASTX
NCBI GI g3510253
BLAST score 194
E value 2.0e-15
Match length 63
% identity 57
NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No. 300348
Seq. ID LIB3180-050-P2-M1-C1
Method BLASTX
NCBI GI g3309243
BLAST score 169
E value 2.0e-12
Match length 41
% identity 78
NCBI Description (AF073507) aconitase-iron regulated protein 1 [Citrus limon]

Seq. No. 300349
Seq. ID LIB3180-050-P2-M1-E11
Method BLASTN
NCBI GI g416150
BLAST score 79
E value 8.0e-37
Match length 115
% identity 92
NCBI Description Zea mays beta-8 tubulin (tub8) mRNA, complete cds

Seq. No. 300350
Seq. ID LIB3180-050-P2-M1-E5
Method BLASTX
NCBI GI g3152581
BLAST score 247
E value 3.0e-21
Match length 69
% identity 65
NCBI Description (AC002986) Similar to E. coli sulfurtransferase (rhodanese)
gb_AE00338. ESTs gb_T03984, gb_T03983 and gb_W43228 come
from this gene. [Arabidopsis thaliana]

Seq. No. 300351
Seq. ID LIB3180-050-P2-M1-F1
Method BLASTX
NCBI GI g1723436

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BLAST score 289
E value 4.0e-26
Match length 106
% identity 58
NCBI Description HYPOTHETICAL 119.9 KD PROTEIN C56F8.03 IN CHROMOSOME I
>gi_1204225_emb_CAA93574 (Z69728) unknown
[Schizosaccharomyces pombe]

Seq. No. 300352
Seq. ID LIB3180-051-P2-M1-A1
Method BLASTX
NCBI GI g1184774
BLAST score 370
E value 2.0e-35
Match length 88
% identity 84
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
GAPC3 [Zea mays]

Seq. No. 300353
Seq. ID LIB3180-051-P2-M1-A2
Method BLASTX
NCBI GI g4406769
BLAST score 247
E value 4.0e-21
Match length 84
% identity 60
NCBI Description (AC006836) putative translin [Arabidopsis thaliana]

Seq. No. 300354
Seq. ID LIB3180-051-P2-M1-B12
Method BLASTX
NCBI GI g82695
BLAST score 326
E value 1.0e-30
Match length 72
% identity 93
NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) 3 -
maize (fragment) >gi_293887 (L13431)
glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 300355
Seq. ID LIB3180-051-P2-M1-D9
Method BLASTX
NCBI GI g22216
BLAST score 184
E value 9.0e-14
Match length 81
% identity 52
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 300356
Seq. ID LIB3180-052-P2-M1-C3
Method BLASTX
NCBI GI g3915826
BLAST score 290
E value 2.0e-26

Match length 80
% identity 71
NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 300357
Seq. ID LIB3180-052-P2-M1-C6
Method BLASTX
NCBI GI g4091008
BLAST score 214.
E value 3.0e-17
Match length 87
% identity 55
NCBI Description (AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No. 300358
Seq. ID LIB3180-052-P2-M1-D10
Method BLASTN
NCBI GI g4206307
BLAST score 36
E value 9.0e-11
Match length 108
% identity 84
NCBI Description Zea mays retrotransposon Cinful-2

Seq. No. 300359
Seq. ID LIB3180-052-P2-M1-E12
Method BLASTX
NCBI GI g4585966
BLAST score 156
E value 2.0e-10
Match length 70
% identity 54
NCBI Description (AC005287) Putative dihydrolipoamide acetyltransferase [Arabidopsis thaliana]

Seq. No. 300360
Seq. ID LIB3180-052-P2-M1-F6
Method BLASTX
NCBI GI g135398
BLAST score 313
E value 5.0e-29
Match length 58
% identity 98
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir_S15773 tubulin alpha-1 chain - maize >gi_22147_emb_CAA33734_ (X15704) alpha1-tubulin [Zea mays]

Seq. No. 300361
Seq. ID LIB3180-052-P2-M1-G11
Method BLASTX
NCBI GI g3452091
BLAST score 268
E value 1.0e-23
Match length 86
% identity 57
NCBI Description (AJ004899) rudimentary enhancer [Glycine max]

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Seq. No.	300362
Seq. ID	LIB3180-052-P2-M1-G12
Method	BLASTX
NCBI GI	g3318615
BLAST score	212
E value	3.0e-17
Match length	46
% identity	91
NCBI Description	(AB016065) mitochondrial phosphate transporter [Oryza sativa]
Seq. No.	300363
Seq. ID	LIB3180-052-P2-M1-G3
Method	BLASTX
NCBI GI	g168586
BLAST score	433
E value	7.0e-43
Match length	138
% identity	69
NCBI Description	(M58656) pyruvate,orthophosphate dikinase [Zea mays]
Seq. No.	300364
Seq. ID	LIB3180-052-P2-M1-H10
Method	BLASTX
NCBI GI	g4263722
BLAST score	411
E value	3.0e-40
Match length	131
% identity	60
NCBI Description	(AC006223) putative glucan synthase [Arabidopsis thaliana]
Seq. No.	300365
Seq. ID	LIB3180-053-P2-M1-A6
Method	BLASTX
NCBI GI	g3914557
BLAST score	322
E value	8.0e-30
Match length	77
% identity	84
NCBI Description	RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED PROTEIN) >gi_1155265 (U40219) possible apospory-associated protein [Pennisetum ciliare]
Seq. No.	300366
Seq. ID	LIB3180-053-P2-M1-B11
Method	BLASTX
NCBI GI	g2827080
BLAST score	157
E value	8.0e-11
Match length	63
% identity	62
NCBI Description	(AF020271) malate dehydrogenase precursor [Medicago sativa]
Seq. No.	300367
Seq. ID	LIB3180-053-P2-M1-C5
Method	BLASTX
NCBI GI	g3511285

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BLAST score	224
E value	7.0e-19
Match length	62
% identity	68
NCBI Description	(AF081534) cellulose synthase [Populus alba x Populus tremula]
Seq. No.	300368
Seq. ID	LIB3180-053-P2-M1-C7
Method	BLASTN
NCBI GI	g260041
BLAST score	45
E value	2.0e-16
Match length	73
% identity	90
NCBI Description	Sh2=shrunken-2 locus [maize, mRNA Partial, 1867 nt]
Seq. No.	300369
Seq. ID	LIB3180-053-P2-M1-D5
Method	BLASTN
NCBI GI	g463151
BLAST score	119
E value	1.0e-60
Match length	159
% identity	94
NCBI Description	Zea mays high sulfur zein gene, complete cds
Seq. No.	300370
Seq. ID	LIB3180-053-P2-M1-D7
Method	BLASTX
NCBI GI	g730125
BLAST score	426
E value	1.0e-46
Match length	122
% identity	75
NCBI Description	NADPH-CYTOCHROME P450 REDUCTASE >gi_322739_pir_S31502 NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Madagascar periwinkle >gi_18139_emb_CAA49446_ (X69791) NADPH--ferrihemoprotein reductase [Catharanthus roseus]
Seq. No.	300371
Seq. ID	LIB3180-054-P2-M1-A3
Method	BLASTX
NCBI GI	g464707
BLAST score	263
E value	4.0e-23
Match length	66
% identity	76
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir_S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A

[Arabidopsis thaliana]. >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No. 300372
Seq. ID LIB3180-054-P2-M1-F2
Method BLASTX
NCBI GI g2370312
BLAST score 457
E value 1.0e-45
Match length 102
% identity 79
NCBI Description (AJ000995) DnaJ-like protein [Medicago sativa] >gi_3202020 (AF069507) DnaJ-like protein MsJ1 [Medicago sativa]

Seq. No. 300373
Seq. ID LIB3180-054-P2-M1-F3
Method BLASTX
NCBI GI g4008159
BLAST score 156
E value 8.0e-11
Match length 57
% identity 61
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]

Seq. No. 300374
Seq. ID LIB3180-054-P2-M1-G1
Method BLASTX
NCBI GI g2735841
BLAST score 241
E value 2.0e-20
Match length 116
% identity 42
NCBI Description (AF010283) No definition line found [Sorghum bicolor]

Seq. No. 300375
Seq. ID LIB3180-055-P2-M1-A10
Method BLASTX
NCBI GI g1143864
BLAST score 320
E value 7.0e-30
Match length 98
% identity 63
NCBI Description (U28047) beta glucosidase [Oryza sativa]

Seq. No. 300376
Seq. ID LIB3180-055-P2-M1-B6
Method BLASTN
NCBI GI g949979
BLAST score 128
E value 5.0e-66
Match length 184
% identity 92
NCBI Description Z.mays Glossy2 locus DNA

Seq. No. 300377
Seq. ID LIB3180-055-P2-M1-D10
Method BLASTX
NCBI GI g1076746
BLAST score 518
E value 7.0e-53
Match length 101
% identity 97
NCBI Description heat shock protein 70 - rice (fragment)
>gi_763160_emb_CAA47948_(X67711) heat shock protein 70
[Oryza sativa]

Seq. No. 300378
Seq. ID LIB3180-055-P2-M1-F4
Method BLASTX
NCBI GI g126896
BLAST score 271
E value 5.0e-24
Match length 108
% identity 55
NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
>gi_319831_pir_DEPUMW malate dehydrogenase (EC 1.1.1.37)
precursor, mitochondrial - watermelon
>gi_18297_emb_CAA35239_(X17362) precursor protein (AA -27
to 320) [Citrullus lanatus]

Seq. No. 300379
Seq. ID LIB3180-057-P2-M1-E9
Method BLASTN
NCBI GI g22336
BLAST score 59
E value 5.0e-25
Match length 63
% identity 98
NCBI Description Maize mRNA for an 18kDa heat shock protein

Seq. No. 300380
Seq. ID LIB3180-058-P2-M1-F11
Method BLASTX
NCBI GI g4587584
BLAST score 153
E value 1.0e-10
Match length 50
% identity 62
NCBI Description (AC007232) unknown protein [Arabidopsis thaliana]

Seq. No. 300381
Seq. ID LIB3180-058-P2-M1-F12
Method BLASTX
NCBI GI g3560533
BLAST score 202
E value 2.0e-16
Match length 51
% identity 76
NCBI Description (AF042333) 24-methylene lophenol C24(1)methyltransferase
[Oryza sativa]

Seq. No. 300382
Seq. ID LIB3180-058-P2-M1-H1
Method BLASTX
NCBI GI g520582
BLAST score 164
E value 2.0e-11
Match length 52
% identity 62
NCBI Description (D37796) Ids3 [Hordeum vulgare]

Seq. No. 300383
Seq. ID LIB3180-059-P2-M1-A10
Method BLASTN
NCBI GI g1184775
BLAST score 78
E value 5.0e-36
Match length 138
% identity 89
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC4 (gpc4) mRNA, complete cds

Seq. No. 300384
Seq. ID LIB3180-059-P2-M1-A11
Method BLASTX
NCBI GI g4454480
BLAST score 153
E value 1.0e-10
Match length 37
% identity 76
NCBI Description (AC006234) putative (1-4)-beta-mannan endohydrolase [Arabidopsis thaliana]

Seq. No. 300385
Seq. ID LIB3180-059-P2-M1-B3
Method BLASTX
NCBI GI g2668744
BLAST score 243
E value 7.0e-21
Match length 54
% identity 83
NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No. 300386
Seq. ID LIB3180-059-P2-M1-E1
Method BLASTX
NCBI GI g4415996
BLAST score 212
E value 3.0e-17
Match length 61
% identity 66
NCBI Description (AF059290) beta-tubulin 4 [Eleusine indica]

Seq. No. 300387
Seq. ID LIB3180-059-P2-M1-E2
Method BLASTN
NCBI GI g1037129

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BLAST score 42
E value 2.0e-14
Match length 84
% identity 90
NCBI Description (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize, Tuxpeno CMS 450, mRNA Partial, 1889 nt]

Seq. No. 300388
Seq. ID LIB3180-059-P2-M1-F10
Method BLASTN
NCBI GI g2642323
BLAST score 91
E value 1.0e-43
Match length 131
% identity 91
NCBI Description Zea mays profilin (PRO4) mRNA, complete cds

Seq. No. 300389
Seq. ID LIB3180-059-P2-M1-H2
Method BLASTX
NCBI GI g2244971
BLAST score 229
E value 6.0e-19
Match length 52
% identity 77
NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 300390
Seq. ID LIB3180-060-P2-M1-A1
Method BLASTX
NCBI GI g559713
BLAST score 237
E value 4.0e-20
Match length 86
% identity 55
NCBI Description (D38552) The ha1539 protein is related to cyclophilin. [Homo sapiens]

Seq. No. 300391
Seq. ID LIB3180-060-P2-M1-A4
Method BLASTN
NCBI GI g168584
BLAST score 79
E value 4.0e-37
Match length 95
% identity 96
NCBI Description Corn pyruvate,orthophosphate dikinase gene, exons 2-19

Seq. No. 300392
Seq. ID LIB3180-060-P2-M1-B9
Method BLASTN
NCBI GI g22138
BLAST score 60
E value 2.0e-25
Match length 131
% identity 87
NCBI Description Z.mays gene for acetohydroxyacid synthase (AHAS108)

Seq. No. 300393
Seq. ID LIB3180-060-P2-M1-H6
Method BLASTN
NCBI GI g536891
BLAST score 36
E value 5.0e-11
Match length 60
% identity 90
NCBI Description Wheat mRNA for protein H2A, complete cds, clone wch2A-4

Seq. No. 300394
Seq. ID LIB3180-061-P2-M1-A1
Method BLASTX
NCBI GI g3393067
BLAST score 314
E value 5.0e-29
Match length 87
% identity 72
NCBI Description (AJ001117) sucrose synthase type I [Triticum sp.]

Seq. No. 300395
Seq. ID LIB3180-061-P2-M1-A10
Method BLASTX
NCBI GI g2829871
BLAST score 227
E value 8.0e-19
Match length 112
% identity 43
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 300396
Seq. ID LIB3180-061-P2-M1-A9
Method BLASTX
NCBI GI g2194142
BLAST score 331
E value 6.0e-31
Match length 131
% identity 47
NCBI Description (AC002062) ESTs gb_N38288,gb_T43486,gb_AA395242 come from this gene. [Arabidopsis thaliana]

Seq. No. 300397
Seq. ID LIB3180-061-P2-M1-B11
Method BLASTN
NCBI GI g260041
BLAST score 40
E value 2.0e-13
Match length 67
% identity 90
NCBI Description Sh2=shrunken-2 locus [maize, mRNA Partial, 1867 nt]

Seq. No. 300398
Seq. ID LIB3180-061-P2-M1-B2
Method BLASTX
NCBI GI g1370603
BLAST score 294

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E value 9.0e-27
Match length 92
% identity 66
NCBI Description (X98245) annexin p35 [Zea mays]

Seq. No. 300399
Seq. ID LIB3180-061-P2-M1-C3
Method BLASTX
NCBI GI g119355
BLAST score 289
E value 5.0e-26
Match length 57
% identity 100
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
>gi_100869_pir_S16257 phosphopyruvate hydratase (EC
4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
[Zea mays]

Seq. No. 300400
Seq. ID LIB3180-061-P2-M1-D3
Method BLASTN
NCBI GI g168673
BLAST score 61
E value 1.0e-25
Match length 73
% identity 96
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 300401
Seq. ID LIB3180-061-P2-M1-E11
Method BLASTX
NCBI GI g231654
BLAST score 310
E value 2.0e-28
Match length 79
% identity 81
NCBI Description BRITTLE-1 PROTEIN PRECURSOR >gi_82676_pir_JQ1459_Bt1
protein precursor - maize >gi_168426 (M79333) brittle-1
protein [Zea mays]

Seq. No. 300402
Seq. ID LIB3180-061-P2-M1-F1
Method BLASTN
NCBI GI g22516
BLAST score 100
E value 5.0e-49
Match length 176
% identity 89
NCBI Description Maize Zc2 gene for zein Zc2 (28 kD glutelin-2)

Seq. No. 300403
Seq. ID LIB3180-061-P2-M1-F3
Method BLASTN
NCBI GI g248336
BLAST score 72
E value 2.0e-32

DRAFT Sequence

Match length 124
% identity 31
NCBI Description polyubiquitin [maize, Genomic, 3841 nt]

Seq. No. 300404
Seq. ID LIB3180-061-P2-M1-G1
Method BLASTX
NCBI GI g131773
BLAST score 448
E value 1.0e-44
Match length 122
% identity 76
NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
>gi_82724_pir_B30097 ribosomal protein S14 (clone MCH2) - maize

Seq. No. 300405
Seq. ID LIB3180-061-P2-M1-H2
Method BLASTX
NCBI GI g2668742
BLAST score 365
E value 4.0e-35
Match length 86
% identity 87
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 300406
Seq. ID LIB3180-061-P2-M1-H7
Method BLASTX
NCBI GI g421855
BLAST score 264
E value 4.0e-23
Match length 78
% identity 59
NCBI Description alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana (fragment)

Seq. No. 300407
Seq. ID LIB3180-062-P2-M1-A2
Method BLASTX
NCBI GI g1658313
BLAST score 172
E value 3.0e-25
Match length 79
% identity 44
NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 300408
Seq. ID LIB3180-062-P2-M1-C8
Method BLASTX
NCBI GI g2688830
BLAST score 177
E value 3.0e-13
Match length 45
% identity 80
NCBI Description (AF000952) putative sugar transporter [Prunus armeniaca]

Seq. No. 300409
Seq. ID LIB3180-062-P2-M1-D9
Method BLASTX
NCBI GI g4210330
BLAST score 261
E value 7.0e-23
Match length 93
% identity 56
NCBI Description (AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No. 300410
Seq. ID LIB3180-062-P2-M1-E1
Method BLASTN
NCBI GI g3057119
BLAST score 246
E value 1.0e-136
Match length 298
% identity 96
NCBI Description Zea mays starch synthase DULL1 (dull1) mRNA, complete cds

Seq. No. 300411
Seq. ID LIB3180-062-P2-M1-G4
Method BLASTX
NCBI GI g3694807
BLAST score 386
E value 2.0e-37
Match length 87
% identity 86
NCBI Description (AF055898) alanine aminotransferase [Zea mays]

Seq. No. 300412
Seq. ID LIB3181-001-P1-M1-B1
Method BLASTN
NCBI GI g168698
BLAST score 63
E value 5.0e-27
Match length 151
% identity 85
NCBI Description Z.mays zein mRNA, complete cds

Seq. No. 300413
Seq. ID LIB3181-001-P1-M1-B11
Method BLASTX
NCBI GI g2827524
BLAST score 168
E value 3.0e-12
Match length 54
% identity 59
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 300414
Seq. ID LIB3181-001-P1-M1-C7
Method BLASTN
NCBI GI g413792
BLAST score 47
E value 2.0e-17

Match length 139
% identity 83
NCBI Description Cloning vector lambda EMBL3 SP6/T7, left arm

Seq. No. 300415
Seq. ID LIB3181-001-P1-M1-C9
Method BLASTN
NCBI GI g168694
BLAST score 120
E value 4.0e-61
Match length 128
% identity 98
NCBI Description Maize gamma zein mRNA, partial cds

Seq. No. 300416
Seq. ID LIB3181-001-P1-M1-D3
Method BLASTX
NCBI GI g567893
BLAST score 224
E value 2.0e-18
Match length 75
% identity 56
NCBI Description (L37382) beta-galactosidase-complementation protein [Cloning vector]

Seq. No. 300417
Seq. ID LIB3181-001-P1-M1-G8
Method BLASTX
NCBI GI g141605
BLAST score 228
E value 5.0e-19
Match length 73
% identity 68
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cz19c2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 300418
Seq. ID LIB3181-002-P1-M1-B10
Method BLASTX
NCBI GI g3298548
BLAST score 386
E value 2.0e-37
Match length 109
% identity 72
NCBI Description (AC004681) putative spliceosomal protein [Arabidopsis thaliana]

Seq. No. 300419
Seq. ID LIB3181-002-P1-M1-B5
Method BLASTN
NCBI GI g168484
BLAST score 77
E value 1.0e-35
Match length 157
% identity 87
NCBI Description Maize endosperm glutelin-2 gene, complete cds

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Seq. No. 300420
Seq. ID LIB3181-002-P1-M1-C1
Method BLASTN
NCBI GI g22524
BLAST score 110
E value 4.0e-55
Match length 194
% identity 90
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)

Seq. No. 300421
Seq. ID LIB3181-002-P1-M1-C2
Method BLASTX
NCBI GI g168699
BLAST score 214
E value 2.0e-17
Match length 67
% identity 69
NCBI Description (M60836) zein [Zea mays]

Seq. No. 300422
Seq. ID LIB3181-002-P1-M1-D3
Method BLASTX
NCBI GI g1174526
BLAST score 352
E value 2.0e-33
Match length 98
% identity 67
NCBI Description LYSYL-tRNA SYNTHETASE (LYSINE--tRNA LIGASE) (LYSRS)
>gi_1074993_pir_D64110 lysine--tRNA ligase (EC 6.1.1.6) -
Haemophilus influenzae (strain Rd KW20) >gi_1574141
(U32800) lysyl-tRNA synthetase (lysU) [Haemophilus
influenzae Rd]

Seq. No. 300423
Seq. ID LIB3181-002-P1-M1-E5
Method BLASTX
NCBI GI g4204294
BLAST score 314
E value 5.0e-29
Match length 90
% identity 76
NCBI Description (AC003027) lcl_prt_seq No definition line found
[Arabidopsis thaliana]

Seq. No. 300424
Seq. ID LIB3181-002-P1-M1-F5
Method BLASTN
NCBI GI g168696
BLAST score 83
E value 7.0e-39
Match length 103
% identity 95
NCBI Description Z.mays zein mRNA, 3' end

Seq. No. 300425

DRAFT

Seq. ID	LIB3181-003-P1-M1-A12
Method	BLASTX
NCBI GI	g4504165
BLAST score	220
E value	1.0e-21
Match length	79
% identity	62
NCBI Description	gelsolin (amyloidosis, Finnish type) >gi_121116_sp_P06396_GELS HUMAN GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL) >gi_71649_pir_FAHUP gelsolin precursor, plasma - human >gi_736249_emb_CAA28000_ (X04412) plasma gelsolin [Homo sapiens] >gi_225304_prf_1211330A gelsolin [Homo sapiens]
Seq. No.	300426
Seq. ID	LIB3181-003-P1-M1-B1
Method	BLASTN
NCBI GI	g22514
BLAST score	141
E value	2.0e-73
Match length	365
% identity	85
NCBI Description	Maize Zcl gene for Zein Zcl (14 kD zein-2)
Seq. No.	300427
Seq. ID	LIB3181-003-P1-M1-B11
Method	BLASTN
NCBI GI	g4038570
BLAST score	174
E value	4.0e-93
Match length	291
% identity	89
NCBI Description	Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Qu
Seq. No.	300428
Seq. ID	LIB3181-003-P1-M1-B6
Method	BLASTN
NCBI GI	g1684789
BLAST score	62
E value	3.0e-26
Match length	294
% identity	81
NCBI Description	Human epithelial membrane protein (CL-20) mRNA, complete cds
Seq. No.	300429
Seq. ID	LIB3181-003-P1-M1-B7
Method	BLASTX
NCBI GI	g3335226
BLAST score	403
E value	3.0e-39
Match length	119
% identity	65
NCBI Description	(AF077374) small proline-rich protein [Homo sapiens]

DO NOT USE

Seq. No.	300430
Seq. ID	LIB3181-003-P1-M1-B8
Method	BLASTX
NCBI GI	g3293537
BLAST score	142
E value	7.0e-09
Match length	79
% identity	38
NCBI Description	(AF071059) zinc finger RNA binding protein [Mus musculus]
Seq. No.	300431
Seq. ID	LIB3181-003-P1-M1-C12
Method	BLASTX
NCBI GI	g4504165
BLAST score	421
E value	1.0e-41
Match length	103
% identity	84
NCBI Description	gelsolin (amyloidosis, Finnish type) >gi_121116_sp_P06396 GELS HUMAN GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL) >gi_71649_pir_FAHUP gelsolin precursor, plasma - human >gi_736249_emb_CAA28000_ (X04412) plasma gelsolin [Homo sapiens] >gi_225304_prf_1211330A gelsolin [Homo sapiens]
Seq. No.	300432
Seq. ID	LIB3181-003-P1-M1-C5
Method	BLASTX
NCBI GI	g346219
BLAST score	257
E value	1.0e-22
Match length	74
% identity	70
NCBI Description	keratin K4a - human (fragment)
Seq. No.	300433
Seq. ID	LIB3181-003-P1-M1-D10
Method	BLASTN
NCBI GI	g180222
BLAST score	35
E value	4.0e-10
Match length	125
% identity	82
NCBI Description	Human carcinoembryonic antigen mRNA (CEA), complete cds
Seq. No.	300434
Seq. ID	LIB3181-003-P1-M1-D4
Method	BLASTX
NCBI GI	g224507
BLAST score	270
E value	9.0e-24
Match length	97
% identity	61
NCBI Description	zein A1 [Zea mays]
Seq. No.	300435

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Seq. ID	LIB3181-003-P1-M1-E10
Method	BLASTX
NCBI GI	g2224565
BLAST score	712
E value	2.0e-75
Match length	138
% identity	96
NCBI Description	(AB002310) KIAA0312 [Homo sapiens]
Seq. No.	300436
Seq. ID	LIB3181-003-P1-M1-E2
Method	BLASTN
NCBI GI	g22288
BLAST score	107
E value	4.0e-53
Match length	131
% identity	95
NCBI Description	Maize mRNA fragment for endosperm glutelin-2
Seq. No.	300437
Seq. ID	LIB3181-003-P1-M1-F10
Method	BLASTX
NCBI GI	g2118384
BLAST score	170
E value	5.0e-13
Match length	109
% identity	50
NCBI Description	squamous cell carcinoma antigen 2 - human
Seq. No.	300438
Seq. ID	LIB3181-003-P1-M1-F4
Method	BLASTX
NCBI GI	g16073
BLAST score	293
E value	1.0e-26
Match length	67
% identity	88
NCBI Description	(X59526) zein protein [Acetabularia mediterranea]
Seq. No.	300439
Seq. ID	LIB3181-003-P1-M1-F7
Method	BLASTX
NCBI GI	g168691
BLAST score	238
E value	5.0e-20
Match length	89
% identity	56
NCBI Description	(M29628) zein [Zea mays]
Seq. No.	300440
Seq. ID	LIB3181-003-P1-M1-G10
Method	BLASTX
NCBI GI	g2137308
BLAST score	186
E value	3.0e-14
Match length	65
% identity	63

NCBI Description G protein beta subuit like - mouse >gi_475012_dbj_BAA06185_ (D29802) G protein beta subuit like [Mus musculus]

Seq. No. 300441
Seq. ID LIB3181-003-P1-M1-G8
Method BLASTN
NCBI GI g3777595
BLAST score 71
E value 1.0e-31
Match length 119
% identity 90
NCBI Description Homo sapiens TACC2 protein (TACC2) mRNA, partial cds

Seq. No. 300442
Seq. ID LIB3181-003-P1-M1-H1
Method BLASTX
NCBI GI g3763845
BLAST score 220
E value 1.0e-19
Match length 84
% identity 61
NCBI Description (AB018375) early nodulin [Oryza sativa] >gi_3763847_dbj_BAA33814_ (AB018376) early nodulin [Oryza sativa]

Seq. No. 300443
Seq. ID LIB3181-003-P1-M1-H10
Method BLASTN
NCBI GI g3551833
BLAST score 45
E value 3.0e-16
Match length 127
% identity 84
NCBI Description Homo sapiens clone 24 diacylglycerol kinase alpha (DAGK1) mRNA, complete cds

Seq. No. 300444
Seq. ID LIB3181-004-P1-M1-B12
Method BLASTN
NCBI GI g531832
BLAST score 37
E value 2.0e-11
Match length 137
% identity 82
NCBI Description Cloning vector pSport2, complete sequence

Seq. No. 300445
Seq. ID LIB3181-004-P1-M1-B3
Method BLASTX
NCBI GI g2244732
BLAST score 225
E value 9.0e-19
Match length 55
% identity 69
NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No. 300446

Seq. ID LIB3181-004-P1-M1-C1
Method BLASTX
NCBI GI g16073
BLAST score 365
E value 6.0e-35
Match length 127
% identity 61
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 300447
Seq. ID LIB3181-004-P1-M1-D1
Method BLASTN
NCBI GI g168663
BLAST score 56
E value 6.0e-23
Match length 68
% identity 96
NCBI Description Maize sulfur-rich zein protein of Mr 15,000, complete cds

Seq. No. 300448
Seq. ID LIB3181-004-P1-M1-D10
Method BLASTX
NCBI GI g82660
BLAST score 168
E value 5.0e-12
Match length 60
% identity 62
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 300449
Seq. ID LIB3181-004-P1-M1-G3
Method BLASTN
NCBI GI g22524
BLAST score 161
E value 2.0e-85
Match length 320
% identity 89
NCBI Description Zea mays mRNA encoding a zein (clone ZG31A)

Seq. No. 300450
Seq. ID LIB3181-006-P1-K2-E10
Method BLASTN
NCBI GI g168681
BLAST score 119
E value 3.0e-60
Match length 235
% identity 89
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_ Sequence 8 from Patent US

Seq. No. 300451
Seq. ID LIB3181-006-P1-K2-E4
Method BLASTX
NCBI GI g3482913
BLAST score 249
E value 1.0e-21

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Match length 87
& identity 57
NCBI Description (AC003970) Similar to MtN21, gi_2598575, Megicago truncatula nodulation induced gene [Arabidopsis thaliana]

Seq. No. 300452
Seq. ID LIB3181-006-P1-K2-F5
Method BLASTX
NCBI GI g141609
BLAST score 182
E value 5.0e-14
Match length 56
& identity 71
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi_100944_pir_S15656 zein, 19K - maize >gi_22448_emb_CAA41543_ (X58700) 19 kDa zein [Zea mays]

Seq. No. 300453
Seq. ID LIB3181-007-P1-K2-D6
Method BLASTX
NCBI GI g168691
BLAST score 280
E value 6.0e-25
Match length 80
& identity 70
NCBI Description (M29628) zein [Zea mays]

Seq. No. 300454
Seq. ID LIB3181-007-P1-K2-F10
Method BLASTX
NCBI GI g100940
BLAST score 304
E value 1.0e-27
Match length 125
& identity 54
NCBI Description zein zA1 - maize

Seq. No. 300455
Seq. ID LIB3181-007-P1-K2-H3
Method BLASTX
NCBI GI g1709990
BLAST score 155
E value 1.0e-10
Match length 45
& identity 64
NCBI Description 60S RIBOSOMAL PROTEIN L35A

Seq. No. 300456
Seq. ID LIB3181-007-P1-M1-C4
Method BLASTX
NCBI GI g2832247
BLAST score 186
E value 6.0e-14
Match length 111
& identity 43
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

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Seq. No. 300457
Seq. ID LIB3181-007-P1-M1-E2
Method BLASTX
NCBI GI g2506328
BLAST score 314
E value 6.0e-29
Match length 97
% identity 64
NCBI Description CYTOCHROME C >gi_1235929 (L77113) cytochrome c [Helianthus annuus]

Seq. No. 300458
Seq. ID LIB3181-007-P1-M1-E5
Method BLASTN
NCBI GI g168673
BLAST score 41
E value 9.0e-14
Match length 41
% identity 100
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 300459
Seq. ID LIB3181-007-P1-M1-G5
Method BLASTN
NCBI GI g168673
BLAST score 78
E value 7.0e-36
Match length 187
% identity 84
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 300460
Seq. ID LIB3181-008-P1-K2-B12
Method BLASTX
NCBI GI g168699
BLAST score 226
E value 1.0e-18
Match length 60
% identity 83
NCBI Description (M60836) zein [Zea mays]

Seq. No. 300461
Seq. ID LIB3181-008-P1-K2-C10
Method BLASTX
NCBI GI g3924594
BLAST score 289
E value 7.0e-26
Match length 80
% identity 65
NCBI Description (AF069442) putative ribonucleoprotein [Arabidopsis thaliana] >gi_4262139_gb_AAD14439 (AC005275) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No. 300462
Seq. ID LIB3181-008-P1-K2-C6
Method BLASTN
NCBI GI g22544

BLAST score 87
E value 3.0e-41
Match length 200
% identity 87
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 300463
Seq. ID LIB3181-008-P1-M1-B12
Method BLASTX
NCBI GI g168699
BLAST score 258
E value 2.0e-22
Match length 106
% identity 58
NCBI Description (M60836) zein [Zea mays]

Seq. No. 300464
Seq. ID LIB3181-008-P1-M1-D6
Method BLASTX
NCBI GI g1710530
BLAST score 162
E value 1.0e-11
Match length 43
% identity 74
NCBI Description 60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir_S71256
ribosomal protein L27a - Arabidopsis thaliana
>gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
L27a [Arabidopsis thaliana]

Seq. No. 300465
Seq. ID LIB3181-009-P1-K2-A10
Method BLASTX
NCBI GI g168701
BLAST score 169
E value 1.0e-23
Match length 127
% identity 59
NCBI Description (M60837) zein [Zea mays]

Seq. No. 300466
Seq. ID LIB3181-009-P1-K2-A12
Method BLASTX
NCBI GI g2131417
BLAST score 165
E value 2.0e-11
Match length 129
% identity 29
NCBI Description hypothetical protein YDR291w - yeast (Saccharomyces
cerevisiae) >gi_1230655 (U51031) Ydr291wp [Saccharomyces
cerevisiae]

Seq. No. 300467
Seq. ID LIB3181-009-P1-K2-C3
Method BLASTX
NCBI GI g2529340
BLAST score 510
E value 8.0e-52

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Match length 129
% identity 81
NCBI Description (L81162) homologue; putative [Zea mays]

Seq. No. 300468
Seq. ID LIB3181-009-P1-K2-F6
Method BLASTN
NCBI GI g1617473
BLAST score 118
E value 1.0e-59
Match length 202
% identity 99
NCBI Description Z.mays mRNA for Rbl protein

Seq. No. 300469
Seq. ID LIB3181-009-P1-K2-H8
Method BLASTX
NCBI GI g72307
BLAST score 371
E value 1.0e-35
Match length 127
% identity 65
NCBI Description 22K zein precursor (clone pZ22.3) - maize >gi_168686 (J01246) 26.99 kd zein protein [Zea mays]

Seq. No. 300470
Seq. ID LIB3181-010-P1-K2-D5
Method BLASTN
NCBI GI g168673
BLAST score 161
E value 2.0e-85
Match length 240
% identity 95
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 300471
Seq. ID LIB3181-010-P1-K2-H6
Method BLASTX
NCBI GI g2791516
BLAST score 208
E value 4.0e-17
Match length 58
% identity 66
NCBI Description (AL021246) hypothetical protein Rv2476c [Mycobacterium tuberculosis]

Seq. No. 300472
Seq. ID LIB3181-010-P1-M1-F3
Method BLASTN
NCBI GI g168673
BLAST score 39
E value 1.0e-12
Match length 83
% identity 87
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 300473

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Seq. ID LIB3181-011-P1-K2-A10
Method BLASTN
NCBI GI g168579
BLAST score 41
E value 6.0e-14
Match length 112
% identity 86
NCBI Description Maize pyruvate,orthophosphate dikinase mRNA, complete cds

Seq. No. 300474
Seq. ID LIB3181-011-P1-K2-A4
Method BLASTX
NCBI GI g141605
BLAST score 482
E value 1.0e-48
Match length 111
% identity 88
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cz19c2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 300475
Seq. ID LIB3181-011-P1-K2-A5
Method BLASTX
NCBI GI g1698548
BLAST score 260
E value 2.0e-22
Match length 104
% identity 58
NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No. 300476
Seq. ID LIB3181-011-P1-K2-B3
Method BLASTN
NCBI GI g2832242
BLAST score 141
E value 2.0e-73
Match length 293
% identity 12
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 300477
Seq. ID LIB3181-011-P1-K2-F11
Method BLASTX
NCBI GI g115786
BLAST score 169
E value 2.0e-12
Match length 61
% identity 61
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
(CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding
protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
mays]

Seq. No. 300478
Seq. ID LIB3181-011-P1-K2-G6
Method BLASTX

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NCBI GI	g3953466
BLAST score	186
E value	7.0e-22
Match length	89
% identity	54
NCBI Description	(AC002328) F20N2.11 [Arabidopsis thaliana]
Seq. No.	300479
Seq. ID	LIB3181-011-P1-M1-B2
Method	BLASTX
NCBI GI	g224508
BLAST score	172
E value	2.0e-12
Match length	50
% identity	68
NCBI Description	zein A20 [Zea mays]
Seq. No.	300480
Seq. ID	LIB3181-013-P1-K2-A10
Method	BLASTN
NCBI GI	g3449334
BLAST score	186
E value	1.0e-100
Match length	316
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.	300481
Seq. ID	LIB3181-013-P1-K2-A7
Method	BLASTN
NCBI GI	g4490717
BLAST score	76
E value	6.0e-35
Match length	96
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)
Seq. No.	300482
Seq. ID	LIB3181-013-P1-K2-A9
Method	BLASTX
NCBI GI	g1170040
BLAST score	426
E value	3.0e-42
Match length	96
% identity	89
NCBI Description	GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) >gi_451198_dbj_BAA03137_(D14049) glutathione reductase precursor [Arabidopsis thaliana] >gi_1944448_dbj_BAA19653_(D89620) glutathione reductase precursor [Arabidopsis thaliana] >gi_740576_prf_2005376A glutathione reductase [Arabidopsis thaliana]
Seq. No.	300483
Seq. ID	LIB3181-013-P1-K2-C12
Method	BLASTX

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NCBI GI g3915847
BLAST score 455
E value 2.0e-45
Match length 105
% identity 88
NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 300484
Seq. ID LIB3181-013-P1-K2-D12
Method BLASTX
NCBI GI g1769905
BLAST score 259
E value 1.0e-22
Match length 106
% identity 54
NCBI Description (X98108) 23 kDa polypeptide of oxygen-evolving complex (OEC) [Arabidopsis thaliana]

Seq. No. 300485
Seq. ID LIB3181-013-P1-K2-D3
Method BLASTX
NCBI GI g4049341
BLAST score 439
E value 2.0e-43
Match length 126
% identity 69
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 300486
Seq. ID LIB3181-013-P1-K2-G8
Method BLASTX
NCBI GI g2829792
BLAST score 261
E value 5.0e-23
Match length 86
% identity 57
NCBI Description SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS I) >gi_1781353_emb_CAA71442_ (Y10416) soluble starch (bacterial glycogen) synthase [Solanum tuberosum]

Seq. No. 300487
Seq. ID LIB3181-013-P1-K2-H12
Method BLASTX
NCBI GI g3377797
BLAST score 352
E value 1.0e-33
Match length 85
% identity 82
NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara]

Seq. No. 300488
Seq. ID LIB3181-013-P1-K2-H8

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Method	BLASTX
NCBI GI	g2829899
BLAST score	220
E value	3.0e-18
Match length	70
% identity	57
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.	300489
Seq. ID	LIB3181-014-P1-K2-A10
Method	BLASTX
NCBI GI	g168586
BLAST score	382
E value	4.0e-37
Match length	98
% identity	74
NCBI Description	(M58656) pyruvate,orthophosphate dikinase [Zea mays]
Seq. No.	300490
Seq. ID	LIB3181-014-P1-K2-A4
Method	BLASTX
NCBI GI	g2130065
BLAST score	149
E value	9.0e-10
Match length	64
% identity	56
NCBI Description	alpha-globulin precursor - rice >gi_1783206_dbj_BAA09308_(D50643) 26 kDa globulin [Oryza sativa]
Seq. No.	300491
Seq. ID	LIB3181-014-P1-K2-E10
Method	BLASTN
NCBI GI	g22326
BLAST score	78
E value	6.0e-36
Match length	142
% identity	89
NCBI Description	Z.mays gene for Hageman factor inhibitor
Seq. No.	300492
Seq. ID	LIB3181-014-P1-K2-E11
Method	BLASTN
NCBI GI	g532622
BLAST score	77
E value	3.0e-35
Match length	185
% identity	85
NCBI Description	Zea mays lipase (LIP) mRNA, complete cds
Seq. No.	300493
Seq. ID	LIB3181-014-P1-K2-E4
Method	BLASTX
NCBI GI	g2832243
BLAST score	260
E value	7.0e-23

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Match length 93
% identity 59
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 300494
Seq. ID LIB3181-014-P1-K2-F6
Method BLASTX
NCBI GI g16073
BLAST score 223
E value 3.0e-18
Match length 113
% identity 50
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 300495
Seq. ID LIB3181-014-P1-K2-G7
Method BLASTX
NCBI GI g141600
BLAST score 333
E value 4.0e-31
Match length 123
% identity 59
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cz19B1) - maize
>gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 300496
Seq. ID LIB3181-014-P1-K2-H9
Method BLASTN
NCBI GI g531828
BLAST score 39
E value 2.0e-12
Match length 131
% identity 82
NCBI Description Cloning vector pSport1, complete cds

Seq. No. 300497
Seq. ID LIB3181-014-P1-M1-C9
Method BLASTX
NCBI GI g531829
BLAST score 140
E value 5.0e-09
Match length 71
% identity 45
NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No. 300498
Seq. ID LIB3181-014-P1-M1-H1
Method BLASTX
NCBI GI g141617
BLAST score 318
E value 2.0e-29
Match length 115
% identity 58
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize

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>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 300499
Seq. ID LIB3182-001-P1-M1-E5
Method BLASTX
NCBI GI g82659
BLAST score 141
E value 8.0e-09
Match length 57
% identity 53
NCBI Description 19K zein precursor (clone Z4) - maize
>gi_4388702_emb_CAA24719_ (V01472) zein [Zea mays]

Seq. No. 300500
Seq. ID LIB3182-001-P1-M1-F12
Method BLASTX
NCBI GI g141606
BLAST score 300
E value 2.0e-27
Match length 90
% identity 68
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
>gi_72309_pir_ZIZMD1 19K zein precursor (clone cZ19D1) - maize
>gi_168682 (M12144) 19 kDa zein protein [Zea mays]

Seq. No. 300501
Seq. ID LIB3182-001-P1-M1-H5
Method BLASTX
NCBI GI g1707924
BLAST score 537
E value 4.0e-55
Match length 110
% identity 93
NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 1 PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) (SHRUNKEN-2) >gi_1947182 (M81603) shrunken-2 [Zea mays] >gi_444329_prf_1906378A ADP glucose pyrophosphorylase [Zea mays]

Seq. No. 300502
Seq. ID LIB3182-002-P1-M1-C11
Method BLASTX
NCBI GI g511870
BLAST score 206
E value 2.0e-16
Match length 36
% identity 100
NCBI Description (M23537) zein protein [Zea mays]

Seq. No. 300503
Seq. ID LIB3182-002-P1-M1-C4
Method BLASTX
NCBI GI g141606
BLAST score 319

E value 1.0e-29
Match length 107
% identity 63
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
>gi_72309_pir_ZIZMD1 19K zein precursor (clone cZ19D1) - maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]

Seq. No. 300504
Seq. ID LIB3182-002-P1-M1-D11
Method BLASTX
NCBI GI g3868758
BLAST score 144
E value 1.0e-18
Match length 96
% identity 56
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 300505
Seq. ID LIB3182-002-P1-M1-D3
Method BLASTN
NCBI GI g168681
BLAST score 59
E value 1.0e-24
Match length 203
% identity 82
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

Seq. No. 300506
Seq. ID LIB3182-002-P1-M1-E10
Method BLASTX
NCBI GI g1184774
BLAST score 442
E value 4.0e-44
Match length 84
% identity 100
NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No. 300507
Seq. ID LIB3182-002-P1-M1-G3
Method BLASTX
NCBI GI g141600
BLAST score 144
E value 3.0e-09
Match length 66
% identity 58
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) - maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 300508
Seq. ID LIB3182-004-P2-M1-A9
Method BLASTX
NCBI GI g141607
BLAST score 257
E value 3.0e-22

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Match length 66
% identity 77
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE PZ19.1)
>gi_22521_emb_CAA24718_(V01471) zein [Zea mays] >gi_168672
(J01244) zein 19 kd protein (partial) [Zea mays]

Seq. No. 300509
Seq. ID LIB3182-004-P2-M1-B4
Method BLASTX
NCBI GI g224508
BLAST score 348
E value 8.0e-33
Match length 129
% identity 60
NCBI Description zein A20 [Zea mays]

Seq. No. 300510
Seq. ID LIB3182-004-P2-M1-E1
Method BLASTX
NCBI GI g2832243
BLAST score 218
E value 1.0e-17
Match length 127
% identity 46
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 300511
Seq. ID LIB3182-004-P2-M1-E8
Method BLASTX
NCBI GI g121631
BLAST score 242
E value 2.0e-20
Match length 74
% identity 64
NCBI Description GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR
>gi_72323_pir_KNNT2S glycine-rich protein 2 - wood tobacco
>gi_19743_emb_CAA42622_(X60007) nsGRP-2 [Nicotiana
sylvestris]

Seq. No. 300512
Seq. ID LIB3182-004-P2-M1-F10
Method BLASTX
NCBI GI g224509
BLAST score 386
E value 3.0e-37
Match length 138
% identity 64
NCBI Description zein E19 [Zea mays]

Seq. No. 300513
Seq. ID LIB3182-005-P2-M1-B8
Method BLASTX
NCBI GI g419803
BLAST score 323
E value 4.0e-30
Match length 94
% identity 69

NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 300514
Seq. ID LIB3182-005-P2-M1-C3
Method BLASTN
NCBI GI g168673
BLAST score 80
E value 5.0e-37
Match length 303
% identity 84
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 300515
Seq. ID LIB3182-005-P2-M1-D11
Method BLASTN
NCBI GI g4140643
BLAST score 94
E value 2.0e-45
Match length 274
% identity 43
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 300516
Seq. ID LIB3182-005-P2-M1-E11
Method BLASTX
NCBI GI g3885334
BLAST score 354
E value 1.0e-40
Match length 108
% identity 82
NCBI Description (AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No. 300517
Seq. ID LIB3182-005-P2-M1-H12
Method BLASTN
NCBI GI g2832242
BLAST score 60
E value 3.0e-25
Match length 144
% identity 44
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 300518
Seq. ID LIB3182-006-P2-M1-B6
Method BLASTX
NCBI GI g22216
BLAST score 223
E value 2.0e-18
Match length 92
% identity 55
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 300519
Seq. ID LIB3182-008-P2-M1-B10

Method BLASTN
NCBI GI g1212995
BLAST score 35
E value 3.0e-10
Match length 71
% identity 87
NCBI Description H.vulgare mRNA for UDP-glucose pyrophosphorylase

Seq. No. 300520
Seq. ID LIB3182-008-P2-M1-B2
Method BLASTN
NCBI GI g22544
BLAST score 82
E value 3.0e-38
Match length 167
% identity 94
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 300521
Seq. ID LIB3182-008-P2-M1-E5
Method BLASTX
NCBI GI g141612
BLAST score 146
E value 2.0e-09
Match length 36
% identity 83
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)
>gi_72306_pir_ZIZMC2 22K zein precursor (clone cz22C2) -
maize (fragment) >gi_168688 (M12141) 22 kDa zein protein
[Zea mays]

Seq. No. 300522
Seq. ID LIB3182-008-P2-M1-H3
Method BLASTN
NCBI GI g22544
BLAST score 113
E value 1.0e-56
Match length 217
% identity 89
NCBI Description Maize mRNA (clone A30) for zein (a plant storage protein)

Seq. No. 300523
Seq. ID LIB3182-009-P2-M1-A1
Method BLASTX
NCBI GI g141605
BLAST score 202
E value 4.0e-16
Match length 73
% identity 62
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cz19C2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 300524
Seq. ID LIB3182-009-P2-M1-A10
Method BLASTN
NCBI GI g1314396

BLAST score 160
E value 7.0e-85
Match length 221
% identity 92
NCBI Description Zea mays ssp. mays USDA PI 515436 ITS1, 5.8S rRNA, ITS2

Seq. No. 300525
Seq. ID LIB3182-009-P2-M1-A12
Method BLASTX
NCBI GI g141605
BLAST score 303
E value 6.0e-37
Match length 120
% identity 70
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cZ19C2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 300526
Seq. ID LIB3182-009-P2-M1-B1
Method BLASTX
NCBI GI g141606
BLAST score 211
E value 7.0e-17
Match length 78
% identity 62
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
>gi_72309_pir_ZIZMD1 19K zein precursor (clone cZ19D1) -
maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]

Seq. No. 300527
Seq. ID LIB3182-009-P2-M1-B4
Method BLASTX
NCBI GI g1279640
BLAST score 229
E value 4.0e-19
Match length 101
% identity 49
NCBI Description (X92204) NAM [Petunia x hybrida]

Seq. No. 300528
Seq. ID LIB3182-009-P2-M1-D1
Method BLASTX
NCBI GI g2832247
BLAST score 236
E value 8.0e-20
Match length 92
% identity 59
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 300529
Seq. ID LIB3182-009-P2-M1-E10
Method BLASTX
NCBI GI g168695
BLAST score 157
E value 4.0e-11
Match length 48

DRAFT BLAST SEARCHES

% identity 71
NCBI Description (M16218) gamma zein [Zea mays] >gi_225315_prf_1211356A
zein gamma [Zea mays]

Seq. No. 300530
Seq. ID LIB3182-009-P2-M1-E2
Method BLASTX
NCBI GI g1084457
BLAST score 168
E value 5.0e-12
Match length 62
% identity 55
NCBI Description elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_
(D23674) elongation factor 1 beta [Oryza sativa]

Seq. No. 300531
Seq. ID LIB3182-009-P2-M1-E9
Method BLASTX
NCBI GI g508545
BLAST score 213
E value 3.0e-17
Match length 71
% identity 63
NCBI Description (L34340) zein [Zea mays]

Seq. No. 300532
Seq. ID LIB3182-009-P2-M1-F11
Method BLASTX
NCBI GI g141600
BLAST score 354
E value 2.0e-38
Match length 111
% identity 80
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19B1)
>gi_72315_pir_ZIZMB1 19K zein precursor (clone cZ19B1) -
maize >gi_168674 (M12143) 19 kDa zein protein [Zea mays]

Seq. No. 300533
Seq. ID LIB3182-009-P2-M1-G1
Method BLASTX
NCBI GI g141610
BLAST score 177
E value 6.0e-13
Match length 84
% identity 51
NCBI Description ZEIN-ALPHA PRECURSOR (CLONE Z4)

Seq. No. 300534
Seq. ID LIB3182-009-P2-M1-H11
Method BLASTN
NCBI GI g168700
BLAST score 38
E value 3.0e-12
Match length 77
% identity 87
NCBI Description Z.mays zein mRNA, complete cds

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Seq. No.	300535
Seq. ID	LIB3182-009-P2-M1-H6
Method	BLASTX
NCBI GI	g22216
BLAST score	142
E value	2.0e-11
Match length	78
% identity	59
NCBI Description	(X55722) 22kD zein [Zea mays]
Seq. No.	300536
Seq. ID	LIB3182-010-P2-M1-E2
Method	BLASTX
NCBI GI	g4336434
BLAST score	311
E value	1.0e-28
Match length	114
% identity	53
NCBI Description	(AF092431) nodule-enhanced protein phosphatase type 2C [Lotus japonicus]
Seq. No.	300537
Seq. ID	LIB3182-010-P2-M1-E6
Method	BLASTX
NCBI GI	g82654
BLAST score	221
E value	2.0e-20
Match length	83
% identity	65
NCBI Description	10K zein precursor - maize >gi_22541_emb_CAA30409_ (X07535) 10kDa zein (AA 1 - 150) [Zea mays]
Seq. No.	300538
Seq. ID	LIB3182-010-P2-M1-F2
Method	BLASTX
NCBI GI	g82660
BLAST score	183
E value	2.0e-22
Match length	83
% identity	75
NCBI Description	19K zein precursor (clone ZG31A) - maize (fragment) >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
Seq. No.	300539
Seq. ID	LIB3182-010-P2-M1-H1
Method	BLASTN
NCBI GI	g22219
BLAST score	111
E value	9.0e-56
Match length	178
% identity	92
NCBI Description	Z.mays ZSF4C2 gene for 22 kD zein
Seq. No.	300540
Seq. ID	LIB3182-012-P2-M1-B4
Method	BLASTN
NCBI GI	g168484

BLAST score 316
E value 1.0e-178
Match length 360
% identity 97
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 300541
Seq. ID LIB3182-012-P2-M1-B5
Method BLASTN
NCBI GI g22531
BLAST score 68
E value 2.0e-30
Match length 120
% identity 89
NCBI Description Zea mays mRNA encoding a zein (clone pZ22.1)
>gi_270688_gb_I03336_Sequence 10 from Patent US 4885357
>gi_270741_gb_I03273_Sequence 2 from Patent US

Seq. No. 300542
Seq. ID LIB3182-012-P2-M1-B6
Method BLASTN
NCBI GI g168652
BLAST score 100
E value 5.0e-49
Match length 108
% identity 98
NCBI Description Maize amyloplast-specific transit protein (waxy; wx+ locus), complete cds

Seq. No. 300543
Seq. ID LIB3182-012-P2-M1-B9
Method BLASTX
NCBI GI g22216
BLAST score 247
E value 1.0e-32
Match length 111
% identity 70
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 300544
Seq. ID LIB3182-012-P2-M1-D12
Method BLASTX
NCBI GI g16073
BLAST score 364
E value 9.0e-35
Match length 116
% identity 69
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 300545
Seq. ID LIB3182-012-P2-M1-F1
Method BLASTN
NCBI GI g22528
BLAST score 50
E value 4.0e-19
Match length 82
% identity 90

NCBI Description Zea mays mRNA encoding a zein (clone A20)

Seq. No. 300546
Seq. ID LIB3182-012-P2-M1-H3
Method BLASTX
NCBI GI g2832243
BLAST score 386
E value 2.0e-37
Match length 121
% identity 70
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 300547
Seq. ID LIB3182-013-P2-M1-E6
Method BLASTX
NCBI GI g629861
BLAST score 173
E value 1.0e-12
Match length 76
% identity 54
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 300548
Seq. ID LIB3182-014-P2-M1-A2
Method BLASTX
NCBI GI g22216
BLAST score 176
E value 2.0e-27
Match length 92
% identity 74
NCBI Description (X55722) 22kD zein [Zea mays]

Seq. No. 300549
Seq. ID LIB3182-014-P2-M1-A5
Method BLASTN
NCBI GI g16072
BLAST score 107
E value 2.0e-53
Match length 220
% identity 87
NCBI Description Acetabularia mediterranea zein gene

Seq. No. 300550
Seq. ID LIB3182-014-P2-M1-A6
Method BLASTX
NCBI GI g141597
BLAST score 241
E value 2.0e-20
Match length 126
% identity 46
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
>gi_72314_pir_ZIZM3 19K zein precursor (clone A30) - maize
>gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
[Zea mays]

Seq. No. 300551

Seq. ID	LIB3182-014-P2-M1-C1
Method	BLASTX
NCBI GI	g121472
BLAST score	280
E value	6.0e-25
Match length	105
% identity	51
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZMZM19 glutelin-2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea mays] >gi_168485_(M16066) glutelin-2 [Zea mays]
Seq. No.	300552
Seq. ID	LIB3182-014-P2-M1-C4
Method	BLASTX
NCBI GI	g2832247
BLAST score	374
E value	6.0e-36
Match length	120
% identity	68
NCBI Description	(AF031569) 22-kDa alpha zein 10 [Zea mays]
Seq. No.	300553
Seq. ID	LIB3182-014-P2-M1-E12
Method	BLASTN
NCBI GI	g168704
BLAST score	118
E value	8.0e-60
Match length	118
% identity	100
NCBI Description	Zea mays zein protein gene, complete cds
Seq. No.	300554
Seq. ID	LIB3182-014-P2-M1-G3
Method	BLASTX
NCBI GI	g141612
BLAST score	411
E value	3.0e-40
Match length	136
% identity	67
NCBI Description	ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2) >gi_72306_pir_ZIZMC2 22K zein precursor (clone cz22C2) - maize (fragment) >gi_168688_(M12141) 22 kDa zein protein [Zea mays]
Seq. No.	300555
Seq. ID	LIB3182-014-P2-M1-H7
Method	BLASTX
NCBI GI	g16073
BLAST score	272
E value	2.0e-24
Match length	71
% identity	78
NCBI Description	(X59526) zein protein [Acetabularia mediterranea]

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Seq. No.	300556
Seq. ID	LIB3182-015-P2-M1-A7
Method	BLASTN
NCBI GI	g22514
BLAST score	320
E value	1.0e-180
Match length	339
% identity	99
NCBI Description	Maize Zcl gene for Zein Zcl (14 kD zein-2)
Seq. No.	300557
Seq. ID	LIB3182-015-P2-M1-C10
Method	BLASTN
NCBI GI	g2832242
BLAST score	49
E value	6.0e-19
Match length	73
% identity	10
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	300558
Seq. ID	LIB3182-015-P2-M1-C12
Method	BLASTX
NCBI GI	g168701
BLAST score	196
E value	2.0e-15
Match length	81
% identity	60
NCBI Description	(M60837) zein [Zea mays]
Seq. No.	300559
Seq. ID	LIB3182-015-P2-M1-C3
Method	BLASTN
NCBI GI	g340933
BLAST score	84
E value	5.0e-40
Match length	112
% identity	95
NCBI Description	Zea mays 10-kDa zein gene, complete cds
Seq. No.	300560
Seq. ID	LIB3182-015-P2-M1-H5
Method	BLASTN
NCBI GI	g168694
BLAST score	164
E value	2.0e-87
Match length	196
% identity	96
NCBI Description	Maize gamma zein mRNA, partial cds
Seq. No.	300561
Seq. ID	LIB3182-016-P2-M1-A2
Method	BLASTX
NCBI GI	g629861
BLAST score	189
E value	8.0e-24
Match length	84

% identity 77
NCBI Description zein Zd1, 19K - maize >gi_535020_emb_CAA47639_ (X67203)
zein Zd1 (19 kDa zein) [Zea mays]

Seq. No. 300562
Seq. ID LIB3182-016-P2-M1-B6
Method BLASTX
NCBI GI g141617
BLAST score 260
E value 2.0e-22
Match length 130
% identity 46
NCBI Description ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
>gi_100941_pir_S12140 zein Zc1 - maize
>gi_100945_pir_B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]
>gi_168666_ (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 300563
Seq. ID LIB3182-016-P2-M1-B8
Method BLASTX
NCBI GI g141613
BLAST score 140
E value 9.0e-09
Match length 63
% identity 52
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
>gi_72305_pir_ZIZM21_ 22K zein precursor (clone pZ22.1) - maize
>gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]

Seq. No. 300564
Seq. ID LIB3182-016-P2-M1-C5
Method BLASTX
NCBI GI g2832243
BLAST score 171
E value 3.0e-12
Match length 94
% identity 45
NCBI Description (AF031569) 22-kDa alpha zein 4 [Zea mays]

Seq. No. 300565
Seq. ID LIB3182-016-P2-M1-C8
Method BLASTX
NCBI GI g16073
BLAST score 408
E value 6.0e-40
Match length 124
% identity 69
NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 300566
Seq. ID LIB3182-016-P2-M1-D6
Method BLASTX
NCBI GI g141615
BLAST score 218
E value 7.0e-18
Match length 70

% identity 67
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONE PZ22.3)
>gi_22536_emb_CAA24727_ (V01480) zein protein 3 [Zea mays]

Seq. No. 300567
Seq. ID LIB3182-016-P2-M1-D7
Method BLASTX
NCBI GI g508545
BLAST score 161
E value 1.0e-18
Match length 64
% identity 81
NCBI Description (L34340) zein [Zea mays]

Seq. No. 300568
Seq. ID LIB3182-016-P2-M1-D8
Method BLASTN
NCBI GI g22447
BLAST score 95
E value 4.0e-46
Match length 163
% identity 89
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein

Seq. No. 300569
Seq. ID LIB3279-003-P1-K1-B10
Method BLASTN
NCBI GI g473602
BLAST score 151
E value 2.0e-79
Match length 276
% identity 88
NCBI Description Zea mays W-22 histone H2A mRNA, complete cds

Seq. No. 300570
Seq. ID LIB3279-003-P1-K1-B5
Method BLASTX
NCBI GI g4559339
BLAST score 363
E value 1.0e-34
Match length 96
% identity 74
NCBI Description (AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No. 300571
Seq. ID LIB3279-003-P1-K1-B6
Method BLASTX
NCBI GI g3047086
BLAST score 193
E value 1.0e-14
Match length 122
% identity 33
NCBI Description (AF058914) similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]

Seq. No. 300572

Seq. ID LIB3279-003-P1-K1-C12
Method BLASTX
NCBI GI g585338
BLAST score 260
E value 1.0e-22
Match length 80
% identity 64
NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
>gi_391879_dbj_BAA01181_(D10335) adenylate kinase-b [Oryza sativa]

Seq. No. 300573
Seq. ID LIB3279-003-P1-K1-C4
Method BLASTX
NCBI GI g3868758
BLAST score 254
E value 3.0e-33
Match length 128
% identity 58
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 300574
Seq. ID LIB3279-003-P1-K1-G8
Method BLASTX
NCBI GI g3004564
BLAST score 501
E value 6.0e-51
Match length 111
% identity 80
NCBI Description (AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 300575
Seq. ID LIB3279-004-P1-K1-C8
Method BLASTX
NCBI GI g2500497
BLAST score 326
E value 2.0e-30
Match length 80
% identity 82
NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi_1419372_emb_CAA67225_(X98656) ribosomal protein S21 [Zea mays]

Seq. No. 300576
Seq. ID LIB3279-004-P1-K1-C9
Method BLASTX
NCBI GI g1170029
BLAST score 498
E value 2.0e-50
Match length 105
% identity 90
NCBI Description GLUTAMATE-1-SEMALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA)
(GLUTAMATE-1-SEMALDEHYDE AMINOTRANSFERASE) (GSA-AT)
>gi_100581_pir_A35789 glutamate-1-semialdehyde
2,1-aminomutase (EC 5.4.3.8) - barley >gi_506383 (M31545)
glutamate 1-semialdehyde aminotransferase [Hordeum vulgare]

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Seq. No. 300577
Seq. ID LIB3279-004-P1-K1-D8
Method BLASTX
NCBI GI g3080420
BLAST score 168
E value 7.0e-12
Match length 113
% identity 40
NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No. 300578
Seq. ID LIB3279-004-P1-K1-F2
Method BLASTX
NCBI GI g135398
BLAST score 372
E value 4.0e-36
Match length 85
% identity 84
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir_S15773 tubulin alpha-1 chain - maize >gi_22147_emb_CAA33734_ (X15704) alpha1-tubulin [Zea mays]

Seq. No. 300579
Seq. ID LIB3279-004-P1-K1-G8
Method BLASTN
NCBI GI g4585620
BLAST score 41
E value 7.0e-14
Match length 117
% identity 85
NCBI Description Zea mays hmgi/y gene, exons 1-2

Seq. No. 300580
Seq. ID LIB3279-004-P1-K1-G9
Method BLASTN
NCBI GI g984755
BLAST score 46
E value 8.0e-17
Match length 118
% identity 85
NCBI Description O.sativa mRNA for chilling-inducible protein

Seq. No. 300581
Seq. ID LIB3279-004-P1-K1-H7
Method BLASTX
NCBI GI g399854
BLAST score 212
E value 5.0e-17
Match length 90
% identity 58
NCBI Description HISTONE H2B.2 >gi_283042_pir_S28049 histone H2B - maize >gi_22325_emb_CAA40565_ (X57313) H2B histone [Zea mays]

Seq. No. 300582
Seq. ID LIB3279-005-P1-K1-A7
Method BLASTX

NCBI GI g3551245
BLAST score 348
E value 5.0e-33
Match length 76
% identity 86
NCBI Description (AB012702) P40-like protein [Daucus carota]

Seq. No. 300583
Seq. ID LIB3279-005-P1-K1-B7
Method BLASTX
NCBI GI g729671
BLAST score 150
E value 9.0e-10
Match length 95
% identity 41
NCBI Description HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]

Seq. No. 300584
Seq. ID LIB3279-005-P1-K1-D2
Method BLASTX
NCBI GI g2245125
BLAST score 159
E value 8.0e-11
Match length 52
% identity 58
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 300585
Seq. ID LIB3279-005-P1-K1-D5
Method BLASTX
NCBI GI g417103
BLAST score 442
E value 4.0e-44
Match length 92
% identity 97
NCBI Description HISTONE H3.2, MINOR >gi_282871_pir_S24346 histone H3.3-like protein - Arabidopsis thaliana
>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 300586
Seq. ID LIB3279-005-P1-K1-D6

DRAFT

Method BLASTX
NCBI GI g4006877
BLAST score 230
E value 5.0e-19
Match length 77
% identity 61
NCBI Description (Z99707) RNA-binding like protein [Arabidopsis thaliana]

Seq. No. 300587
Seq. ID LIB3279-005-P1-K1-F6
Method BLASTX
NCBI GI g135399
BLAST score 415
E value 1.0e-40
Match length 139
% identity 61
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_100716_pir_S20758 tubulin
alpha-1 chain - rice >gi_20379_emb_CAA77988_ (Z11931) alpha
1 tubulin [Oryza sativa] >gi_1136124_emb_CAA62918_ (X91808)
alfa-tubulin [Oryza sativa]

Seq. No. 300588
Seq. ID LIB3279-005-P1-K1-G9
Method BLASTX
NCBI GI g3885884
BLAST score 148
E value 1.0e-09
Match length 62
% identity 50
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 300589
Seq. ID LIB3279-005-P1-K1-H9
Method BLASTX
NCBI GI g729762
BLAST score 141
E value 7.0e-12
Match length 57
% identity 68
NCBI Description 17.0 KD CLASS II HEAT SHOCK PROTEIN (HSP 18)
>gi_477225_pir_A48425 heat shock protein HSP18 - maize
>gi_300079_bbs_130952 (S59777) HSP18=18 kda heat shock
protein [Zea mays, Oh43, clone cMHSP18-1, Peptide, 154 aa]
[Zea mays]

Seq. No. 300590
Seq. ID LIB3279-006-P1-K1-D12
Method BLASTX
NCBI GI g2245038
BLAST score 254
E value 7.0e-22
Match length 130
% identity 44
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 300591
Seq. ID LIB3279-006-P1-K1-D4

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Method BLASTX
NCBI GI g498707
BLAST score 329
E value 1.0e-30
Match length 133
% identity 52
NCBI Description (X78422) HYP1 [Arabidopsis thaliana]

Seq. No. 300592
Seq. ID LIB3279-006-P1-K1-D6
Method BLASTN
NCBI GI g3341647
BLAST score 45
E value 3.0e-16
Match length 109
% identity 94
NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase

Seq. No. 300593
Seq. ID LIB3279-006-P1-K1-E6
Method BLASTX
NCBI GI g3063455
BLAST score 276
E value 2.0e-24
Match length 71
% identity 68
NCBI Description (AC003981) F22O13.17 [Arabidopsis thaliana]

Seq. No. 300594
Seq. ID LIB3279-006-P1-K1-F10
Method BLASTX
NCBI GI g1363492
BLAST score 292
E value 2.0e-26
Match length 116
% identity 54
NCBI Description outer envelope membrane protein OEP75 precursor - garden pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720 (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No. 300595
Seq. ID LIB3279-007-P1-K1-A9
Method BLASTX
NCBI GI g2654088
BLAST score 207
E value 2.0e-16
Match length 123
% identity 35
NCBI Description (AF033118) potassium transporter [Arabidopsis thaliana] >gi_2688979 (AF029876) high-affinity potassium transporter; AtKUP1p [Arabidopsis thaliana] >gi_3150413 (AC004165) high-affinity potassium transporter (AtKUP1) [Arabidopsis thaliana] >gi_3420045 (AC004680) high-affinity potassium transporter (AtKUP1) [Arabidopsis thaliana]

Seq. No. 300596

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Seq. ID	LIB3279-007-P1-K1-C1
Method	BLASTN
NCBI GI	g312180
BLAST score	40
E value	3.0e-13
Match length	100
% identity	85
NCBI Description	Z.mays GapC4 gene
Seq. No.	300597
Seq. ID	LIB3279-007-P1-K1-E4
Method	BLASTX
NCBI GI	g2673906
BLAST score	526
E value	9.0e-54
Match length	139
% identity	76
NCBI Description	(AC002561) putative DNA polymerase delta small subunit [Arabidopsis thaliana]
Seq. No.	300598
Seq. ID	LIB3279-007-P1-K1-H7
Method	BLASTX
NCBI GI	g4559333
BLAST score	154
E value	3.0e-10
Match length	120
% identity	28
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]
Seq. No.	300599
Seq. ID	LIB3279-008-P1-K1-A1
Method	BLASTX
NCBI GI	g4580515
BLAST score	218
E value	3.0e-18
Match length	62
% identity	60
NCBI Description	(AF036301) scarecrow-like 3 [Arabidopsis thaliana]
Seq. No.	300600
Seq. ID	LIB3279-008-P1-K1-F11
Method	BLASTN
NCBI GI	g473602
BLAST score	51
E value	7.0e-20
Match length	107
% identity	87
NCBI Description	Zea mays W-22 histone H2A mRNA, complete cds
Seq. No.	300601
Seq. ID	LIB3279-008-P1-K1-F5
Method	BLASTX
NCBI GI	g2262111
BLAST score	248
E value	3.0e-21
Match length	82

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% identity 63
NCBI Description (AC002343) ribitol dehydrogenase isolog [Arabidopsis thaliana]

Seq. No. 300602
Seq. ID LIB3279-008-P1-K1-F8
Method BLASTX
NCBI GI g2262143
BLAST score 301
E value 2.0e-27
Match length 93
% identity 61
NCBI Description (AC002330) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 300603
Seq. ID LIB3279-008-P1-K1-G11
Method BLASTX
NCBI GI g2443857
BLAST score 147
E value 3.0e-09
Match length 40
% identity 72
NCBI Description (U79961) vacuolar sorting receptor homolog [Zea mays]

Seq. No. 300604
Seq. ID LIB3279-008-P1-K1-H6
Method BLASTX
NCBI GI g3914020
BLAST score 262
E value 8.0e-23
Match length 137
% identity 42
NCBI Description (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
(HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
>gi_1561641_emb_CAA69388_ (Y08211) mandelonitrile lyase
[Prunus dulcis]

Seq. No. 300605
Seq. ID LIB3279-009-P1-K1-A4
Method BLASTX
NCBI GI g2660669
BLAST score 164
E value 2.0e-11
Match length 51
% identity 57
NCBI Description (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis thaliana]

Seq. No. 300606
Seq. ID LIB3279-009-P1-K1-C4
Method BLASTX
NCBI GI g1703201
BLAST score 235
E value 9.0e-20
Match length 67
% identity 66

NCBI Description PROTEIN KINASE AFC3 >gi_601791 (U16178) protein kinase [Arabidopsis thaliana]

Seq. No. 300607
Seq. ID LIB3279-009-P1-K1-E4
Method BLASTX
NCBI GI g1806283
BLAST score 161
E value 2.0e-11
Match length 48
% identity 73

NCBI Description (Z79637) Histone H4 homologue [Sesbania rostrata]

Seq. No. 300608
Seq. ID LIB3279-009-P1-K1-E6
Method BLASTX
NCBI GI g553073
BLAST score 233
E value 9.0e-20
Match length 78
% identity 60

NCBI Description (M94481) reverse transcriptase [Zea mays]

Seq. No. 300609
Seq. ID LIB3279-009-P1-K1-F1
Method BLASTX
NCBI GI g3176726
BLAST score 294
E value 6.0e-27
Match length 82
% identity 70

NCBI Description (AC002392) putative serine proteinase [Arabidopsis thaliana]

Seq. No. 300610
Seq. ID LIB3279-009-P1-K1-F7
Method BLASTX
NCBI GI g1076678
BLAST score 319
E value 6.0e-30
Match length 68
% identity 94

NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No. 300611
Seq. ID LIB3279-009-P1-K1-G4
Method BLASTX
NCBI GI g4512696
BLAST score 195
E value 4.0e-15
Match length 64
% identity 55

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 300612
Seq. ID LIB3279-009-P1-K1-G8
Method BLASTX

NCBI GI g283051
BLAST score 160
E value 3.0e-11
Match length 57
% identity 61
NCBI Description RNA-directed DNA polymerase (EC 2.7.7.49) - maize transposon (fragment)

Seq. No. 300613
Seq. ID LIB3279-009-P1-K1-H9
Method BLASTX
NCBI GI g2828279
BLAST score 170
E value 3.0e-12
Match length 41
% identity 73
NCBI Description (AL021687) hypothetical protein [Arabidopsis thaliana]

Seq. No. 300614
Seq. ID LIB3279-010-P1-K1-C4
Method BLASTX
NCBI GI g2213594
BLAST score 240
E value 2.0e-20
Match length 103
% identity 45
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No. 300615
Seq. ID LIB3279-010-P1-K1-E12
Method BLASTX
NCBI GI g1711036
BLAST score 205
E value 3.0e-16
Match length 63
% identity 71
NCBI Description (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]

Seq. No. 300616
Seq. ID LIB3279-011-P1-K1-A2
Method BLASTX
NCBI GI g4589961
BLAST score 321
E value 1.0e-29
Match length 150
% identity 47
NCBI Description (AC007169) unknown protein [Arabidopsis thaliana]

Seq. No. 300617
Seq. ID LIB3279-011-P1-K1-A4
Method BLASTX
NCBI GI g4314388
BLAST score 531
E value 2.0e-54
Match length 126
% identity 77

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NCBI Description (AC006232) hypothetical protein [Arabidopsis thaliana]

Seq. No. 300618
Seq. ID LIB3279-011-P1-K1-A5
Method BLASTX
NCBI GI g3451071
BLAST score 273
E value 2.0e-24
Match length 87
% identity 67
NCBI Description (AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No. 300619
Seq. ID LIB3279-011-P1-K1-B8
Method BLASTX
NCBI GI g2982266
BLAST score 381
E value 9.0e-37
Match length 83
% identity 90
NCBI Description (AF051216) probable fibrillarin [Picea mariana]

Seq. No. 300620
Seq. ID LIB3279-011-P1-K1-D1
Method BLASTN
NCBI GI g577824
BLAST score 49
E value 1.0e-18
Match length 104
% identity 87
NCBI Description Z.mays gene for H2B histone (gH2B3)

Seq. No. 300621
Seq. ID LIB3279-011-P1-K1-D3
Method BLASTN
NCBI GI g886400
BLAST score 40
E value 2.0e-13
Match length 52
% identity 94
NCBI Description Oryza sativa MADS-box protein (MADS2) mRNA, complete cds

Seq. No. 300622
Seq. ID LIB3279-011-P1-K1-F11
Method BLASTX
NCBI GI g4455300
BLAST score 179
E value 3.0e-13
Match length 69
% identity 49
NCBI Description (AL035528) putative pectate lyase A11 (fragment) [Arabidopsis thaliana]

Seq. No. 300623
Seq. ID LIB3279-011-P1-K1-G6
Method BLASTX

NCBI GI g2498077
BLAST score 296
E value 5.0e-27
Match length 81
% identity 75
NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
(PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase
[Saccharum officinarum]

Seq. No. 300624
Seq. ID LIB3279-011-P1-K1-H2
Method BLASTX
NCBI GI g3913804
BLAST score 236
E value 7.0e-20
Match length 60
% identity 82
NCBI Description HISTONE H2B.3 >gi_577825_emb_CAA49584_ (X69960) H2B histone
[Zea mays]

Seq. No. 300625
Seq. ID LIB3279-011-P1-K1-H6
Method BLASTX
NCBI GI g121974
BLAST score 343
E value 2.0e-32
Match length 71
% identity 97
NCBI Description HISTONE H2A.2.1 >gi_70710_pir_HSWT2A histone H2A.2 - wheat

Seq. No. 300626
Seq. ID LIB3279-011-P1-K1-H7
Method BLASTX
NCBI GI g1703380
BLAST score 442
E value 6.0e-44
Match length 100
% identity 87
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760)
ADP-ribosylation factor [Oryza sativa]

Seq. No. 300627
Seq. ID LIB3279-012-P1-K1-A10
Method BLASTX
NCBI GI g3461835
BLAST score 262
E value 7.0e-23
Match length 83
% identity 61
NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana]
>gi_3927840 (AC005727) putative protein kinase [Arabidopsis thaliana]

Seq. No. 300628
Seq. ID LIB3279-012-P1-K1-C10
Method BLASTX
NCBI GI g1550814

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BLAST score 203
E value 5.0e-16
Match length 51
% identity 84
NCBI Description (Y07959) 60S acidic ribosomal protein P0 [Zea mays]

Seq. No. 300629
Seq. ID LIB3279-012-P1-K1-E10
Method BLASTX
NCBI GI g131772
BLAST score 375
E value 4.0e-36
Match length 94
% identity 82
NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
>gi_82723_pir_A30097 ribosomal protein S14 (clone MCH1) - maize

Seq. No. 300630
Seq. ID LIB3279-012-P1-K1-E11
Method BLASTX
NCBI GI g1173027
BLAST score 167
E value 4.0e-12
Match length 52
% identity 60
NCBI Description 60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal protein L31 [Nicotiana glutinosa]

Seq. No. 300631
Seq. ID LIB3279-012-P1-K1-F10
Method BLASTX
NCBI GI g399854
BLAST score 144
E value 3.0e-09
Match length 57
% identity 58
NCBI Description HISTONE H2B.2 >gi_283042_pir_S28049 histone H2B - maize
>gi_22325_emb_CAA40565_ (X57313) H2B histone [Zea mays]

Seq. No. 300632
Seq. ID LIB3279-012-P1-K1-F4
Method BLASTN
NCBI GI g22324
BLAST score 111
E value 1.0e-55
Match length 207
% identity 88
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No. 300633
Seq. ID LIB3279-012-P1-K1-F7
Method BLASTX
NCBI GI g4585908
BLAST score 181
E value 2.0e-13
Match length 92

% identity 37
NCBI Description (AC006298) putative lysosomal acid lipase [Arabidopsis thaliana]

Seq. No. 300634
Seq. ID LIB3279-012-P1-K1-G2
Method BLASTN
NCBI GI g459267
BLAST score 131
E value 1.0e-67
Match length 155
% identity 97
NCBI Description Z.mays gene for HMG protein

Seq. No. 300635
Seq. ID LIB3279-012-P1-K1-G6
Method BLASTN
NCBI GI g3452287
BLAST score 58
E value 7.0e-24
Match length 148
% identity 91
NCBI Description Zea mays retrotransposon Fourf 3' LTR, partial sequence

Seq. No. 300636
Seq. ID LIB3279-013-P1-K1-C10
Method BLASTX
NCBI GI g1723958
BLAST score 325
E value 3.0e-30
Match length 135
% identity 51
NCBI Description PUTATIVE KINESIN-LIKE PROTEIN YGL216W
>gi_2131622_pir_S64238 hypothetical protein YGL216w -
yeast (Saccharomyces cerevisiae) >gi_1322862_emb_CAA96933_
(Z72739) ORF YGL216w [Saccharomyces cerevisiae]

Seq. No. 300637
Seq. ID LIB3279-013-P1-K1-C11
Method BLASTX
NCBI GI g2832625
BLAST score 205
E value 4.0e-16
Match length 79
% identity 54
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 300638
Seq. ID LIB3279-013-P1-K1-D10
Method BLASTX
NCBI GI g728882
BLAST score 258
E value 2.0e-23
Match length 114
% identity 61
NCBI Description ADP-RIBOSYLATION FACTOR 3 >gi_541846_pir_S41938
ADP-ribosylation factor 3 - Arabidopsis thaliana

DRAFT Sequence

>gi_453191_emb_CAA54564_ (X77385) ADP-ribosylation factor 3
[Arabidopsis thaliana]

Seq. No. 300639
Seq. ID LIB3279-013-P1-K1-H3
Method BLASTX
NCBI GI g122022
BLAST score 338
E value 1.0e-31
Match length 93
% identity 76
NCBI Description HISTONE H2B >gi_283025_pir_S22323 histone H2B - wheat
>gi_21801_emb_CAA42530_ (X59873) histone H2B [Triticum aestivum]

Seq. No. 300640
Seq. ID LIB3279-014-P1-K1-A9
Method BLASTX
NCBI GI g3608485
BLAST score 292
E value 1.0e-42
Match length 101
% identity 88
NCBI Description (AF088915) proteasome beta subunit [Petunia x hybrida]

Seq. No. 300641
Seq. ID LIB3279-014-P1-K1-C9
Method BLASTX
NCBI GI g3023713
BLAST score 178
E value 3.0e-13
Match length 58
% identity 66
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372
(U09450) enolase [Oryza sativa]

Seq. No. 300642
Seq. ID LIB3279-014-P1-K1-D12
Method BLASTX
NCBI GI g133867
BLAST score 198
E value 1.0e-15
Match length 70
% identity 63
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal
protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
ribosomal protein S11 [Zea mays]

Seq. No. 300643
Seq. ID LIB3279-014-P1-K1-D8
Method BLASTN
NCBI GI g168492
BLAST score 149
E value 3.0e-78
Match length 221
% identity 92

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NCBI Description Corn histone H3 (H3C3) gene, complete cds

Seq. No. 300644
Seq. ID LIB3279-014-P1-K1-E9
Method BLASTX
NCBI GI g1519253
BLAST score 262
E value 7.0e-23
Match length 85
% identity 64
NCBI Description (U65958) GF14-d protein [Oryza sativa]

Seq. No. 300645
Seq. ID LIB3279-015-P1-K1-C4
Method BLASTX
NCBI GI g2865394
BLAST score 365
E value 7.0e-35
Match length 133
% identity 49
NCBI Description (AF036949) basic leucine zipper protein [Zea mays]

Seq. No. 300646
Seq. ID LIB3279-015-P1-K1-C6
Method BLASTX
NCBI GI g2129635
BLAST score 440
E value 1.0e-43
Match length 145
% identity 58
NCBI Description light repressible receptor protein kinase - Arabidopsis thaliana >gi_1321686_emb_CAA66376_ (X97774) light repressible receptor protein kinase [Arabidopsis thaliana]

Seq. No. 300647
Seq. ID LIB3279-015-P1-K1-E5
Method BLASTN
NCBI GI g22483
BLAST score 58
E value 6.0e-24
Match length 146
% identity 86
NCBI Description Z.mays RNA for superoxide dismutase Sod4

Seq. No. 300648
Seq. ID LIB3279-016-P1-K1-A3
Method BLASTN
NCBI GI g22121
BLAST score 214
E value 1.0e-117
Match length 218
% identity 100
NCBI Description Maize alcohol dehydrogenase 1 gene (Adh1-1F)

Seq. No. 300649
Seq. ID LIB3279-016-P1-K1-C4
Method BLASTN

NCBI GI g22243
 BLAST score 44
 E value 1.0e-15
 Match length 88
 % identity 88
 NCBI Description Zea mays Cin1 repeat from Cin1 middle repetitive family

Seq. No. 300650
 Seq. ID LIB3279-016-P1-K1-C8
 Method BLASTN
 NCBI GI g3821780
 BLAST score 36
 E value 8.0e-11
 Match length 48
 % identity 67
 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 300651
 Seq. ID LIB3279-016-P1-K1-C9
 Method BLASTX
 NCBI GI g3355468
 BLAST score 156
 E value 6.0e-12
 Match length 109
 % identity 42
 NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No. 300652
 Seq. ID LIB3279-016-P1-K1-H5
 Method BLASTX
 NCBI GI g498931
 BLAST score 289
 E value 7.0e-26
 Match length 94
 % identity 64
 NCBI Description (Z12825) ORF167; homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]

Seq. No. 300653
 Seq. ID LIB3279-016-P1-K1-H8
 Method BLASTX
 NCBI GI g118104
 BLAST score 610
 E value 1.0e-63
 Match length 131
 % identity 89
 NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
 >gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) - maize >gi_168461 (M55021) cyclophilin [Zea mays]
 >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 300654
 Seq. ID LIB3279-017-P1-K1-A1
 Method BLASTX

NCBI GI g2315449
BLAST score 253
E value 9.0e-22
Match length 109
% identity 44
NCBI Description (AF016448) similar to *Saccharomyces cerevisiae* nuclear protein SNF7 (SP:P39929) in one region and the chromosome segregation protein SMC2 (SP:P38989) in another [Caenorhabditis elegans]

Seq. No. 300655
Seq. ID LIB3279-017-P1-K1-D5
Method BLASTX
NCBI GI g3080398
BLAST score 238
E value 4.0e-25
Match length 142
% identity 34
NCBI Description (AL022603) putative protein [*Arabidopsis thaliana*]

Seq. No. 300656
Seq. ID LIB3279-017-P1-K1-D9
Method BLASTX
NCBI GI g4455255
BLAST score 176
E value 1.0e-12
Match length 69
% identity 58
NCBI Description (AL035523) putative protein [*Arabidopsis thaliana*]

Seq. No. 300657
Seq. ID LIB3279-017-P1-K1-E6
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100
NCBI Description *Xenopus laevis* cDNA clone 27A6-1

Seq. No. 300658
Seq. ID LIB3279-017-P1-K1-F8
Method BLASTX
NCBI GI g2982435
BLAST score 215
E value 2.0e-17
Match length 89
% identity 56
NCBI Description (AL022224) retrotransposon like protein (fragment) [*Arabidopsis thaliana*]

Seq. No. 300659
Seq. ID LIB3279-017-P1-K1-G5
Method BLASTX
NCBI GI g2245012
BLAST score 217
E value 1.0e-17

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Match length 131
% identity 43
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 300660
Seq. ID LIB3279-018-P1-K1-A8
Method BLASTX
NCBI GI g3915131
BLAST score 158
E value 4.0e-11
Match length 50
% identity 60
NCBI Description THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
>gi_426442_dbj_BAA04864 (D21836) thioredoxin h [Oryza sativa] >gi_454882_dbj_BAA05546 (D26547) rice thioredoxin h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza sativa]

Seq. No. 300661
Seq. ID LIB3279-018-P1-K1-B6
Method BLASTX
NCBI GI g576886
BLAST score 311
E value 4.0e-29
Match length 59
% identity 97
NCBI Description (L37750) kaurene synthase A [Zea mays]

Seq. No. 300662
Seq. ID LIB3279-018-P1-K1-C10
Method BLASTX
NCBI GI g544125
BLAST score 153
E value 2.0e-10
Match length 42
% identity 64
NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
>gi_81651_pir_S22496 peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis thaliana >gi_16248_emb_CAA45161 (X63616) cyclophilin-like protein [Arabidopsis thaliana]

Seq. No. 300663
Seq. ID LIB3279-018-P1-K1-D10
Method BLASTX
NCBI GI g728826
BLAST score 209
E value 6.0e-17
Match length 90
% identity 49
NCBI Description ALDO-KETO REDUCTASE >gi_155867 (M93122) aldo-keto reductase [Babesia bovis]

Seq. No. 300664
Seq. ID LIB3279-018-P1-K1-E2
Method BLASTX
NCBI GI g3096949

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BLAST score	331
E value	3.0e-31
Match length	91
% identity	66
NCBI Description	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]
Seq. No.	300665
Seq. ID	LIB3279-018-P1-K1-E9
Method	BLASTX
NCBI GI	g1078813
BLAST score	163
E value	2.0e-11
Match length	53
% identity	21
NCBI Description	polyubiquitin - Euplotes eurystomus (SGC9) >gi_159038 (M57231) ubiquitin [Euplotes eurystomus]
Seq. No.	300666
Seq. ID	LIB3279-049-P1-K1-C4
Method	BLASTX
NCBI GI	g231573
BLAST score	298
E value	7.0e-31
Match length	100
% identity	71
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_99970_pir_S24757 asparaginase (EC 3.5.1.1) - narrow-leaved blue lupine >gi_19135_emb_CAA43099_ (X60691) developing seed L-asparaginase [Lupinus angustifolius]
Seq. No.	300667
Seq. ID	LIB3279-049-P1-K1-D9
Method	BLASTX
NCBI GI	g3334133
BLAST score	155
E value	1.0e-10
Match length	87
% identity	44
NCBI Description	CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1) >gi_1432145 (U61231) cytochrome P450 [Arabidopsis thaliana]
Seq. No.	300668
Seq. ID	LIB3279-050-P1-K1-A3
Method	BLASTN
NCBI GI	g2832242
BLAST score	71
E value	1.0e-31
Match length	266
% identity	87
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	300669
Seq. ID	LIB3279-050-P1-K1-C1
Method	BLASTX
NCBI GI	g3860277

BLAST score 146
E value 4.0e-17
Match length 50
% identity 92
NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb AAD15604 (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 300670
Seq. ID LIB3279-050-P1-K1-G5
Method BLASTX
NCBI GI g1917019
BLAST score 155
E value 3.0e-13
Match length 63
% identity 70
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]

Seq. No. 300671
Seq. ID LIB3279-051-P1-K1-A4
Method BLASTX
NCBI GI g2668742
BLAST score 267
E value 4.0e-25
Match length 79
% identity 81
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 300672
Seq. ID LIB3279-051-P1-K1-C10
Method BLASTN
NCBI GI g575425
BLAST score 65
E value 4.0e-28
Match length 129
% identity 88
NCBI Description Z.mays mRNA for sugar-starvation induced protein

Seq. No. 300673
Seq. ID LIB3279-051-P1-K1-C7
Method BLASTX
NCBI GI g462229
BLAST score 271
E value 5.0e-24
Match length 91
% identity 58
NCBI Description HISTONE H2A.1 >gi_542442_pir_S41471 histone H2A.1 - Tetrahymena thermophila (SGC5) >gi_310870 (L18892) histone H2A.1 [Tetrahymena thermophila]

Seq. No. 300674
Seq. ID LIB3279-051-P1-K1-D7
Method BLASTX
NCBI GI g1172553
BLAST score 289
E value 1.0e-31
Match length 126

% identity	58
NCBI Description	OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi_456672_emb_CAA54788_ (X77733) voltage dependent anion channel (VDAC) [Triticum aestivum]
Seq. No.	300675
Seq. ID	LIB3279-051-P1-K1-F1
Method	BLASTX
NCBI GI	g131773
BLAST score	222
E value	3.0e-21
Match length	82
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH2) >gi_82724_pir_B30097 ribosomal protein S14 (clone MCH2) - maize
Seq. No.	300676
Seq. ID	LIB3279-051-P1-K1-F9
Method	BLASTX
NCBI GI	g1865677
BLAST score	254
E value	5.0e-22
Match length	86
% identity	62
NCBI Description	(Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]
Seq. No.	300677
Seq. ID	LIB3279-052-P1-K1-A2
Method	BLASTX
NCBI GI	g2668742
BLAST score	298
E value	3.0e-27
Match length	73
% identity	78
NCBI Description	(AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.	300678
Seq. ID	LIB3279-052-P1-K1-A8
Method	BLASTX
NCBI GI	g2191169
BLAST score	199
E value	6.0e-20
Match length	94
% identity	54
NCBI Description	(AF007270). Similar to shaggy related protein kinase. Belongs to the CDC2/CDKX subfamily [Arabidopsis thaliana]
Seq. No.	300679
Seq. ID	LIB3279-052-P1-K1-D5
Method	BLASTX
NCBI GI	g3128168
BLAST score	415
E value	3.0e-45
Match length	131

% identity 66
NCBI Description (AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No. 300680
Seq. ID LIB3279-052-P1-K1-F2
Method BLASTX
NCBI GI g409007
BLAST score 247
E value 4.0e-21
Match length 74
% identity 68
NCBI Description BBI-M=Bowman-Birk trypsin inhibitor-related protein [Zea mays=corn, Peptide, 102 aa] >gi_447268_prf_1914141A trypsin inhibitor-related protein [Zea mays]

Seq. No. 300681
Seq. ID LIB3279-052-P1-K1-G12
Method BLASTX
NCBI GI g112994
BLAST score 262
E value 4.0e-23
Match length 60
% identity 85
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN >gi_82685_pir_S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564) ABA-inducible gene protein [Zea mays] >gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 300682
Seq. ID LIB3279-053-P1-K1-A12
Method BLASTX
NCBI GI g2961346
BLAST score 333
E value 3.0e-31
Match length 73
% identity 75
NCBI Description (AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No. 300683
Seq. ID LIB3279-053-P1-K1-F7
Method BLASTX
NCBI GI g2765837
BLAST score 168
E value 7.0e-12
Match length 41
% identity 76
NCBI Description (Z96936) NAP16kDa protein [Arabidopsis thaliana]

Seq. No. 300684
Seq. ID LIB3279-053-P1-K1-G1
Method BLASTN
NCBI GI g1546918
BLAST score 63

E value 5.0e-27
Match length 71
% identity 97
NCBI Description Z.mays mRNA for translation initiation factor 5A

Seq. No. 300685
Seq. ID LIB3279-053-P1-K1-G5
Method BLASTX
NCBI GI g2190547
BLAST score 298
E value 4.0e-27
Match length 114
% identity 66
NCBI Description (AC001229) ESTs
gb_T43256, gb_46316, gb_N64930, gb_AA395255, gb_AA404382 come
from this gene. [Arabidopsis thaliana]

Seq. No. 300686
Seq. ID LIB3279-054-P1-K1-B1
Method BLASTX
NCBI GI g2982289
BLAST score 162
E value 1.0e-11
Match length 75
% identity 56
NCBI Description (AF051229) 60S ribosomal protein L17 [Picea mariana]

Seq. No. 300687
Seq. ID LIB3279-054-P1-K1-D6
Method BLASTX
NCBI GI g1346251
BLAST score 260
E value 1.0e-22
Match length 73
% identity 77
NCBI Description HISTONE H2B.4 >gi_577819_emb_CAA49585_ (X69961) H2B histone
[Zea mays]

Seq. No. 300688
Seq. ID LIB3279-054-P1-K1-E7
Method BLASTX
NCBI GI g2829889
BLAST score 175
E value 1.0e-12
Match length 61
% identity 64
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 300689
Seq. ID LIB3279-054-P1-K1-F7
Method BLASTX
NCBI GI g4091010
BLAST score 161
E value 5.0e-11
Match length 69
% identity 52
NCBI Description (AF042275) anther-specific protein [Oryza sativa]

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Seq. No. 300690
Seq. ID LIB3279-055-P1-K1-A1
Method BLASTX
NCBI GI g2245394
BLAST score 168
E value 7.0e-12
Match length 43
% identity 63
NCBI Description (U89771) ARF1-binding protein [Arabidopsis thaliana]

Seq. No. 300691
Seq. ID LIB3279-055-P1-K1-C11
Method BLASTX
NCBI GI g2344899
BLAST score 184
E value 1.0e-13
Match length 68
% identity 50
NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 300692
Seq. ID LIB3279-055-P1-K1-C12
Method BLASTX
NCBI GI g132849
BLAST score 189
E value 2.0e-14
Match length 54
% identity 69
NCBI Description 60S RIBOSOMAL PROTEIN L2 >gi_20001_emb CAA44362.1_ (X62500)
60S ribosomal protein L2 [Nicotiana tabacum]

Seq. No. 300693
Seq. ID LIB3279-055-P1-K1-D12
Method BLASTX
NCBI GI g1143864
BLAST score 222
E value 2.0e-18
Match length 70
% identity 60
NCBI Description (U28047) beta glucosidase [Oryza sativa]

Seq. No. 300694
Seq. ID LIB3279-055-P1-K1-H6
Method BLASTN
NCBI GI g473604
BLAST score 113
E value 6.0e-57
Match length 164
% identity 93
NCBI Description Zea mays W-22 histone H2B mRNA, complete cds

Seq. No. 300695
Seq. ID LIB3279-057-P1-K1-A1
Method BLASTN
NCBI GI g498642
BLAST score 40

E value 2.0e-13
Match length 60
% identity 92
NCBI Description Zea mays G-box binding factor 1 (GBF1) mRNA, complete cds

Seq. No. 300696
Seq. ID LIB3279-057-P1-K1-B6
Method BLASTX
NCBI GI g4371282
BLAST score 305
E value 6.0e-28
Match length 99
% identity 67
NCBI Description (AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No. 300697
Seq. ID LIB3279-057-P1-K1-B9
Method BLASTX
NCBI GI g1815681
BLAST score 189
E value 2.0e-14
Match length 35
% identity 94
NCBI Description (U85246) expansin [Oryza sativa]

Seq. No. 300698
Seq. ID LIB3279-057-P1-K1-C11
Method BLASTN
NCBI GI g2623247
BLAST score 99
E value 2.0e-48
Match length 135
% identity 93
NCBI Description Zea mays SU1 isoamylase (sugary1) gene, complete cds

Seq. No. 300699
Seq. ID LIB3279-057-P1-K1-D4
Method BLASTX
NCBI GI g3292820
BLAST score 158
E value 1.0e-10
Match length 83
% identity 42
NCBI Description (AL031018) putative MADS Box / AGL protein [Arabidopsis thaliana]

Seq. No. 300700
Seq. ID LIB3279-057-P1-K1-E11
Method BLASTX
NCBI GI g2244952
BLAST score 163
E value 6.0e-19
Match length 103
% identity 51
NCBI Description (Z97340) strong similarity to ZK688.3 protein - Caenorhabditis elegans [Arabidopsis thaliana]

Seq. No. 300701
Seq. ID LIB3279-057-P1-K1-E12
Method BLASTX
NCBI GI g3894393
BLAST score 158
E value 1.0e-10
Match length 130
% identity 33
NCBI Description (AF053998) Hcr2-5D [Lycopersicon esculentum]

Seq. No. 300702
Seq. ID LIB3279-057-P1-K1-H7
Method BLASTX
NCBI GI g4455309
BLAST score 272
E value 5.0e-24
Match length 71
% identity 72
NCBI Description (AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No. 300703
Seq. ID LIB3279-059-P1-K1-A7
Method BLASTN
NCBI GI g4234859
BLAST score 53
E value 5.0e-21
Match length 61
% identity 97
NCBI Description Zea mays copia-like retrotransposon St1-14 leader region, partial sequence

Seq. No. 300704
Seq. ID LIB3279-059-P1-K1-C4
Method BLASTX
NCBI GI g629846
BLAST score 233
E value 2.0e-19
Match length 49
% identity 88
NCBI Description initiator-binding protein - maize >gi_483444_emb_CAA55693_(X79086) initiator-binding protein [Zea mays]

Seq. No. 300705
Seq. ID LIB3279-059-P1-K1-C9
Method BLASTN
NCBI GI g2062705
BLAST score 35
E value 2.0e-10
Match length 35
% identity 100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 300706
Seq. ID LIB3279-059-P1-K1-F3
Method BLASTX
NCBI GI g4469009

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BLAST score 163
E value 4.0e-18
Match length 99
% identity 54
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 300707
Seq. ID LIB3279-059-P1-K1-G4
Method BLASTX
NCBI GI g3123270
BLAST score 215
E value 1.0e-21
Match length 67
% identity 80
NCBI Description 40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)
>gi_2463335_emb_CAA75242_ (Y15009) ribosomal protein S4
[Oryza sativa]

Seq. No. 300708
Seq. ID LIB3279-059-P1-K1-H8
Method BLASTX
NCBI GI g1870700
BLAST score 227
E value 4.0e-19
Match length 60
% identity 75
NCBI Description (U84116) cleavage stage histone H3 [Psammechinus miliaris]

Seq. No. 300709
Seq. ID LIB3279-060-P1-K1-A10
Method BLASTX
NCBI GI g3201541
BLAST score 292
E value 2.0e-26
Match length 111
% identity 52
NCBI Description (AJ005077) TCTR2 protein [Lycopersicon esculentum]

Seq. No. 300710
Seq. ID LIB3279-060-P1-K1-B10
Method BLASTX
NCBI GI g728777
BLAST score 238
E value 5.0e-20
Match length 61
% identity 70
NCBI Description ACTIVATOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD
SUBUNIT) (A1 36 KD SUBUNIT) (RF-C 36 KD SUBUNIT) (RFC36)
>gi_1498257 (L07540) replication factor C, 36-kDa subunit
[Homo sapiens]

Seq. No. 300711
Seq. ID LIB3279-060-P1-K1-B12
Method BLASTX
NCBI GI g2832672
BLAST score 305
E value 6.0e-28

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Match length 74
% identity 76
NCBI Description (AL021712) nifU-like protein [Arabidopsis thaliana]

Seq. No. 300712
Seq. ID LIB3279-060-P1-K1-B2
Method BLASTX
NCBI GI g445612
BLAST score 231
E value 3.0e-19
Match length 56
% identity 79
NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No. 300713
Seq. ID LIB3279-060-P1-K1-B7
Method BLASTX
NCBI GI g1171429
BLAST score 337
E value 1.0e-31
Match length 90
% identity 68
NCBI Description (U44028) CKC [Arabidopsis thaliana]

Seq. No. 300714
Seq. ID LIB3279-060-P1-K1-F7
Method BLASTN
NCBI GI g1657766
BLAST score 39
E value 2.0e-12
Match length 55
% identity 95
NCBI Description Zea mays retrotransposon Opie-2 5' LTR, primer binding site, gag gene, pol gene, complete cds, polypurine tract and 3' LTR

Seq. No. 300715
Seq. ID LIB3279-060-P1-K1-G1
Method BLASTX
NCBI GI g3738304
BLAST score 263
E value 6.0e-23
Match length 80
% identity 60
NCBI Description (AC005309) hypothetical protein [Arabidopsis thaliana]

Seq. No. 300716
Seq. ID LIB36-001-Q1-E1-C6
Method BLASTX
NCBI GI g1084479
BLAST score 262
E value 9.0e-23
Match length 53
% identity 98
NCBI Description H+-transporting ATP synthase (EC 3.6.1.34) delta chain - maize (fragment) >gi_311237_emb_CAA46804 (X66005)
H(+)-transporting ATP synthase [Zea mays]

Seq. No. 300717
Seq. ID LIB36-001-Q1-E1-D2
Method BLASTX
NCBI GI g3021506
BLAST score 538
E value 1.0e-63
Match length 138
% identity 92
NCBI Description (X96727) isocitrate dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No. 300718
Seq. ID LIB36-001-Q1-E1-F6
Method BLASTX
NCBI GI g1172818
BLAST score 172
E value 8.0e-13
Match length 48
% identity 73
NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal protein S16 [Oryza sativa] >gi_1096552_prf_2111468A ribosomal protein S16 [Oryza sativa]

Seq. No. 300719
Seq. ID LIB36-001-Q1-E1-H3
Method BLASTX
NCBI GI g3789952
BLAST score 517
E value 1.0e-52
Match length 129
% identity 80
NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No. 300720
Seq. ID LIB36-002-Q1-E1-B4
Method BLASTX
NCBI GI g4191348
BLAST score 557
E value 2.0e-57
Match length 125
% identity 85
NCBI Description (AF087661) NADH-ubiquinone oxidoreductase 42 kDa subunit [Homo sapiens]

Seq. No. 300721
Seq. ID LIB36-002-Q1-E1-D12
Method BLASTN
NCBI GI g3093334
BLAST score 37
E value 8.0e-12
Match length 89
% identity 85
NCBI Description Homo sapiens mRNA from HIV-associated non-Hodgkin's lymphoma (clone h12-22)

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Seq. No.	300722
Seq. ID	LIB36-003-Q1-E1-B5
Method	BLASTX
NCBI GI	g3810596
BLAST score	337
E value	1.0e-31
Match length	105
% identity	56
NCBI Description	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
Seq. No.	300723
Seq. ID	LIB36-003-Q1-E1-D3
Method	BLASTN
NCBI GI	g3420038
BLAST score	56
E value	6.0e-23
Match length	165
% identity	43
NCBI Description	Zea mays gypsy/Ty3-type retrotransposon Tekay, complete sequence
Seq. No.	300724
Seq. ID	LIB36-004-Q1-E1-A1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	300725
Seq. ID	LIB36-004-Q1-E1-C12
Method	BLASTX
NCBI GI	g1171579
BLAST score	207
E value	2.0e-16
Match length	69
% identity	55
NCBI Description	(X95342) cytochrome P450 [Nicotiana tabacum]
Seq. No.	300726
Seq. ID	LIB36-004-Q1-E1-D9
Method	BLASTX
NCBI GI	g2191161
BLAST score	147
E value	2.0e-09
Match length	56
% identity	61
NCBI Description	(AF007270) contains similarity to B. subtilis flagellar biosynthesis protein FLHA (SW:P35620) [Arabidopsis thaliana]
Seq. No.	300727
Seq. ID	LIB36-004-Q1-E1-F5
Method	BLASTN

NCBI GI g2062705
 BLAST score 36
 E value 7.0e-11
 Match length 36
 % identity 100
 NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 300728
 Seq. ID LIB36-004-Q1-E1-H4
 Method BLASTX
 NCBI GI g4240035
 BLAST score 397
 E value 1.0e-38
 Match length 112
 % identity 70
 NCBI Description (AB018588) ZmGR1b [Zea mays]

Seq. No. 300729
 Seq. ID LIB36-005-Q1-E1-D11
 Method BLASTX
 NCBI GI g168586
 BLAST score 170
 E value 4.0e-12
 Match length 95
 % identity 48
 NCBI Description (M58656) pyruvate,orthophosphate dikinase [Zea mays]

Seq. No. 300730
 Seq. ID LIB36-005-Q1-E1-D6
 Method BLASTX
 NCBI GI g3193330
 BLAST score 172
 E value 3.0e-12
 Match length 73
 % identity 42
 NCBI Description (AF069299) contains similarity to Medicago sativa corC
 (GB:L22305) [Arabidopsis thaliana]

Seq. No. 300731
 Seq. ID LIB36-006-Q1-E1-D9
 Method BLASTX
 NCBI GI g120670
 BLAST score 404
 E value 1.0e-39
 Match length 77
 % identity 100
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 >gi_100879_pir_S06879 glyceraldehyde-3-phosphate
 dehydrogenase (EC 1.2.1.12) C - maize
 >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]

Seq. No. 300732
 Seq. ID LIB36-006-Q1-E1-E8
 Method BLASTX
 NCBI GI g126737
 BLAST score 151
 E value 3.0e-20

Match length 84
% identity 70
NCBI Description MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)
(ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)
>gi_65939_pir_DEZMMX malate dehydrogenase
(oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40)
precursor, chloroplast - maize >gi_168528 (J05130)
NADP-dependent malic enzyme (EC 1.1.1.40) [Zea mays]

Seq. No. 300733
Seq. ID LIB36-006-Q1-E1-F11
Method BLASTX
NCBI GI g1835731
BLAST score 218
E value 9.0e-18
Match length 80
% identity 54
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 300734
Seq. ID LIB36-006-Q1-E1-G3
Method BLASTX
NCBI GI g2345154
BLAST score 322
E value 4.0e-30
Match length 70
% identity 86
NCBI Description (AF015522) ribosomal protein S4 [Zea mays]

Seq. No. 300735
Seq. ID LIB36-006-Q1-E1-H3
Method BLASTX
NCBI GI g115786
BLAST score 174
E value 4.0e-13
Match length 46
% identity 85
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
(CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding
protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
mays]

Seq. No. 300736
Seq. ID LIB36-007-Q1-E1-A1
Method BLASTX
NCBI GI g3063471
BLAST score 303
E value 1.0e-27
Match length 95
% identity 58
NCBI Description (AC003981) F22013.33 [Arabidopsis thaliana]

Seq. No. 300737
Seq. ID LIB36-007-Q1-E1-C4
Method BLASTX
NCBI GI g2677824
BLAST score 196

E value 5.0e-15
Match length 96
% identity 44
NCBI Description (U93164) abscisic stress ripening protein homolog [Prunus armeniaca]

Seq. No. 300738
Seq. ID LIB36-008-Q1-E1-A2
Method BLASTX
NCBI GI g902525
BLAST score 463
E value 2.0e-46
Match length 125
% identity 78
NCBI Description (U29160) ubiquitin fusion protein [Zea mays]
>gi_1589387_prf_2211240A ubiquitin fusion protein [Zea mays]

Seq. No. 300739
Seq. ID LIB36-008-Q1-E1-C8
Method BLASTN
NCBI GI g22356
BLAST score 118
E value 5.0e-60
Match length 196
% identity 91
NCBI Description Maize mRNA for light-harvesting chlorophyll a/b binding protein LHCP

Seq. No. 300740
Seq. ID LIB36-008-Q1-E1-E5
Method BLASTX
NCBI GI g131225
BLAST score 218
E value 4.0e-18
Match length 60
% identity 73
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 300741
Seq. ID LIB36-008-Q1-E1-F11
Method BLASTX
NCBI GI g115771
BLAST score 277
E value 6.0e-25
Match length 59
% identity 90
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll a/b-binding protein precursor - maize
>gi_22224_emb_CAA32900 (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

Seq. No. 300742

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Seq. ID	LIB36-008-Q1-E1-F2
Method	BLASTX
NCBI GI	g115815
BLAST score	329
E value	8.0e-31
Match length	84
% identity	75
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-M9) (LHCP) >gi_100866_pir_S13098 chlorophyll a/b-binding protein precursor - maize >gi_22355_emb_CAA39376_ (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays]
Seq. No.	300743
Seq. ID	LIB36-009-Q1-E1-C3
Method	BLASTX
NCBI GI	g114551
BLAST score	726
E value	3.0e-77
Match length	147
% identity	99
NCBI Description	ATP SYNTHASE BETA CHAIN >gi_67833_pir_PWZMB H+-transporting ATP synthase (EC 3.6.1.34) beta chain - maize chloroplast >gi_552732 (J01421) coupling factor beta-subunit [Zea mays] >gi_902229_emb_CAA60293_ (X86563) ATPase beta subunit [Zea mays]
Seq. No.	300744
Seq. ID	LIB36-009-Q1-E1-D11
Method	BLASTX
NCBI GI	g2642154
BLAST score	272
E value	6.0e-24
Match length	110
% identity	46
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana] >gi_3790595 (AF079186) RING-H2 finger protein RHC2a [Arabidopsis thaliana]
Seq. No.	300745
Seq. ID	LIB36-009-Q1-E1-F12
Method	BLASTX
NCBI GI	g4416302
BLAST score	281
E value	1.0e-25
Match length	67
% identity	84
NCBI Description	(AF105716) copia-type pol polyprotein [Zea mays]
Seq. No.	300746
Seq. ID	LIB36-009-Q1-E1-F3
Method	BLASTX
NCBI GI	g4587597
BLAST score	319
E value	2.0e-29
Match length	89
% identity	61

NCBI Description (AC006951) putative MAP kinase phosphatase [Arabidopsis thaliana]

Seq. No. 300747
Seq. ID LIB36-010-Q1-E1-A12
Method BLASTN
NCBI GI g433459
BLAST score 135
E value 5.0e-70
Match length 161
% identity 97
NCBI Description Z.mays mRNA for ferredoxin-thioredoxin reductase

Seq. No. 300748
Seq. ID LIB36-010-Q1-E1-B12
Method BLASTN
NCBI GI g1255218
BLAST score 138
E value 9.0e-72
Match length 234
% identity 91
NCBI Description Zea mays blue-light photoreceptor-like mRNA

Seq. No. 300749
Seq. ID LIB36-010-Q1-E1-C3
Method BLASTN
NCBI GI g902200
BLAST score 190
E value 1.0e-102
Match length 254
% identity 94
NCBI Description Z.mays complete chloroplast genome

Seq. No. 300750
Seq. ID LIB36-010-Q1-E1-D6
Method BLASTX
NCBI GI g2668742
BLAST score 376
E value 4.0e-36
Match length 86
% identity 87
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 300751
Seq. ID LIB36-010-Q1-E1-E1
Method BLASTX
NCBI GI g3885896
BLAST score 192
E value 9.0e-15
Match length 101
% identity 49
NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

Seq. No. 300752
Seq. ID LIB36-010-Q1-E1-E6
Method BLASTX
NCBI GI g4544402

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BLAST score	403
E value	3.0e-39
Match length	149
% identity	58
NCBI Description	(AC007047) putative leucine rich repeat protein [Arabidopsis thaliana]
Seq. No.	300753
Seq. ID	LIB36-010-Q1-E1-F7
Method	BLASTX
NCBI GI	g3218550
BLAST score	163
E value	4.0e-11
Match length	75
% identity	40
NCBI Description	(AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]
Seq. No.	300754
Seq. ID	LIB36-011-Q1-E1-A11
Method	BLASTX
NCBI GI	g4581156
BLAST score	139
E value	5.0e-09
Match length	58
% identity	50
NCBI Description	(AC006919) putative pyruvate kinase [Arabidopsis thaliana]
Seq. No.	300755
Seq. ID	LIB36-011-Q2-E2-A10
Method	BLASTX
NCBI GI	g2244987
BLAST score	150
E value	1.0e-09
Match length	50
% identity	54
NCBI Description	(Z97340) similarity to protein kinase - slime mold (Dictyostelium) [Arabidopsis thaliana]
Seq. No.	300756
Seq. ID	LIB36-011-Q2-E2-A11
Method	BLASTX
NCBI GI	g1174845
BLAST score	398
E value	1.0e-38
Match length	88
% identity	80
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE 2) (UBIQUITIN CARRIER PROTEIN) >gi_101070_pir_S12529 ubiquitin-conjugating enzyme rhp6 - fission yeast (Schizosaccharomyces pombe) >gi_929893_emb_CAA90592_ (250728) ubiquitin-conjugating enzyme e2-17 kd [Schizosaccharomyces pombe]
Seq. No.	300757
Seq. ID	LIB36-011-Q2-E2-A12
Method	BLASTX
NCBI GI	g3327033

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BLAST score 440
E value 1.0e-43
Match length 148
% identity 61
NCBI Description (Z68198) 40S ribosomal protein [Schizosaccharomyces pombe]

Seq. No. 300758
Seq. ID LIB36-011-Q2-E2-A7
Method BLASTX
NCBI GI g1708366
BLAST score 145
E value 4.0e-09
Match length 64
% identity 45
NCBI Description HEXOKINASE >gi_1041966_bbs_168854 (S78714)
hexokinase=hexose-phosphorylating enzyme [Schwanniomyces occidentalis, CBS819, ATCC2322, Peptide, 478 aa]
[Debaryomyces occidentalis]

Seq. No. 300759
Seq. ID LIB36-011-Q2-E2-A8
Method BLASTX
NCBI GI g4406372
BLAST score 310
E value 2.0e-28
Match length 139
% identity 47
NCBI Description (AF109156) thiosulfate sulfurtransferase [Datisca glomerata]

Seq. No. 300760
Seq. ID LIB36-011-Q2-E2-B1
Method BLASTX
NCBI GI g4506635
BLAST score 448
E value 2.0e-44
Match length 124
% identity 69
NCBI Description ribosomal protein L32 >gi_132886_sp_P02433_RL32_HUMAN 60S
RIBOSOMAL PROTEIN L32 >gi_71335_pir_R5HU32 ribosomal protein L32 - human >gi_71336_pir_R5MS32 ribosomal protein L32 - mouse >gi_71337_pir_R5RT32 ribosomal protein L32 - rat >gi_36132_emb_CAA27048 (X03342) rpL32 (aa 1-135) [Homo sapiens] >gi_57117_emb_CAA29777 (X06483) ribosomal protein L32 [Rattus norvegicus] >gi_200781 (K02060) ribosomal protein L32-3A [Mus musculus] >gi_226004_prf_1405339A ribosomal protein L32 [Rattus norvegicus]

Seq. No. 300761
Seq. ID LIB36-011-Q2-E2-B12
Method BLASTX
NCBI GI g2443753
BLAST score 352
E value 3.0e-33
Match length 128
% identity 54
NCBI Description (AF020346) pyridoxal kinase [Rattus norvegicus]

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Seq. No.	300762
Seq. ID	LIB36-011-Q2-E2-B4
Method	BLASTX
NCBI GI	g4406378
BLAST score	210
E value	1.0e-16
Match length	77
% identity	51
NCBI Description	(AF109913) plasma membrane H+-ATPase [Pichia angusta]
Seq. No.	300763
Seq. ID	LIB36-011-Q2-E2-B7
Method	BLASTX
NCBI GI	g1749582
BLAST score	469
E value	5.0e-47
Match length	150
% identity	57
NCBI Description	(D89187) similar to <i>Saccharomyces cerevisiae</i> hypothetical TRP-ASP repeats containing protein in MDS1-SWP1 intergenic region, SWISS-PROT Accession Number P40217 [<i>Schizosaccharomyces pombe</i>]
Seq. No.	300764
Seq. ID	LIB36-011-Q2-E2-B8
Method	BLASTX
NCBI GI	g119119
BLAST score	340
E value	7.0e-32
Match length	106
% identity	60
NCBI Description	ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (SHORT CHAIN ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1) >gi_92216_pir_S06477 enoyl-CoA hydratase (EC 4.2.1.17) precursor, mitochondrial - rat >gi_56072_emb_CAA34080_(X15958) precursor polypeptide (AA -29 to 261) [<i>Rattus norvegicus</i>] >gi_227489_prf_1704377A enoyl-CoA hydratase [<i>Rattus norvegicus</i>]
Seq. No.	300765
Seq. ID	LIB36-011-Q2-E2-B9
Method	BLASTX
NCBI GI	g3122971
BLAST score	224
E value	3.0e-18
Match length	68
% identity	54
NCBI Description	PROBABLE tRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE >gi_2388924_emb_CAB11659_ (Z98977) hypothetical protein [<i>Schizosaccharomyces pombe</i>]
Seq. No.	300766
Seq. ID	LIB36-011-Q2-E2-C10
Method	BLASTX
NCBI GI	g1168328

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BLAST score 402
E value 4.0e-39
Match length 130
% identity 58
NCBI Description ACTIN-LIKE PROTEIN 3 >gi_629878_pir_S48844 actin-like protein - slime mold (*Dictyostelium discoideum*)
>gi_2130164_pir_S69002 actin-like protein - slime mold (*Dictyostelium discoideum*) >gi_563346_emb_CAA86553 (Z46418) actin-like protein [*Dictyostelium discoideum*]

Seq. No. 300767
Seq. ID LIB36-011-Q2-E2-C12
Method BLASTX
NCBI GI g133978
BLAST score 550
E value 2.0e-56
Match length 147
% identity 70
NCBI Description 40S RIBOSOMAL PROTEIN S6 (PHOSPHOPROTEIN NP33)
>gi_70932_pir_R3RTS6 ribosomal protein S6 - rat
>gi_70933_pir_R3MS6 ribosomal protein S6 - mouse
>gi_319910_pir_R3HU6 ribosomal protein S6 - human
>gi_36148_emb_CAA47719 (X67309) ribosomal protein S6 [Homo sapiens] >gi_54010_emb_CAA68430 (Y00348) ribosomal protein S6 [Mus musculus] >gi_206747 (M29358) ribosomal protein S6 [Rattus norvegicus] >gi_307393 (M77232) ribosomal protein S6 [Homo sapiens] >gi_1177549_emb_CAA90936 (Z54209) rpS6 [Mus musculus]

Seq. No. 300768
Seq. ID LIB36-011-Q2-E2-C2
Method BLASTX
NCBI GI g2499017
BLAST score 455
E value 2.0e-45
Match length 118
% identity 69
NCBI Description ALPHA, ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 1
(TREHALOSE-6-PHOSPHATE SYNTHASE)
(UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE)
>gi_551471 (U07184) trehalose-6-phosphate synthase subunit 1 [*Aspergillus niger*]

Seq. No. 300769
Seq. ID LIB36-011-Q2-E2-C4
Method BLASTX
NCBI GI g4557467
BLAST score 229
E value 7.0e-19
Match length 111
% identity 41
NCBI Description Cockayne syndrome 1 protein >gi_3121917_sp_Q13216_CSA_HUMAN
COCKAYNE SYNDROME WD-REPEAT PROTEIN CSA
>gi_1362773_pir_A57090 CSA protein - human >gi_975302 (U28413) CSA protein [Homo sapiens]

Seq. No. 300770

Seq. ID LIB36-011-Q2-E2-C6
Method BLASTX
NCBI GI g1513298
BLAST score 238
E value 6.0e-20
Match length 129
% identity 35
NCBI Description (U66526) AbcA [Dictyostelium discoideum]

Seq. No. 300771
Seq. ID LIB36-011-Q2-E2-C8
Method BLASTX
NCBI GI g3204175
BLAST score 164
E value 3.0e-11
Match length 101
% identity 39
NCBI Description (AJ006405) prostaglandin-D synthase [Gallus gallus]

Seq. No. 300772
Seq. ID LIB36-011-Q2-E2-C9
Method BLASTX
NCBI GI g3334494
BLAST score 523
E value 2.0e-53
Match length 140
% identity 74
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_2388954_emb_CAB11687
(Z98979) 40s ribosomal protein s11 [Schizosaccharomyces pombe]

Seq. No. 300773
Seq. ID LIB36-011-Q2-E2-D1
Method BLASTX
NCBI GI g478005
BLAST score 293
E value 2.0e-26
Match length 121
% identity 50
NCBI Description profilin-IB - Acanthamoeba sp. (tentative sequence)

Seq. No. 300774
Seq. ID LIB36-011-Q2-E2-D12
Method BLASTX
NCBI GI g182403
BLAST score 352
E value 3.0e-33
Match length 125
% identity 51
NCBI Description (M74090) TB2 [Homo sapiens]

Seq. No. 300775
Seq. ID LIB36-011-Q2-E2-D5
Method BLASTX
NCBI GI g3023751
BLAST score 320
E value 2.0e-29

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Match length 133
% identity 30
NCBI Description 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir_S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No. 300776
Seq. ID LIB36-011-Q2-E2-D6
Method BLASTX
NCBI GI g2414627
BLAST score 269
E value 6.0e-24
Match length 92
% identity 58
NCBI Description (Z99259) 40s ribosomal protein [Schizosaccharomyces pombe]

Seq. No. 300777
Seq. ID LIB36-011-Q2-E2-D7
Method BLASTX
NCBI GI g114517
BLAST score 422
E value 2.0e-41
Match length 120
% identity 71
NCBI Description ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR >gi_67811_pir_PWHUA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain precursor - human >gi_28938_emb_CAA41789_ (X59066) H(+) -transporting ATP synthase [Homo sapiens] >gi_34468_emb_CAA46452_ (X65460) ATP synthase alpha subunit [Homo sapiens] >gi_559317_dbj_BAA05672_ (D28126) ATP synthase alpha subunit [Homo sapiens] >gi_559325_dbj_BAA03531_ (D14710) import precursor of human ATP synthase alpha subunit [Homo sapiens] >gi_1090507_prf_2019238A ATP synthase:SUBUNIT=alpha [Homo sapiens]

Seq. No. 300778
Seq. ID LIB36-011-Q2-E2-D8
Method BLASTX
NCBI GI g3947746
BLAST score 211
E value 1.0e-16
Match length 132
% identity 33
NCBI Description (AJ009960) DNA photolyase [Trichoderma harzianum]

Seq. No. 300779
Seq. ID LIB36-011-Q2-E2-E2
Method BLASTX
NCBI GI g600159
BLAST score 361
E value 2.0e-34
Match length 93
% identity 78
NCBI Description (U17362) elongation factor 2 [Cricetulus griseus]

Seq. No. 300780
Seq. ID LIB36-011-Q2-E2-E3
Method BLASTX
NCBI GI g3643267
BLAST score 169
E value 5.0e-24
Match length 125
% identity 52
NCBI Description (AF090443) catalase [Dictyostelium discoideum]

Seq. No. 300781
Seq. ID LIB36-011-Q2-E2-E8
Method BLASTX
NCBI GI g2160185
BLAST score 199
E value 2.0e-15
Match length 76
% identity 51
NCBI Description (AC000132) Similar to S. pombe ISP4 (gb_D83992).
[Arabidopsis thaliana]

Seq. No. 300782
Seq. ID LIB36-011-Q2-E2-F10
Method BLASTX
NCBI GI g1749752
BLAST score 442
E value 7.0e-44
Match length 148
% identity 60
NCBI Description (D89272) similar to Saccharomyces cerevisiae T-complex
protein 1, theta subunit, SWISS-PROT Accession Number P47079
[Schizosaccharomyces pombe]

Seq. No. 300783
Seq. ID LIB36-011-Q2-E2-F11
Method BLASTN
NCBI GI g2618602
BLAST score 64
E value 2.0e-27
Match length 306
% identity 83
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 300784
Seq. ID LIB36-011-Q2-E2-F8
Method BLASTX
NCBI GI g134509
BLAST score 165
E value 2.0e-11
Match length 68
% identity 50
NCBI Description SIS1 PROTEIN >gi_101623_pir_A39660 heat shock protein SIS1
- yeast (Saccharomyces cerevisiae) >gi_4474_emb_CAA41366
(X58460) SIS1 protein [Saccharomyces cerevisiae]
>gi_1301824_emb_CAA95866_ (Z71283) ORF YNL007c

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[Saccharomyces cerevisiae]

Seq. No. 300785
Seq. ID LIB36-011-Q2-E2-F9
Method BLASTX
NCBI GI g4160343
BLAST score 247
E value 5.0e-21
Match length 151
% identity 38
NCBI Description (AL035216) similar to rat synaptic glycoprotein sc2
[Schizosaccharomyces pombe]

Seq. No. 300786
Seq. ID LIB36-011-Q2-E2-G11
Method BLASTX
NCBI GI g115390
BLAST score 173
E value 3.0e-12
Match length 127
% identity 37
NCBI Description SQUIDULIN (OPTIC LOBE CALCIUM-BINDING PROTEIN) (SCABP)
>gi_102715_pir_A33353 calcium-binding protein - squid
(Watasenia scintillans)

Seq. No. 300787
Seq. ID LIB36-011-Q2-E2-G3
Method BLASTX
NCBI GI g4029330
BLAST score 279
E value 7.0e-25
Match length 89
% identity 57
NCBI Description (Y16743) ketol-acid reductoisomerase [Piromyces sp. E2]

Seq. No. 300788
Seq. ID LIB36-011-Q2-E2-G7
Method BLASTX
NCBI GI g98110
BLAST score 382
E value 8.0e-37
Match length 129
% identity 56
NCBI Description alpha-amylase (EC 3.2.1.1) - Bacillus circulans
>gi_39412_emb_CAA43194_ (X60779) amylase [Bacillus circulans]

Seq. No. 300789
Seq. ID LIB36-011-Q2-E2-H4
Method BLASTX
NCBI GI g135399
BLAST score 440
E value 1.0e-43
Match length 109
% identity 73
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_100716_pir_S20758 tubulin
alpha-1 chain - rice >gi_20379_emb_CAA77988_ (Z11931) alpha

1 tubulin [Oryza sativa] >gi_1136124_emb_CAA62918_ (X91808)
alfa-tubulin [Oryza sativa]

Seq. No. 300790
Seq. ID LIB36-011-Q2-E2-H5
Method BLASTX
NCBI GI g3152297
BLAST score 606
E value 4.0e-63
Match length 150
% identity 75
NCBI Description (Y17297) 6-phosphogluconate dehydrogenase [Cunninghamella elegans]

Seq. No. 300791
Seq. ID LIB36-011-Q2-E2-H8
Method BLASTX
NCBI GI g3860277
BLAST score 395
E value 2.0e-38
Match length 130
% identity 59
NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604 (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 300792
Seq. ID LIB36-012-Q1-E1-A10
Method BLASTX
NCBI GI g131388
BLAST score 235
E value 9.0e-20
Match length 74
% identity 78
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670 (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No. 300793
Seq. ID LIB36-012-Q1-E1-B10
Method BLASTX
NCBI GI g2129454
BLAST score 155
E value 3.0e-10
Match length 41
% identity 33
NCBI Description chlorophyll a/b-binding protein (clone GC18 and others) - Euglena gracilis (var. bacillaris) (fragment) >gi_510388_emb_CAA43633_ (X61361) light harvesting chlorophyll a/b binding protein of PSII [Euglena gracilis]

Seq. No. 300794
Seq. ID LIB36-012-Q1-E1-D6

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Method	BLASTX
NCBI GI	g3024018
BLAST score	344
E value	1.0e-32
Match length	79
% identity	84
NCBI Description	INITIATION FACTOR 5A (EIF-5A) (EIF-4D) >gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation initiation factor 5A [Zea mays]
Seq. No.	300795
Seq. ID	LIB36-012-Q1-E1-D8
Method	BLASTX
NCBI GI	g4580461
BLAST score	244
E value	1.0e-20
Match length	97
% identity	51
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]
Seq. No.	300796
Seq. ID	LIB36-012-Q1-E1-F3
Method	BLASTX
NCBI GI	g133726
BLAST score	181
E value	7.0e-14
Match length	34
% identity	100
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S11 >gi_70943_pir_R3RZ11 ribosomal protein S11 - rice chloroplast >gi_12019_emb_CAA33980_ (X15901) ribosomal protein S11 [Oryza sativa] >gi_226640_prf_1603356BP ribosomal protein S11 [Oryza sativa]
Seq. No.	300797
Seq. ID	LIB36-013-Q1-E1-B2
Method	BLASTX
NCBI GI	g3800853
BLAST score	226
E value	3.0e-19
Match length	53
% identity	87
NCBI Description	(AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase activase precursor [Zea mays]
Seq. No.	300798
Seq. ID	LIB36-013-Q1-E1-B9
Method	BLASTX
NCBI GI	g112994
BLAST score	236
E value	2.0e-20
Match length	46
% identity	100
NCBI Description	GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN >gi_82685_pir_S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 300799
Seq. ID LIB36-013-Q1-E1-C4
Method BLASTN
NCBI GI g22312
BLAST score 128
E value 5.0e-66
Match length 167
% identity 94
NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)

Seq. No. 300800
Seq. ID LIB36-013-Q1-E1-C9
Method BLASTX
NCBI GI g1076336
BLAST score 342
E value 3.0e-32
Match length 125
% identity 58
NCBI Description hypothetical protein H1.1flk - Arabidopsis thaliana (fragment)

Seq. No. 300801
Seq. ID LIB36-013-Q1-E1-E10
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 5.0e-11
Match length 48
% identity 67
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 300802
Seq. ID LIB36-013-Q1-E1-F1
Method BLASTN
NCBI GI g596079
BLAST score 120
E value 3.0e-61
Match length 120
% identity 100
NCBI Description Zea mays thiamine biosynthetic enzyme (thi1-2) mRNA, complete cds

Seq. No. 300803
Seq. ID LIB36-013-Q1-E1-F6
Method BLASTN
NCBI GI g606814
BLAST score 64
E value 1.0e-27
Match length 170
% identity 97
NCBI Description Zea mays Golden Bantam carbonic anhydrase mRNA, complete cds

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Seq. No. 300804
Seq. ID LIB36-013-Q1-E1-G10
Method BLASTX
NCBI GI g1708993
BLAST score 425
E value 5.0e-42
Match length 99
% identity 82
NCBI Description CYSTATHIONINE BETA-LYASE PRECURSOR (CBL)
(BETA-CYSTATHIONASE) (CYSTEINE LYASE)
>gi_2129567_pir_S61429 cystathionine beta-lyase (EC
4.4.1.8) - Arabidopsis thaliana >gi_704397 (L40511)
cystathionine beta-lyase [Arabidopsis thaliana]

Seq. No. 300805
Seq. ID LIB36-014-Q1-E1-A8
Method BLASTX
NCBI GI g1122317
BLAST score 208
E value 2.0e-16
Match length 69
% identity 64
NCBI Description (X94193) heat shock protein 17.9 [Pennisetum glaucum]

Seq. No. 300806
Seq. ID LIB36-014-Q1-E1-B12
Method BLASTN
NCBI GI g2062691
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100
NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete
cds

Seq. No. 300807
Seq. ID LIB36-014-Q1-E1-D11
Method BLASTX
NCBI GI g2980793
BLAST score 189
E value 3.0e-14
Match length 60
% identity 58
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 300808
Seq. ID LIB36-014-Q1-E1-G10
Method BLASTX
NCBI GI g1708993
BLAST score 208
E value 1.0e-16
Match length 76
% identity 54
NCBI Description CYSTATHIONINE BETA-LYASE PRECURSOR (CBL)
(BETA-CYSTATHIONASE) (CYSTEINE LYASE)
>gi_2129567_pir_S61429 cystathionine beta-lyase (EC

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4.4.1.8) - *Arabidopsis thaliana* >gi_704397 (L40511)
cystathione beta-lyase [*Arabidopsis thaliana*]

Seq. No. 300809
Seq. ID LIB36-015-Q1-E1-A4
Method BLASTX
NCBI GI g4585972
BLAST score 209
E value 9.0e-17
Match length 113
% identity 35
NCBI Description (AC005287) Putative ATPase [*Arabidopsis thaliana*]

Seq. No. 300810
Seq. ID LIB36-015-Q1-E1-B4
Method BLASTX
NCBI GI g3885886
BLAST score 545
E value 6.0e-56
Match length 105
% identity 92
NCBI Description (AF093631) Rieske Fe-S precursor protein [*Oryza sativa*]

Seq. No. 300811
Seq. ID LIB36-015-Q1-E1-C1
Method BLASTN
NCBI GI g829147
BLAST score 120
E value 3.0e-61
Match length 183
% identity 92
NCBI Description Z.mays gene for cyclophilin

Seq. No. 300812
Seq. ID LIB36-015-Q1-E1-C2
Method BLASTX
NCBI GI g548603
BLAST score 152
E value 2.0e-10
Match length 53
% identity 62
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
>gi_478404_pir_JQ2247 photosystem I chain D precursor -
barley >gi_167085 (M98254) PSI-D subunit [*Hordeum vulgare*]

Seq. No. 300813
Seq. ID LIB36-015-Q1-E1-C5
Method BLASTN
NCBI GI g2062705
BLAST score 36
E value 6.0e-11
Match length 48
% identity 67
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 300814

SPECIMEN SOURCE

Seq. ID	LIB36-015-Q1-E1-F2
Method	BLASTX
NCBI GI	g1632831
BLAST score	157
E value	4.0e-13
Match length	71
% identity	61
NCBI Description	(Z49698) orf [Ricinus communis]
Seq. No.	300815
Seq. ID	LIB36-015-Q1-E1-G6
Method	BLASTX
NCBI GI	g294845
BLAST score	175
E value	6.0e-13
Match length	58
% identity	57
NCBI Description	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]
Seq. No.	300816
Seq. ID	LIB36-015-Q1-E1-G8
Method	BLASTX
NCBI GI	g312179
BLAST score	240
E value	3.0e-20
Match length	95
% identity	55
NCBI Description	(X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.	300817
Seq. ID	LIB36-016-Q1-E1-C12
Method	BLASTN
NCBI GI	g559531
BLAST score	57
E value	9.0e-24
Match length	105
% identity	89
NCBI Description	Z.mays mRNA for cysteine proteinase
Seq. No.	300818
Seq. ID	LIB36-016-Q2-E2-D11
Method	BLASTX
NCBI GI	g2062169
BLAST score	290
E value	5.0e-26
Match length	123
% identity	44
NCBI Description	(AC001645) ABC transporter (PDR5-like) isoform [Arabidopsis thaliana]
Seq. No.	300819
Seq. ID	LIB36-016-Q2-E2-D12

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Method BLASTX
NCBI GI g2062169
BLAST score 141
E value 6.0e-09
Match length 34
% identity 65
NCBI Description (AC001645) ABC transporter (PDR5-like) isoform [Arabidopsis thaliana]

Seq. No. 300820
Seq. ID LIB36-017-Q1-E1-B3
Method BLASTX
NCBI GI g1707928
BLAST score 358
E value 5.0e-34
Match length 87
% identity 84
NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 2 PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi_1076806_pir_S49439 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) - maize >gi_558365_emb_CAA86227_ (Z38111) ADP-glucose pyrophosphorylase [Zea mays]

Seq. No. 300821
Seq. ID LIB36-017-Q1-E1-B4
Method BLASTN
NCBI GI g2832242
BLAST score 76
E value 5.0e-35
Match length 160
% identity 87
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 300822
Seq. ID LIB36-017-Q1-E1-C1
Method BLASTN
NCBI GI g3819189
BLAST score 44
E value 2.0e-15
Match length 76
% identity 91
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0654

Seq. No. 300823
Seq. ID LIB36-017-Q1-E1-F10
Method BLASTX
NCBI GI g4468817
BLAST score 207
E value 2.0e-16
Match length 44
% identity 84
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 300824
Seq. ID LIB36-017-Q1-E1-F7

Method BLASTX
NCBI GI g115786
BLAST score 686
E value 2.0e-72
Match length 132
% identity 95
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays]

Seq. No. 300825
Seq. ID LIB36-017-Q1-E1-F8
Method BLASTX
NCBI GI g2997591
BLAST score 299
E value 4.0e-27
Match length 63
% identity 90
NCBI Description (AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]

Seq. No. 300826
Seq. ID LIB36-017-Q1-E1-H8
Method BLASTN
NCBI GI g311236
BLAST score 71
E value 1.0e-31
Match length 119
% identity 92
NCBI Description Z.mays mRNA for ATPase (delta subunit)

Seq. No. 300827
Seq. ID LIB36-018-Q1-E1-D3
Method BLASTX
NCBI GI g2980779
BLAST score 252
E value 7.0e-22
Match length 84
% identity 60
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 300828
Seq. ID LIB36-018-Q1-E1-D6
Method BLASTX
NCBI GI g1871187
BLAST score 159
E value 4.0e-11
Match length 42
% identity 74
NCBI Description (U90439) unknown protein [Arabidopsis thaliana]

Seq. No. 300829
Seq. ID LIB36-018-Q1-E1-D7
Method BLASTN
NCBI GI g22378
BLAST score 174

E value 2.0e-93
Match length 182
% identity 99
NCBI Description Z.mays gene for nucleic acid binding protein

Seq. No. 300830
Seq. ID LIB36-018-Q1-E1-F9
Method BLASTX
NCBI GI g464981
BLAST score 248
E value 3.0e-21
Match length 47
% identity 98
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 300831
Seq. ID LIB36-018-Q1-E1-G3
Method BLASTX
NCBI GI g1209756
BLAST score 171
E value 4.0e-12
Match length 40
% identity 75
NCBI Description (U43629) integral membrane protein [Beta vulgaris]

Seq. No. 300832
Seq. ID LIB36-018-Q1-E1-G6
Method BLASTX
NCBI GI g3885896
BLAST score 169
E value 4.0e-12
Match length 72
% identity 51
NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

Seq. No. 300833
Seq. ID LIB36-018-Q1-E1-H8
Method BLASTX
NCBI GI g4322323
BLAST score 180
E value 3.0e-13
Match length 116
% identity 34
NCBI Description (AF080543) amino acid transporter [Nepenthes alata]

Seq. No. 300834
Seq. ID LIB36-019-Q1-E1-A8
Method BLASTX
NCBI GI g482311
BLAST score 161
E value 8.0e-18
Match length 73
% identity 70
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf_2002393A oxygen-evolving

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complex protein 1 [Oryza sativa]

Seq. No. 300835
Seq. ID LIB36-019-Q1-E1-B9
Method BLASTX
NCBI GI g131388
BLAST score 329
E value 1.0e-30
Match length 94
% identity 81
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir_S16260 photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum aestivum]

Seq. No. 300836
Seq. ID LIB36-019-Q1-E1-D5
Method BLASTX
NCBI GI g115786
BLAST score 358
E value 5.0e-34
Match length 106
% identity 71
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays]

Seq. No. 300837
Seq. ID LIB36-019-Q1-E1-G12
Method BLASTN
NCBI GI g758352
BLAST score 252
E value 1.0e-139
Match length 287
% identity 97
NCBI Description Z.mays mRNA for cysteine synthase

Seq. No. 300838
Seq. ID LIB36-019-Q1-E1-H6
Method BLASTX
NCBI GI g3885886
BLAST score 378
E value 2.0e-36
Match length 99
% identity 81
NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No. 300839
Seq. ID LIB36-020-Q1-E1-A5
Method BLASTX
NCBI GI g2826844
BLAST score 212
E value 6.0e-17

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Match length 60
% identity 62
NCBI Description (AJ002237) loxc homologue [Lycopersicon esculentum]

Seq. No. 300840
Seq. ID LIB36-020-Q1-E1-A8
Method BLASTX
NCBI GI g3882356
BLAST score 268
E value 1.0e-23
Match length 103
% identity 52
NCBI Description (U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis thaliana]

Seq. No. 300841
Seq. ID LIB36-020-Q1-E1-E2
Method BLASTX
NCBI GI g1709846
BLAST score 323
E value 5.0e-30
Match length 89
% identity 43
NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336)
22 kDa component of photosystem II [Lycopersicon esculentum]

Seq. No. 300842
Seq. ID LIB36-020-Q1-E1-E8
Method BLASTX
NCBI GI g4585882
BLAST score 661
E value 1.0e-69
Match length 133
% identity 89
NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 300843
Seq. ID LIB36-020-Q1-E1-G10
Method BLASTX
NCBI GI g1658313
BLAST score 360
E value 2.0e-34
Match length 98
% identity 39
NCBI Description (Y08987) osr40g2 [Oryza sativa]

Seq. No. 300844
Seq. ID LIB36-020-Q1-E1-G12
Method BLASTN
NCBI GI g902200
BLAST score 302
E value 1.0e-169
Match length 402
% identity 93
NCBI Description Z.mays complete chloroplast genome

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Seq. No. 300845
Seq. ID LIB36-020-Q1-E1-G5
Method BLASTX
NCBI GI g115771
BLAST score 736
E value 2.0e-78
Match length 141
% identity 99
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll a/b-binding protein precursor - maize >gi_22224_emb_CAA32900 (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

Seq. No. 300846
Seq. ID LIB36-021-Q1-E1-D2
Method BLASTX
NCBI GI g1261917
BLAST score 285
E value 1.0e-25
Match length 76
% identity 66
NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]

Seq. No. 300847
Seq. ID LIB36-021-Q1-E1-F4
Method BLASTX
NCBI GI g2911078
BLAST score 145
E value 3.0e-09
Match length 46
% identity 61
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 300848
Seq. ID LIB36-021-Q1-E1-G2
Method BLASTX
NCBI GI g122022
BLAST score 192
E value 9.0e-15
Match length 86
% identity 53
NCBI Description HISTONE H2B >gi_283025_pir_S22323 histone H2B - wheat >gi_21801_emb_CAA42530 (X59873) histone H2B [Triticum aestivum]

Seq. No. 300849
Seq. ID LIB36-021-Q1-E1-G5
Method BLASTN
NCBI GI g1617470
BLAST score 186
E value 1.0e-100
Match length 301
% identity 91
NCBI Description Z.diploperennis DNA for Grandel-4 retrotransposon

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Seq. No.	300850
Seq. ID	LIB36-021-Q1-E1-G6
Method	BLASTN
NCBI GI	g3821780
BLAST score	37
E value	2.0e-11
Match length	49
% identity	67
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	300851
Seq. ID	LIB36-022-Q1-E1-E3
Method	BLASTN
NCBI GI	g1673455
BLAST score	164
E value	2.0e-87
Match length	181
% identity	98
NCBI Description	Z.mays rubisco small subunit gene
Seq. No.	300852
Seq. ID	LIB36-022-Q1-E1-F7
Method	BLASTN
NCBI GI	g236729
BLAST score	283
E value	1.0e-158
Match length	348
% identity	95
NCBI Description	metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
Seq. No.	300853
Seq. ID	LIB36-022-Q1-E1-G5
Method	BLASTN
NCBI GI	g483411
BLAST score	229
E value	1.0e-126
Match length	354
% identity	96
NCBI Description	Zea Mays calmodulin-binding protein mRNA, 3'end
Seq. No.	300854
Seq. ID	LIB36-022-Q1-E1-H3
Method	BLASTX
NCBI GI	g132147
BLAST score	593
E value	1.0e-61
Match length	112
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_68089_pir_RKZMS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - maize >gi_22474_emb_CAA29784_ (X06535) ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi_359512_prf_1312317A ribulosebisphosphate carboxylase [Zea mays]

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Seq. No.	300855
Seq. ID	LIB83-001-Q1-E1-B11
Method	BLASTX
NCBI GI	g1931639
BLAST score	498
E value	2.0e-50
Match length	141
% identity	66
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]
Seq. No.	300856
Seq. ID	LIB83-001-Q1-E1-B12
Method	BLASTN
NCBI GI	g236729
BLAST score	138
E value	9.0e-72
Match length	180
% identity	95
NCBI Description	metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
Seq. No.	300857
Seq. ID	LIB83-001-Q1-E1-E9
Method	BLASTX
NCBI GI	g1172861
BLAST score	350
E value	2.0e-33
Match length	66
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR (RUBISCO LARGE SUBUNIT) >gi_1363613_pir_S58560 ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - maize chloroplast >gi_18036_emb_CAA78027_ (Z11973) Ribulose bisphosphate carboxylase [Zea mays] >gi_902230_emb_CAA60294_ (X86563) rubisco large subunit [Zea mays]
Seq. No.	300858
Seq. ID	LIB83-001-Q1-E1-G1
Method	BLASTN
NCBI GI	g311236
BLAST score	80
E value	2.0e-37
Match length	142
% identity	89
NCBI Description	Z.mays mRNA for ATPase (delta subunit)
Seq. No.	300859
Seq. ID	LIB83-001-Q1-E1-G3
Method	BLASTX
NCBI GI	g4415938
BLAST score	193
E value	9.0e-21
Match length	87
% identity	56
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana]

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Seq. No.	300860
Seq. ID	LIB83-002-Q1-E1-B9
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	300861
Seq. ID	LIB83-002-Q1-E1-C11
Method	BLASTX
NCBI GI	g3885886
BLAST score	353
E value	2.0e-36
Match length	94
% identity	81
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]
Seq. No.	300862
Seq. ID	LIB83-002-Q1-E1-D3
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	46
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	300863
Seq. ID	LIB83-002-Q1-E1-E11
Method	BLASTX
NCBI GI	g4455323
BLAST score	250
E value	2.0e-21
Match length	124
% identity	43
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]
Seq. No.	300864
Seq. ID	LIB83-002-Q1-E1-E8
Method	BLASTX
NCBI GI	g115771
BLAST score	528
E value	5.0e-54
Match length	117
% identity	87
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll a/b-binding protein precursor - maize >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]
Seq. No.	300865
Seq. ID	LIB83-002-Q1-E1-F4

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Method BLASTN
NCBI GI g168527
BLAST score 115
E value 4.0e-58
Match length 124
% identity 98
NCBI Description Maize NADP-dependent malic enzyme (Me1) mRNA, complete cds

Seq. No. 300866
Seq. ID LIB83-002-Q1-E1-F5
Method BLASTX
NCBI GI g2827002
BLAST score 557
E value 2.0e-57
Match length 125
% identity 84
NCBI Description (AF005993) HSP70 [Triticum aestivum]

Seq. No. 300867
Seq. ID LIB83-002-Q1-E1-G1
Method BLASTX
NCBI GI g3249064
BLAST score 438
E value 2.0e-43
Match length 132
% identity 59
NCBI Description (AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb_2245136 from A. thaliana chromosome 4 contig gb_Z97344. [Arabidopsis thaliana]

Seq. No. 300868
Seq. ID LIB83-003-Q1-E1-A2
Method BLASTX
NCBI GI g266578
BLAST score 241
E value 2.0e-20
Match length 56
% identity 77
NCBI Description METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir_S17560 metallothionein-like protein - maize >gi_236730_bbs_57629 (S57628) metallothionein homologue [Zea mays, Peptide, 76 aa] [Zea mays] >gi_559536_emb_CAA57676_(X82186) metallothionein- like protein [Zea mays] >gi_228095_prf_1717215A metallothionein-like protein [Zea mays]

Seq. No. 300869
Seq. ID LIB83-003-Q1-E1-A6
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 300870

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Seq. ID	LIB83-003-Q1-E1-C10
Method	BLASTX
NCBI GI	g629669
BLAST score	152
E value	6.0e-10
Match length	102
% identity	38
NCBI Description	hypothetical protein - tomato
Seq. No.	300871
Seq. ID	LIB83-003-Q1-E1-E12
Method	BLASTX
NCBI GI	g3004565
BLAST score	215
E value	2.0e-17
Match length	67
% identity	60
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]
Seq. No.	300872
Seq. ID	LIB83-003-Q1-E1-E2
Method	BLASTX
NCBI GI	g4580461
BLAST score	612
E value	8.0e-64
Match length	142
% identity	81
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]
Seq. No.	300873
Seq. ID	LIB83-003-Q1-E1-F10
Method	BLASTX
NCBI GI	g4415937
BLAST score	240
E value	3.0e-20
Match length	83
% identity	59
NCBI Description	(AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.	300874
Seq. ID	LIB83-003-Q1-E1-F11
Method	BLASTX
NCBI GI	g131176
BLAST score	351
E value	3.0e-33
Match length	101
% identity	73
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir_F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf_1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]
Seq. No.	300875
Seq. ID	LIB83-003-Q1-E1-F6

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Method	BLASTX
NCBI GI	g2499931
BLAST score	296
E value	9.0e-27
Match length	77
% identity	74
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT) >gi_2129534_pir_S71272 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi_1321681_emb_CAA65609 (X96866) adenine phosphoribosyltransferase [Arabidopsis thaliana]
Seq. No.	300876
Seq. ID	LIB83-003-Q1-E1-H11
Method	BLASTX
NCBI GI	g112994
BLAST score	194
E value	8.0e-15
Match length	46
% identity	91
NCBI Description	GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN >gi_82685_pir_S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564) ABA-inducible gene protein [Zea mays] >gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]
Seq. No.	300877
Seq. ID	LIB83-004-Q1-E1-G10
Method	BLASTX
NCBI GI	g1657851
BLAST score	197
E value	4.0e-15
Match length	49
% identity	35
NCBI Description	(U73214) cold acclimation protein WCOR518 [Triticum aestivum]
Seq. No.	300878
Seq. ID	LIB83-004-Q1-E2-A11
Method	BLASTX
NCBI GI	g1171864
BLAST score	293
E value	2.0e-26
Match length	81
% identity	70
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K >gi_902226_emb_CAA60290_ (X86563) ndhK [Zea mays]
Seq. No.	300879
Seq. ID	LIB83-004-Q1-E2-A2
Method	BLASTN
NCBI GI	g1575129
BLAST score	97
E value	3.0e-47
Match length	197
% identity	87

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NCBI Description Zea mays luminal binding protein cBiPe3 mRNA, complete cds
Seq. No. 300880
Seq. ID LIB83-004-Q1-E2-C12
Method BLASTX
NCBI GI g132819
BLAST score 277
E value 1.0e-24
Match length 67
% identity 72
NCBI Description 50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24)
>gi_71307_pir_R5PM24 ribosomal protein L24 precursor,
chloroplast - garden pea >gi_20873_emb_CAA32185_ (X14020)
CL24 ribosomal preprotein (AA -39 to 155) [Pisum sativum]

Seq. No. 300881
Seq. ID LIB83-004-Q1-E2-G11
Method BLASTX
NCBI GI g481190
BLAST score 198
E value 1.0e-15
Match length 84
% identity 54
NCBI Description plastocyanin precursor - barley >gi_22705_emb_CAA68696_
(Y00704) plastocyanin precursor [Hordeum vulgare]
>gi_431920_emb_CAA82201_ (Z28347) plastocyanin [Hordeum
vulgare]

Seq. No. 300882
Seq. ID LIB83-005-Q1-E1-B10
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 300883
Seq. ID LIB83-005-Q1-E1-B5
Method BLASTX
NCBI GI g3297823
BLAST score 354
E value 1.0e-33
Match length 125
% identity 50
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 300884
Seq. ID LIB83-005-Q1-E1-D11
Method BLASTX
NCBI GI g1399183
BLAST score 279
E value 8.0e-25
Match length 98
% identity 65
NCBI Description (U50739) Lycopene beta cyclase [Arabidopsis thaliana]

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Seq. No. 300885
Seq. ID LIB83-005-Q1-E1-D2
Method BLASTX
NCBI GI g4585576
BLAST score 257
E value 8.0e-36
Match length 108
% identity 73
NCBI Description (AF134051) fructose-1,6-bisphosphatase precursor [Solanum tuberosum]

Seq. No. 300886
Seq. ID LIB83-005-Q1-E1-E5
Method BLASTN
NCBI GI g405634
BLAST score 191
E value 1.0e-103
Match length 207
% identity 99
NCBI Description Z.mays zmcpt mRNA triose phosphate/phosphate translocator

Seq. No. 300887
Seq. ID LIB83-005-Q1-E1-E8
Method BLASTX
NCBI GI g3367519
BLAST score 537
E value 5.0e-55
Match length 134
% identity 78
NCBI Description (AC004392) Contains similarity to gb_U51898
Ca²⁺-independent phospholipase A2 from Rattus norvegicus.
[Arabidopsis thaliana]

Seq. No. 300888
Seq. ID LIB83-005-Q1-E1-F4
Method BLASTX
NCBI GI g2460251
BLAST score 190
E value 2.0e-14
Match length 41
% identity 93
NCBI Description (AF020791) ferrochelatase [Hordeum vulgare]

Seq. No. 300889
Seq. ID LIB83-005-Q1-E1-G1
Method BLASTX
NCBI GI g3885896
BLAST score 354
E value 1.0e-33
Match length 106
% identity 67
NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

Seq. No. 300890
Seq. ID LIB83-005-Q1-E1-H10
Method BLASTX

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NCBI GI g2500130
BLAST score 518
E value 8.0e-53
Match length 136
% identity 73
NCBI Description THIOREDOXIN REDUCTASE 2 (NADPH-DEPENDENT THIOREDOXIN REDUCTASE 2) (NTR 2) >gi_1076358_pir_S44026 thioredoxin reductase (NADPH) (EC 1.6.4.5) A - Arabidopsis thaliana (fragment) >gi_468524_emb_CAA80655_ (Z23108) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No. 300891
Seq. ID LIB83-005-Q1-E1-H11
Method BLASTX
NCBI GI g4038043
BLAST score 256
E value 4.0e-22
Match length 110
% identity 61
NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No. 300892
Seq. ID LIB83-006-Q1-E1-A5
Method BLASTX
NCBI GI g2501190
BLAST score 307
E value 6.0e-31
Match length 106
% identity 72
NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR >gi_2130147_pir_S61420 thiamine biosynthetic enzyme thil-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme [Zea mays]

Seq. No. 300893
Seq. ID LIB83-006-Q1-E1-E3
Method BLASTX
NCBI GI g3252866
BLAST score 209
E value 1.0e-16
Match length 116
% identity 37
NCBI Description (AF033535) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 300894
Seq. ID LIB83-006-Q1-E1-F7
Method BLASTX
NCBI GI g2696227
BLAST score 438
E value 2.0e-43
Match length 98
% identity 84
NCBI Description (D55711) chitinase [Oryza sativa]

Seq. No. 300895
Seq. ID LIB83-006-Q1-E1-G9

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Method BLASTX
NCBI GI g2369690
BLAST score 219
E value 8.0e-18
Match length 89
% identity 55
NCBI Description (Y11988) FPF1 protein [Arabidopsis thaliana]

Seq. No. 300896
Seq. ID LIB83-006-Q1-E1-H11
Method BLASTX
NCBI GI g1648931
BLAST score 607
E value 3.0e-63
Match length 137
% identity 87
NCBI Description (X92428) HOX1B protein [Zea mays]

Seq. No. 300897
Seq. ID LIB83-007-Q1-E1-A10
Method BLASTN
NCBI GI g3821780
BLAST score 35
E value 3.0e-10
Match length 35
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 300898
Seq. ID LIB83-007-Q1-E1-A11
Method BLASTX
NCBI GI g3004555
BLAST score 143
E value 7.0e-09
Match length 135
% identity 27
NCBI Description (AC003673) similar to salt inducible protein [Arabidopsis thaliana]

Seq. No. 300899
Seq. ID LIB83-007-Q1-E1-B7
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 300900
Seq. ID LIB83-007-Q1-E1-C2
Method BLASTN
NCBI GI g4416300
BLAST score 132
E value 2.0e-68
Match length 178
% identity 48

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NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No. 300901
Seq. ID LIB83-007-Q1-E1-D7
Method BLASTN
NCBI GI g3821780
BLAST score 35
E value 3.0e-10
Match length 35
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 300902
Seq. ID LIB83-007-Q1-E1-E3
Method BLASTX
NCBI GI g2149640
BLAST score 156
E value 1.0e-10
Match length 63
% identity 56
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No. 300903
Seq. ID LIB83-007-Q1-E1-E7
Method BLASTX
NCBI GI g3885896
BLAST score 174
E value 1.0e-12
Match length 83
% identity 51
NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

Seq. No. 300904
Seq. ID LIB83-007-Q1-E1-E8
Method BLASTX
NCBI GI g4539009
BLAST score 313
E value 8.0e-29
Match length 102
% identity 56
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 300905
Seq. ID LIB83-007-Q1-E1-H4
Method BLASTX
NCBI GI g3242328
BLAST score 326
E value 7.0e-31
Match length 60
% identity 100
NCBI Description (X98083) cinnamoyl-CoA reductase [Zea mays]

Seq. No. 300906
Seq. ID LIB83-008-Q1-E1-B10
Method BLASTN
NCBI GI g3041776

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BLAST score	49
E value	1.0e-18
Match length	93
% identity	88
NCBI Description	Oryza sativa mRNA for fructose-1,6-bisphosphatase (plastidic isoform), complete cds
Seq. No.	300907
Seq. ID	LIB83-008-Q1-E1-B4
Method	BLASTX
NCBI GI	g4504079
BLAST score	185
E value	8.0e-14
Match length	112
% identity	39
NCBI Description	UNKNOWN >gi_2706632_dbj_BAA24035_ (AB006969) hGAA1 [Homo sapiens]
Seq. No.	300908
Seq. ID	LIB83-008-Q1-E1-E1
Method	BLASTN
NCBI GI	g1816587
BLAST score	61
E value	3.0e-26
Match length	61
% identity	100
NCBI Description	Zea mays LON2 protease (LON2) mRNA, complete cds
Seq. No.	300909
Seq. ID	LIB83-008-Q1-E1-E12
Method	BLASTX
NCBI GI	g1001111
BLAST score	152
E value	6.0e-10
Match length	115
% identity	30
NCBI Description	(D64001) hypothetical protein [Synechocystis sp.]
Seq. No.	300910
Seq. ID	LIB83-008-Q1-E1-G6
Method	BLASTN
NCBI GI	g3282393
BLAST score	38
E value	6.0e-12
Match length	122
% identity	83
NCBI Description	Oryza sativa aie2 mRNA, partial cds
Seq. No.	300911
Seq. ID	LIB83-008-Q1-E1-H10
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	4.0e-10
Match length	35
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

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Seq. No. 300912
Seq. ID LIB83-008-Q1-E1-H12
Method BLASTX
NCBI GI g3643610
BLAST score 353
E value 1.0e-33
Match length 75
% identity 88
NCBI Description (AC005395) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 300913
Seq. ID LIB83-008-Q1-E1-H6
Method BLASTX
NCBI GI g2217970
BLAST score 189
E value 3.0e-14
Match length 134
% identity 13
NCBI Description (Z97074) p40 [Homo sapiens]

Seq. No. 300914
Seq. ID LIB83-009-Q1-E1-D11
Method BLASTX
NCBI GI g2062167
BLAST score 284
E value 2.0e-25
Match length 104
% identity 54
NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No. 300915
Seq. ID LIB83-009-Q1-E1-E10
Method BLASTX
NCBI GI g4544415
BLAST score 196
E value 4.0e-15
Match length 109
% identity 39
NCBI Description (AC006955) putative polyprotein [Arabidopsis thaliana]

Seq. No. 300916
Seq. ID LIB83-009-Q1-E1-E12
Method BLASTX
NCBI GI g4415919
BLAST score 200
E value 8.0e-16
Match length 56
% identity 70
NCBI Description (AC006282) hypothetical protein [Arabidopsis thaliana]

Seq. No. 300917
Seq. ID LIB83-009-Q1-E1-E3
Method BLASTN
NCBI GI g2668741

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BLAST score	124
E value	2.0e-63
Match length	244
% identity	88
NCBI Description	Zea mays glycine-rich RNA binding protein (GRP) mRNA, complete cds
Seq. No.	300918
Seq. ID	LIB83-009-Q1-E1-G8
Method	BLASTN
NCBI GI	g4336609
BLAST score	311
E value	1.0e-175
Match length	376
% identity	96
NCBI Description	Zea mays sigma factor (sig3) mRNA, nuclear gene encoding chloroplast protein, complete cds
Seq. No.	300919
Seq. ID	LIB83-009-Q1-E1-H9
Method	BLASTN
NCBI GI	g2326946
BLAST score	55
E value	4.0e-22
Match length	126
% identity	93
NCBI Description	Z. mays mRNA for chlorophyll a/b-binding protein CP29
Seq. No.	300920
Seq. ID	LIB83-010-Q1-E1-A11
Method	BLASTX
NCBI GI	g1707364
BLAST score	144
E value	4.0e-11
Match length	50
% identity	76
NCBI Description	(X94626) AATP2 [Arabidopsis thaliana]
Seq. No.	300921
Seq. ID	LIB83-010-Q1-E1-A5
Method	BLASTX
NCBI GI	g3643599
BLAST score	540
E value	2.0e-55
Match length	137
% identity	74
NCBI Description	(AC005395) putative tryptophanyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.	300922
Seq. ID	LIB83-010-Q1-E1-F4
Method	BLASTX
NCBI GI	g3252866
BLAST score	189
E value	3.0e-15
Match length	74
% identity	61

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NCBI Description (AF033535) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 300923
Seq. ID LIB83-010-Q1-E1-G7
Method BLASTX
NCBI GI g2244996
BLAST score 191
E value 2.0e-14
Match length 44
% identity 77
NCBI Description (Z97341) similarity to a membrane-associated salt-inducible protein [Arabidopsis thaliana]

Seq. No. 300924
Seq. ID LIB83-011-Q1-E1-A11
Method BLASTX
NCBI GI g2088651
BLAST score 232
E value 2.0e-19
Match length 118
% identity 47
NCBI Description (AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No. 300925
Seq. ID LIB83-011-Q1-E1-A4
Method BLASTX
NCBI GI g1170660
BLAST score 255
E value 5.0e-22
Match length 79
% identity 65
NCBI Description MEVALONATE KINASE (MK) >gi_541880_pir_S42088 mevalonate kinase (EC 2.7.1.36) - Arabidopsis thaliana
>gi_456614_emb_CAA54820_ (X77793) mevalonate kinase [Arabidopsis thaliana]

Seq. No. 300926
Seq. ID LIB83-011-Q1-E1-B1
Method BLASTX
NCBI GI g549986
BLAST score 185
E value 2.0e-22
Match length 78
% identity 72
NCBI Description (U13149) possible apospory-associated protein [Pennisetum ciliare]

Seq. No. 300927
Seq. ID LIB83-011-Q1-E1-D9
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 8.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

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Seq. No. 300928
Seq. ID LIB83-011-Q1-E1-F4
Method BLASTX
NCBI GI g3608137
BLAST score 182
E value 2.0e-13
Match length 73
% identity 48
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 300929
Seq. ID LIB83-011-Q1-E1-F6
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 300930
Seq. ID LIB83-011-Q1-E1-F8
Method BLASTX
NCBI GI g1653230
BLAST score 158
E value 1.0e-10
Match length 55
% identity 60
NCBI Description (D90912) hypothetical protein [Synechocystis sp.]

Seq. No. 300931
Seq. ID LIB83-011-Q1-E1-G11
Method BLASTX
NCBI GI g3426035
BLAST score 153
E value 4.0e-10
Match length 45
% identity 62
NCBI Description (AC005168) putative ripening-associated protein [Arabidopsis thaliana]

Seq. No. 300932
Seq. ID LIB83-012-Q1-E1-A7
Method BLASTX
NCBI GI g1655536
BLAST score 160
E value 5.0e-11
Match length 69
% identity 48
NCBI Description (Y09095) chloride channel [Arabidopsis thaliana]
>gi_1742957_emb_CAA96059 (Z71447) CLC-c chloride channel protein [Arabidopsis thaliana]

Seq. No. 300933
Seq. ID LIB83-012-Q1-E1-B4
Method BLASTX

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NCBI GI g4557657
BLAST score 165
E value 2.0e-11
Match length 101
% identity 35
NCBI Description immature colon carcinoma transcript 1
>gi_2136011_pir_S63540 protein DS 1, 24K - human
>gi_1045059_emb_CAA57387_ (X81788) ICT1 protein [Homo sapiens]

Seq. No. 300934
Seq. ID LIB83-012-Q1-E1-C5
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 300935
Seq. ID LIB83-012-Q1-E1-C9
Method BLASTX
NCBI GI g2224810
BLAST score 394
E value 2.0e-38
Match length 105
% identity 70
NCBI Description (Z97022) cysteine proteinase [Hordeum vulgare]

Seq. No. 300936
Seq. ID LIB83-012-Q1-E1-D6
Method BLASTX
NCBI GI g1323748
BLAST score 240
E value 3.0e-20
Match length 122
% identity 47
NCBI Description (U32430) thiol protease [Triticum aestivum]

Seq. No. 300937
Seq. ID LIB83-012-Q1-E1-F7
Method BLASTX
NCBI GI g2760836
BLAST score 191
E value 2.0e-14
Match length 75
% identity 51
NCBI Description (AC003105) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 300938
Seq. ID LIB83-012-Q1-E1-G1
Method BLASTX
NCBI GI g3451473
BLAST score 146
E value 3.0e-09

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Match length 44
% identity 57
NCBI Description (AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces pombe]

Seq. No. 300939
Seq. ID LIB83-012-Q1-E1-G10
Method BLASTX
NCBI GI g4467128
BLAST score 221
E value 4.0e-18
Match length 112
% identity 46
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 300940
Seq. ID LIB83-013-Q1-E1-A3
Method BLASTX
NCBI GI g2213611
BLAST score 155
E value 3.0e-10
Match length 115
% identity 30
NCBI Description (AC000103) F21J9.5 [Arabidopsis thaliana]

Seq. No. 300941
Seq. ID LIB83-013-Q1-E1-B8
Method BLASTX
NCBI GI g3608412
BLAST score 369
E value 2.0e-35
Match length 118
% identity 59
NCBI Description (AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum]

Seq. No. 300942
Seq. ID LIB83-013-Q1-E1-B9
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 4.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 300943
Seq. ID LIB83-013-Q1-E1-D5
Method BLASTX
NCBI GI g1170949
BLAST score 158
E value 1.0e-10
Match length 105
% identity 34
NCBI Description SERINE/THREONINE-PROTEIN KINASE MHK >gi_481207_pir_S38327
protein kinase - Arabidopsis thaliana >gi_166811 (L07249)
protein kinase [Arabidopsis thaliana]

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Seq. No. 300944
Seq. ID LIB83-013-Q1-E1-E10
Method BLASTX
NCBI GI g3201680
BLAST score 246
E value 4.0e-21
Match length 90
% identity 57
NCBI Description (AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No. 300945
Seq. ID LIB83-013-Q1-E1-E11
Method BLASTX
NCBI GI g2809246
BLAST score 363
E value 1.0e-34
Match length 119
% identity 56
NCBI Description (AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No. 300946
Seq. ID LIB83-013-Q1-E1-E12
Method BLASTN
NCBI GI g168527
BLAST score 130
E value 4.0e-67
Match length 144
% identity 98
NCBI Description Maize NADP-dependent malic enzyme (Me1) mRNA, complete cds

Seq. No. 300947
Seq. ID LIB83-013-Q1-E1-F6
Method BLASTX
NCBI GI g1497987
BLAST score 548
E value 2.0e-56
Match length 133
% identity 79
NCBI Description (U62798) SCARECROW [Arabidopsis thaliana]

Seq. No. 300948
Seq. ID LIB83-013-Q1-E1-H4
Method BLASTX
NCBI GI g2961383
BLAST score 216
E value 1.0e-17
Match length 46
% identity 85
NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No. 300949
Seq. ID LIB83-014-Q1-E1-B8
Method BLASTX
NCBI GI g3212866
BLAST score 153
E value 5.0e-10

EST Database

Match length	64
% identity	53
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.	300950
Seq. ID	LIB83-014-Q1-E1-C5
Method	BLASTX
NCBI GI	g4262146
BLAST score	154
E value	4.0e-10
Match length	111
% identity	32
NCBI Description	(AC005275) predicted protein of unknown function [Arabidopsis thaliana]
Seq. No.	300951
Seq. ID	LIB83-014-Q1-E1-C8
Method	BLASTX
NCBI GI	g132918
BLAST score	202
E value	8.0e-16
Match length	56
% identity	79
NCBI Description	50S RIBOSOMAL PROTEIN L35, CHLOROPLAST PRECURSOR (CL35) >gi_81486_pir_A36107 ribosomal protein L35 precursor, chloroplast - spinach >gi_170139 (M60449) ribosomal protein L35 [Spinacia oleracea]
Seq. No.	300952
Seq. ID	LIB83-014-Q1-E1-D6
Method	BLASTN
NCBI GI	g1159878
BLAST score	48
E value	7.0e-18
Match length	80
% identity	90
NCBI Description	A.fatua mRNA for DNA-binding protein (clone ABF2)
Seq. No.	300953
Seq. ID	LIB83-014-Q1-E1-D8
Method	BLASTX
NCBI GI	g4115388
BLAST score	488
E value	3.0e-49
Match length	133
% identity	68
NCBI Description	(AC005967) putative prolylcarboxypeptidase [Arabidopsis thaliana]
Seq. No.	300954
Seq. ID	LIB83-014-Q1-E1-E11
Method	BLASTX
NCBI GI	g4099921
BLAST score	209
E value	9.0e-17
Match length	72
% identity	54

NCBI Description (U91982) EREBP-3 homolog [Stylosanthes hamata]
Seq. No. 300955
Seq. ID LIB83-014-Q1-E1-E2
Method BLASTX
NCBI GI g4376637
BLAST score 195
E value 5.0e-15
Match length 134
% identity 34
NCBI Description (AE001620) tyrosyl tRNA Synthetase [Chlamydia pneumoniae]
Seq. No. 300956
Seq. ID LIB83-015-Q1-E1-A11
Method BLASTX
NCBI GI g2642158
BLAST score 292
E value 2.0e-26
Match length 79
% identity 68
NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No. 300957
Seq. ID LIB83-015-Q1-E1-C6
Method BLASTX
NCBI GI g825756
BLAST score 157
E value 2.0e-10
Match length 71
% identity 51
NCBI Description (U12391) beta-galactosidase alpha peptide [Cloning vector pSport2]
Seq. No. 300958
Seq. ID LIB83-015-Q1-E1-C8
Method BLASTX
NCBI GI g3334150
BLAST score 146
E value 3.0e-09
Match length 43
% identity 67
NCBI Description MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR
(MG-PROTOPORPHYRIN IX CHELATASE) >gi_2129847_pir_JC4312
chlorophyll magnesium chelatase (EC 4.99.-.-) - soybean
chloroplast >gi_1732469_dbj_BAA08291_ (D45857) Mg chelatase
subunit (46 kD) [Glycine max]
Seq. No. 300959
Seq. ID LIB83-015-Q1-E1-D11
Method BLASTN
NCBI GI g296593
BLAST score 52
E value 3.0e-20
Match length 72
% identity 93
NCBI Description H. vulgare pZE40 gene

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Seq. No.	300960
Seq. ID	LIB83-015-Q1-E1-G12
Method	BLASTX
NCBI GI	g602292
BLAST score	217
E value	1.0e-17
Match length	93
% identity	54
NCBI Description	(U17987) RCH2 protein [Brassica napus]
Seq. No.	300961
Seq. ID	LIB83-015-Q1-E1-G6
Method	BLASTX
NCBI GI	g2406563
BLAST score	356
E value	8.0e-34
Match length	139
% identity	18
NCBI Description	(U62897) carboxypeptidase D precursor [Rattus norvegicus]
Seq. No.	300962
Seq. ID	LIB83-015-Q1-E1-H1
Method	BLASTX
NCBI GI	g3355474
BLAST score	284
E value	2.0e-25
Match length	92
% identity	59
NCBI Description	(AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.	300963
Seq. ID	LIB83-016-Q1-E1-C1
Method	BLASTX
NCBI GI	g2213632
BLAST score	498
E value	2.0e-50
Match length	127
% identity	67
NCBI Description	(AC000103) F21J9.24 [Arabidopsis thaliana]
Seq. No.	300964
Seq. ID	LIB83-016-Q1-E1-C2
Method	BLASTX
NCBI GI	g483410
BLAST score	195
E value	6.0e-15
Match length	74
% identity	57
NCBI Description	(L01496) calmodulin-binding protein [Zea mays]
Seq. No.	300965
Seq. ID	LIB83-016-Q1-E1-H6
Method	BLASTX
NCBI GI	g1838961
BLAST score	284
E value	2.0e-25
Match length	112

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% identity	62
NCBI Description	(Y10994) acyl carrier protein [Casuarina glauca]
Seq. No.	300966
Seq. ID	LIB84-001-Q1-E1-A4
Method	BLASTX
NCBI GI	g4056456
BLAST score	258
E value	2.0e-22
Match length	74
% identity	70
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]
Seq. No.	300967
Seq. ID	LIB84-001-Q1-E1-E9
Method	BLASTX
NCBI GI	g3024440
BLAST score	217
E value	4.0e-20
Match length	76
% identity	72
NCBI Description	PROTEASOME DELTA CHAIN PRECURSOR (MULTICATALYTIC ENDOPEPTIDASE COMPLEX DELTA CHAIN) >gi_1743356_emb_CAA70699_ (Y09505) proteasome delta subunit [Nicotiana tabacum]
Seq. No.	300968
Seq. ID	LIB84-001-Q1-E1-G11
Method	BLASTX
NCBI GI	g2673913
BLAST score	200
E value	2.0e-15
Match length	128
% identity	37
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]
Seq. No.	300969
Seq. ID	LIB84-003-Q1-E1-B11
Method	BLASTX
NCBI GI	g4139264
BLAST score	157
E value	2.0e-13
Match length	69
% identity	61
NCBI Description	(AF111812) actin [Brassica napus]
Seq. No.	300970
Seq. ID	LIB84-003-Q1-E1-B7
Method	BLASTX
NCBI GI	g1652591
BLAST score	201
E value	1.0e-15
Match length	66
% identity	56

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NCBI Description (D90906) chloroplast import-associated channel IAP75
[Synechocystis sp.]

Seq. No. 300971
Seq. ID LIB84-003-Q1-E1-C10
Method BLASTX
NCBI GI g115771
BLAST score 412
E value 1.0e-40
Match length 80
% identity 93

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
(CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll
a/b-binding protein precursor - maize
>gi_22224_emb_CAA32900 (X14794) chlorophyll a/b-binding
preprotein (AA 1 - 262) [Zea mays]

Seq. No. 300972
Seq. ID LIB84-003-Q1-E1-D12
Method BLASTX
NCBI GI g3335355
BLAST score 162
E value 1.0e-11
Match length 45
% identity 24

NCBI Description (AC004512) Match to polyubiquitin DNA gb_L05401 from A.
thaliana. Contains insertion of mitochondrial NADH
dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene
with an expressed insert. EST gb_AA586248 comes from this
region. [Arabi

Seq. No. 300973
Seq. ID LIB84-003-Q1-E1-D2
Method BLASTX
NCBI GI g4220592
BLAST score 364
E value 9.0e-35
Match length 141
% identity 53

NCBI Description (AB010086) nicotianamine synthase 1 [Hordeum vulgare]

Seq. No. 300974
Seq. ID LIB84-003-Q1-E1-E6
Method BLASTX
NCBI GI g4455287
BLAST score 184
E value 7.0e-14
Match length 61
% identity 61

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 300975
Seq. ID LIB84-003-Q1-E1-F10
Method BLASTN
NCBI GI g12474
BLAST score 114
E value 3.0e-57

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Match length 282
% identity 86
NCBI Description Zea mays chloroplast tV-UAC gene for transfer RNA-Val (UAC)

Seq. No. 300976
Seq. ID LIB84-003-Q1-E1-G11
Method BLASTX
NCBI GI g3377950
BLAST score 326
E value 2.0e-30
Match length 113
% identity 55
NCBI Description (AJ009830) cysteine proteinase precursor, AN11 [Ananas comosus]

Seq. No. 300977
Seq. ID LIB84-003-Q1-E1-G7
Method BLASTX
NCBI GI g1877221
BLAST score 267
E value 2.0e-23
Match length 109
% identity 51
NCBI Description (Z83834) Mlo [Hordeum vulgare] >gi_2894377_emb_CAA74909.1_(Y14573) Mlo protein [Hordeum vulgare]

Seq. No. 300978
Seq. ID LIB84-003-Q1-E1-H10
Method BLASTN
NCBI GI g902200
BLAST score 156
E value 2.0e-82
Match length 354
% identity 99
NCBI Description Z.mays complete chloroplast genome

Seq. No. 300979
Seq. ID LIB84-004-Q1-E1-A2
Method BLASTX
NCBI GI g132147
BLAST score 326
E value 2.0e-30
Match length 90
% identity 72
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi_68089_pir_RKZMS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - maize >gi_22474_emb_CAA29784_ (X06535) ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi_359512_prf_1312317A ribulosebisphosphate carboxylase [Zea mays]

Seq. No. 300980
Seq. ID LIB84-004-Q1-E1-A5
Method BLASTX

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NCBI GI g3024762
BLAST score 166
E value 4.0e-16
Match length 130
% identity 41
NCBI Description TRNA PSEUDOURIDINE SYNTHASE B (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE) >gi_2624315_emb_CAA15588_ (AL008967)
truB:[Mycobacterium tuberculosis]

Seq. No. 300981
Seq. ID LIB84-004-Q1-E1-C2
Method BLASTX
NCBI GI g2668742
BLAST score 432
E value 1.0e-42
Match length 86
% identity 98
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 300982
Seq. ID LIB84-004-Q1-E1-C5
Method BLASTX
NCBI GI g1352200
BLAST score 185
E value 2.0e-14
Match length 69
% identity 75
NCBI Description CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
>gi_480909_pir_S37497 triose
phosphate/3-phosphoglycerate/phosphate translocator - maize
>gi_405635_emb_CAA81349_ (Z26595) triose
phosphate/phosphate translocator [Zea mays]

Seq. No. 300983
Seq. ID LIB84-004-Q1-E1-D9
Method BLASTN
NCBI GI g19090
BLAST score 46
E value 1.0e-16
Match length 98
% identity 87
NCBI Description H.vulgare PsAG mRNA

Seq. No. 300984
Seq. ID LIB84-004-Q1-E1-F3
Method BLASTN
NCBI GI g596077
BLAST score 114
E value 2.0e-57
Match length 298
% identity 85
NCBI Description Zea mays thiamine biosynthetic enzyme (thil-1) mRNA,
complete cds

Seq. No. 300985
Seq. ID LIB84-004-Q1-E1-F7

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Method	BLASTX
NCBI GI	g3152613
BLAST score	271
E value	7.0e-24
Match length	127
% identity	41
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]
Seq. No.	300986
Seq. ID	LIB84-004-Q1-E1-G12
Method	BLASTX
NCBI GI	g3925363
BLAST score	379
E value	1.0e-43
Match length	127
% identity	76
NCBI Description	(AF067961) homeodomain protein [Malus domestica]
Seq. No.	300987
Seq. ID	LIB84-005-Q1-E1-E10
Method	BLASTX
NCBI GI	g4508077
BLAST score	177
E value	2.0e-13
Match length	49
% identity	65
NCBI Description	(AC005882) 62114 [Arabidopsis thaliana]
Seq. No.	300988
Seq. ID	LIB84-005-Q1-E1-F12
Method	BLASTX
NCBI GI	g4455309
BLAST score	223
E value	3.0e-18
Match length	70
% identity	61
NCBI Description	(AL035528) hypothetical protein [Arabidopsis thaliana]
Seq. No.	300989
Seq. ID	LIB84-005-Q1-E1-F7
Method	BLASTX
NCBI GI	g4115536
BLAST score	345
E value	1.0e-32
Match length	121
% identity	57
NCBI Description	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
Seq. No.	300990
Seq. ID	LIB84-006-Q1-E1-A3
Method	BLASTX
NCBI GI	g1800219
BLAST score	327
E value	7.0e-31
Match length	81
% identity	78

NCBI Description (U56731) phytochrome C [Sorghum bicolor]

Seq. No. 300991
Seq. ID LIB84-006-Q1-E1-B3
Method BLASTX
NCBI GI g4454472
BLAST score 169
E value 2.0e-12
Match length 54
% identity 57
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 300992
Seq. ID LIB84-006-Q1-E1-C3
Method BLASTX
NCBI GI g1174745
BLAST score 262
E value 4.0e-23
Match length 73
% identity 73
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
>gi_1363523_pir_S53761 triose-phosphate isomerase (EC
5.3.1.1) precursor, chloroplast - rye
>gi_609262_emb_CAA83533 (Z32521) triosephosphate isomerase
[Secale cereale] >gi_1095494_prf_2109226B triosephosphate
isomerase [Secale cereale]

Seq. No. 300993
Seq. ID LIB84-006-Q1-E1-E6
Method BLASTX
NCBI GI g4006872
BLAST score 266
E value 2.0e-23
Match length 95
% identity 52
NCBI Description (Z99707) methionyl aminopeptidase-like protein [Arabidopsis
thaliana]

Seq. No. 300994
Seq. ID LIB84-008-Q1-E1-A3
Method BLASTX
NCBI GI g3290006
BLAST score 315
E value 4.0e-29
Match length 73
% identity 77
NCBI Description (U82201) pathogenesis related protein-5 [Zea mays]

Seq. No. 300995
Seq. ID LIB84-008-Q1-E1-A8
Method BLASTX
NCBI GI g2505870
BLAST score 333
E value 4.0e-31
Match length 76
% identity 82
NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]

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Seq. No.	300996
Seq. ID	LIB84-008-Q1-E1-A9
Method	BLASTX
NCBI GI	g2244876
BLAST score	222
E value	9.0e-19
Match length	112
% identity	50
NCBI Description	(Z97338) hypothetical protein [Arabidopsis thaliana]
Seq. No.	300997
Seq. ID	LIB84-008-Q1-E1-B12
Method	BLASTN
NCBI GI	g902200
BLAST score	78
E value	8.0e-36
Match length	141
% identity	90
NCBI Description	Z.mays complete chloroplast genome
Seq. No.	300998
Seq. ID	LIB84-008-Q1-E1-G11
Method	BLASTX
NCBI GI	g4185141
BLAST score	410
E value	4.0e-40
Match length	122
% identity	67
NCBI Description	(AC005724) putative calmodulin-binding protein [Arabidopsis thaliana]
Seq. No.	300999
Seq. ID	LIB84-008-Q1-E1-G4
Method	BLASTX
NCBI GI	g4191779
BLAST score	259
E value	2.0e-22
Match length	132
% identity	44
NCBI Description	(AC005917) putative recA protein [Arabidopsis thaliana]
Seq. No.	301000
Seq. ID	LIB84-010-Q1-E1-C4
Method	BLASTN
NCBI GI	g5091496
BLAST score	44
E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence
Seq. No.	301001
Seq. ID	LIB84-010-Q1-E1-D7
Method	BLASTN
NCBI GI	g998429

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BLAST score 36
E value 9.0e-11
Match length 64
% identity 89
NCBI Description GRF1-general regulatory factor [Zea mays, XL80, Genomic, 5348 nt]

Seq. No. 301002
Seq. ID LIB84-011-Q1-E1-C8
Method BLASTX
NCBI GI g2246378
BLAST score 220
E value 7.0e-18
Match length 87
% identity 51
NCBI Description (Z86094) plastid protein [Arabidopsis thaliana]

Seq. No. 301003
Seq. ID LIB84-011-Q1-E1-F9
Method BLASTX
NCBI GI g4512684
BLAST score 160
E value 6.0e-11
Match length 76
% identity 47
NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]
>gi_4559324_gb AAD22986.1 AC007087_5 (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 301004
Seq. ID LIB84-012-Q1-E1-C9
Method BLASTN
NCBI GI g236729
BLAST score 69
E value 8.0e-31
Match length 126
% identity 89
NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]

Seq. No. 301005
Seq. ID LIB84-012-Q1-E12-D5
Method BLASTN
NCBI GI g2668739
BLAST score 78
E value 8.0e-36
Match length 192
% identity 93
NCBI Description Zea mays translation initiation factor GOS2 (TIF) mRNA, complete cds

Seq. No. 301006
Seq. ID LIB84-012-Q1-E12-E4
Method BLASTX
NCBI GI g417103
BLAST score 184
E value 5.0e-16
Match length 89

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% identity 57
NCBI Description HISTONE H3.2, MINOR >gi_282871_pir_S24346 histone H3.3-like protein - *Arabidopsis thaliana*
>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [*Arabidopsis thaliana*] >gi_404825_emb_CAA42958_ (X60429)
histone H3.3 like protein [*Arabidopsis thaliana*] >gi_488563 (U09458) histone H3.2 [*Medicago sativa*] >gi_488567 (U09460)
histone H3.2 [*Medicago sativa*] >gi_488569 (U09461) histone H3.2 [*Medicago sativa*] >gi_488575 (U09464) histone H3.2 [*Medicago sativa*] >gi_488577 (U09465) histone H3.2 [*Medicago sativa*] >gi_510911_emb_CAA56153_ (X79714) histone H3 [*Lolium temulentum*] >gi_1435157_emb_CAA58445_ (X83422)
histone H3 variant H3.3 [*Lycopersicon esculentum*] >gi_2558944 (AF024716) histone 3 [*Gossypium hirsutum*] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [*Nicotiana tabacum*] >gi_3885890 (AF093633) histone H3 [*Oryza sativa*] >gi_4038469_gb AAC97380_ (AF109910) histone H3 [*Portereria coarctata*] >gi_4490754_emb CAB38916.1_ (AL035708) histone H3.3 [*Arabidopsis thaliana*] >gi_4490755_emb CAB38917.1_ (AL035708) Histon H3 [*Arabidopsis thaliana*]

Seq. No. 301007
Seq. ID LIB84-013-Q1-E1-D10
Method BLASTX
NCBI GI g4262183
BLAST score 283
E value 2.0e-25
Match length 71
% identity 77
NCBI Description (AC005508) 51434 [*Arabidopsis thaliana*]

Seq. No. 301008
Seq. ID LIB84-013-Q1-E1-F2
Method BLASTX
NCBI GI g3281861
BLAST score 182
E value 2.0e-13
Match length 116
% identity 32
NCBI Description (AL031004) putative protein [*Arabidopsis thaliana*]

Seq. No. 301009
Seq. ID LIB84-013-Q1-E1-G11
Method BLASTX
NCBI GI g3643605
BLAST score 176
E value 9.0e-13
Match length 67
% identity 52
NCBI Description (AC005395) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 301010
Seq. ID LIB84-013-Q1-E1-G4
Method BLASTX
NCBI GI g3650028
BLAST score 375
E value 4.0e-36

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Match length 104
% identity 62
NCBI Description (AC005396) putative 22 kDa peroxisomal membrane protein [Arabidopsis thaliana]

Seq. No. 301011
Seq. ID LIB84-013-Q1-E1-H10
Method BLASTX
NCBI GI g2832643
BLAST score 300
E value 2.0e-27
Match length 93
% identity 61
NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301012
Seq. ID LIB84-013-Q1-E1-H3
Method BLASTX
NCBI GI g1653665
BLAST score 219
E value 8.0e-18
Match length 130
% identity 37
NCBI Description (D90915) peptide chain release factor [Synechocystis sp.]

Seq. No. 301013
Seq. ID LIB84-013-Q1-E1-H4
Method BLASTX
NCBI GI g4099914
BLAST score 216
E value 2.0e-17
Match length 83
% identity 54
NCBI Description (U91857) ethylene-responsive element binding protein homolog [Stylosanthes hamata]

Seq. No. 301014
Seq. ID LIB84-013-Q1-E1-H6
Method BLASTX
NCBI GI g115786
BLAST score 333
E value 3.0e-31
Match length 82
% identity 79
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays]

Seq. No. 301015
Seq. ID LIB84-014-Q1-E1-A1
Method BLASTN
NCBI GI g2062691
BLAST score 37
E value 2.0e-11
Match length 37
% identity 100

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Q U T P R T C D E G E

NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete cds

Seq. No. 301016
Seq. ID LIB84-014-Q1-E1-C6
Method BLASTX
NCBI GI g2494893
BLAST score 392
E value 5.0e-38
Match length 100
% identity 64
NCBI Description CHROMATIN ASSEMBLY FACTOR 1 P48 SUBUNIT (CAF-1 P48 SUBUNIT)
(RETINOBLASTOMA BINDING PROTEIN P48)
(RETINOBLASTOMA-BINDING PROTEIN 4) >gi_2137734_pir_I49366
retinoblastoma-binding protein mRbAp48 - mouse >gi_1016275
(U35141) retinoblastoma-binding protein mRbAp48 [Mus
musculus] >gi_1585656_prf_2201425A retinoblastoma-binding
protein [Mus musculus]

Seq. No. 301017
Seq. ID LIB84-014-Q1-E1-D9
Method BLASTN
NCBI GI g4176423
BLAST score 53
E value 5.0e-21
Match length 73
% identity 93
NCBI Description Oryza sativa rpl12-2 gene for chloroplast ribosomal protein
L12, complete cds

Seq. No. 301018
Seq. ID LIB84-014-Q1-E1-G7
Method BLASTN
NCBI GI g2446997
BLAST score 111
E value 1.0e-55
Match length 292
% identity 91
NCBI Description Zea mays FAD7 gene for fatty acid desaturase, complete cds

Seq. No. 301019
Seq. ID LIB84-015-Q1-E1-B6
Method BLASTX
NCBI GI g4582468
BLAST score 209
E value 1.0e-32
Match length 101
% identity 76
NCBI Description (AC007071) putative 40S ribosomal protein; contains
C-terminal domain [Arabidopsis thaliana]

Seq. No. 301020
Seq. ID LIB84-015-Q1-E1-C4
Method BLASTX
NCBI GI g3377762
BLAST score 390
E value 8.0e-38

Match length 129
% identity 63
NCBI Description (AF079850) nodule-enhanced malate dehydrogenase [Pisum sativum]

Seq. No. 301021
Seq. ID LIB84-015-Q1-E1-C6
Method BLASTX
NCBI GI g3738329
BLAST score 381
E value 9.0e-37
Match length 95
% identity 81
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 301022
Seq. ID LIB84-015-Q1-E1-F6
Method BLASTX
NCBI GI g2664210
BLAST score 380
E value 1.0e-36
Match length 79
% identity 90
NCBI Description (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 301023
Seq. ID LIB84-015-Q1-E1-H5
Method BLASTX
NCBI GI g1076800
BLAST score 340
E value 5.0e-32
Match length 118
% identity 59
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme - maize >gi_600116_emb_CAA84406 (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi_1096503_prf_2111423A ascorbate peroxidase [Zea mays]

Seq. No. 301024
Seq. ID LIB84-016-Q1-E1-E8
Method BLASTX
NCBI GI g2459446
BLAST score 264
E value 5.0e-23
Match length 135
% identity 43
NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No. 301025
Seq. ID LIB84-016-Q1-E1-F2
Method BLASTX
NCBI GI g115815
BLAST score 518
E value 6.0e-53
Match length 105

% identity 90
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
(CAB-M9) (LHCP) >gi_100866_pir_S13098 chlorophyll
a/b-binding protein precursor - maize
>gi_22355_emb_CAA39376_ (X55892) light-harvesting
chlorophyll a/b binding protein [Zea mays]

Seq. No. 301026
Seq. ID LIB84-016-Q1-E1-G9
Method BLASTN
NCBI GI g607147
BLAST score 54
E value 4.0e-22
Match length 66
% identity 95
NCBI Description P.abies (L.) Karst. Lhcbl*1 mRNA for light-harvesting
chlorophyll a/b-binding protein

Seq. No. 301027
Seq. ID LIB84-017-Q1-E1-A6
Method BLASTX
NCBI GI g2425066
BLAST score 153
E value 1.0e-10
Match length 61
% identity 49
NCBI Description (AF019147) cysteine proteinase Mir3 [Zea mays]

Seq. No. 301028
Seq. ID LIB84-017-Q1-E1-B6
Method BLASTX
NCBI GI g2407279
BLAST score 213
E value 4.0e-17
Match length 101
% identity 50
NCBI Description (AF017362) aldolase [Oryza sativa]

Seq. No. 301029
Seq. ID LIB84-017-Q1-E1-C11
Method BLASTN
NCBI GI g22324
BLAST score 42
E value 9.0e-15
Match length 110
% identity 85
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No. 301030
Seq. ID LIB84-017-Q1-E1-F2
Method BLASTX
NCBI GI g4455248
BLAST score 271
E value 7.0e-24
Match length 77
% identity 74
NCBI Description (AL035523) acyl carrier-like protein [Arabidopsis thaliana]

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Seq. No. 301031
Seq. ID LIB84-021-Q1-E1-A8
Method BLASTN
NCBI GI g4140643
BLAST score 52
E value 2.0e-20
Match length 108
% identity 87
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 301032
Seq. ID LIB84-021-Q1-E1-B1
Method BLASTX
NCBI GI g2828292
BLAST score 411
E value 2.0e-40
Match length 121
% identity 68
NCBI Description (AL021687) neoxanthin cleavage enzyme-like protein [Arabidopsis thaliana]

Seq. No. 301033
Seq. ID LIB84-021-Q1-E1-B5
Method BLASTX
NCBI GI g4505337
BLAST score 146
E value 8.0e-10
Match length 69
% identity 52
NCBI Description nucleotide binding protein 1 (E.coli MinD like)
>gi_1709232_sp_P53384_NBP_HUMAN NUCLEOTIDE-BINDING PROTEIN (NBP) >gi_1082661_pir_JC4010 nucleotide-binding protein - human >gi_515644 (U01833) putative nucleotide-binding protein [Homo sapiens]

Seq. No. 301034
Seq. ID LIB84-021-Q1-E1-F12
Method BLASTX
NCBI GI g531467
BLAST score 304
E value 7.0e-28
Match length 119
% identity 52
NCBI Description (U12977) similar to glycerol-3-phosphate-dehydrogenase, GenBank Accession Number U00039, and Swiss-Prot Accession Number P13706 [Pseudomonas lemoignei]

Seq. No. 301035
Seq. ID LIB84-022-Q1-E1-G12
Method BLASTX
NCBI GI g2632254
BLAST score 396
E value 8.0e-39
Match length 95
% identity 83

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NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No. 301036
Seq. ID LIB84-023-Q1-E1-B3
Method BLASTX
NCBI GI g2239260
BLAST score 533
E value 1.0e-54
Match length 109
% identity 95

NCBI Description (Y13734) cinnamoyl CoA reductase [Zea mays]

Seq. No. 301037
Seq. ID LIB84-023-Q1-E1-B4
Method BLASTX
NCBI GI g3738333
BLAST score 141
E value 3.0e-11
Match length 63
% identity 53

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 301038
Seq. ID LIB84-023-Q1-E1-B6
Method BLASTN
NCBI GI g2062705
BLAST score 33
E value 3.0e-09
Match length 41
% identity 95

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 301039
Seq. ID LIB84-023-Q1-E1-D5
Method BLASTX
NCBI GI g4587589
BLAST score 242
E value 1.0e-20
Match length 107
% identity 45

NCBI Description (AC007232) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301040
Seq. ID LIB84-023-Q1-E1-E2
Method BLASTX
NCBI GI g4539437
BLAST score 304
E value 7.0e-28
Match length 111
% identity 56

NCBI Description (AL049523) putative protein [Arabidopsis thaliana]

Seq. No. 301041
Seq. ID LIB84-023-Q1-E1-E6
Method BLASTX
NCBI GI g1658313
BLAST score 397

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E value	9.0e-39
Match length	91
% identity	45
NCBI Description	(Y08987) osr40g2 [Oryza sativa]
Seq. No.	301042
Seq. ID	LIB84-023-Q1-E1-F11
Method	BLASTX
NCBI GI	g3873752
BLAST score	185
E value	7.0e-14
Match length	85
% identity	46
NCBI Description	(Z66519) similar to oxalyl-CoA decarboxylase; cDNA EST EMBL:D71591 comes from this gene; cDNA EST EMBL:D66565 comes from this gene; cDNA EST EMBL:D73312 comes from this gene; cDNA EST EMBL:D70388 comes from this gene; cDNA EST
Seq. No.	301043
Seq. ID	LIB84-024-Q1-E1-D1
Method	BLASTN
NCBI GI	g433459
BLAST score	104
E value	1.0e-51
Match length	192
% identity	90
NCBI Description	Z.mays mRNA for ferredoxin-thioredoxin reductase
Seq. No.	301044
Seq. ID	LIB84-024-Q1-E1-E4
Method	BLASTX
NCBI GI	g1431629
BLAST score	151
E value	7.0e-10
Match length	56
% identity	46
NCBI Description	(X99348) pectinacetylesterase precursor [Vigna radiata]
Seq. No.	301045
Seq. ID	LIB84-024-Q1-E1-E5
Method	BLASTX
NCBI GI	g115771
BLAST score	567
E value	1.0e-58
Match length	109
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll a/b-binding protein precursor - maize >gi_22224_emb CAA32900 (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]
Seq. No.	301046
Seq. ID	LIB84-024-Q1-E1-G10
Method	BLASTX
NCBI GI	g3522943
BLAST score	336

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E value 1.0e-31
 Match length 83
 % identity 41
 NCBI Description (AC004411) putative p-glycoprotein [Arabidopsis thaliana]

 Seq. No. 301047
 Seq. ID LIB84-024-Q1-E1-G9
 Method BLASTX
 NCBI GI g1708899
 BLAST score 139
 E value 6.0e-09
 Match length 56
 % identity 54
 NCBI Description MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1
 (MAN(9)-ALPHA-MANNOSIDASE) >gi_2133635_pir_S60709 alpha
 1,2 mannosidase precursor - fruit fly (Drosophila
 melanogaster) >gi_840754_emb_CAA57962_ (X82640) alpha 1,2
 mannosidase [Drosophila melanogaster]

 Seq. No. 301048
 Seq. ID LIB84-025-Q1-E1-B12
 Method BLASTX
 NCBI GI g3335060
 BLAST score 342
 E value 1.0e-36
 Match length 100
 % identity 85
 NCBI Description (AF025842) plasma membrane-type calcium ATPase [Arabidopsis
 thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma
 membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

 Seq. No. 301049
 Seq. ID LIB84-025-Q1-E1-B9
 Method BLASTX
 NCBI GI g3643605
 BLAST score 158
 E value 8.0e-11
 Match length 55
 % identity 53
 NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]

 Seq. No. 301050
 Seq. ID LIB84-026-Q1-E1-A11
 Method BLASTN
 NCBI GI g218171
 BLAST score 46
 E value 8.0e-17
 Match length 98
 % identity 87
 NCBI Description Oryza sativa mRNA for type I light-harvesting chlorophyll
 a/b binding protein of photosystem II (LHCPII), complete
 cds

 Seq. No. 301051
 Seq. ID LIB84-026-Q1-E1-B5
 Method BLASTX
 NCBI GI g3293555

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BLAST score 364
E value 8.0e-35
Match length 71
% identity 97
NCBI Description (AF072931) chlorophyll a/b binding protein [Medicago sativa]

Seq. No. 301052
Seq. ID LIB84-026-Q1-E1-B7
Method BLASTX
NCBI GI g115800
BLAST score 430
E value 1.0e-42
Match length 101
% identity 81
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-3) (LHCP) >gi_81771_pir_S01962 chlorophyll a/b-binding protein 3 precursor - soybean >gi_18552_emb_CAA31419_ (X12981) chlorophyll a/b binding preprotein (AA - 32 to 231) [Glycine max]

Seq. No. 301053
Seq. ID LIB84-026-Q1-E1-D1
Method BLASTN
NCBI GI g12429
BLAST score 143
E value 1.0e-74
Match length 247
% identity 90
NCBI Description Maize chloroplast ORF170 and psaA gene

Seq. No. 301054
Seq. ID LIB84-026-Q1-E1-D6
Method BLASTX
NCBI GI g1170029
BLAST score 149
E value 4.0e-27
Match length 99
% identity 77
NCBI Description GLUTAMATE-1-SEMALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) (GLUTAMATE-1-SEMALDEHYDE AMINOTRANSFERASE) (GSA-AT) >gi_100581_pir_A35789 glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - barley >gi_506383 (M31545) glutamate 1-semialdehyde aminotransferase [Hordeum vulgare]

Seq. No. 301055
Seq. ID LIB84-026-Q1-E1-F3
Method BLASTX
NCBI GI g2979559
BLAST score 214
E value 3.0e-17
Match length 45
% identity 89
NCBI Description (AC003680) putative DNA binding protein [Arabidopsis thaliana]

Seq. No. 301056

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Seq. ID	LIB84-026-Q1-E1-H7
Method	BLASTN
NCBI GI	g405634
BLAST score	166
E value	1.0e-88
Match length	238
% identity	93
NCBI Description	Z.mays zmcpt mRNA triose phosphate/phosphate translocator
Seq. No.	301057
Seq. ID	LIB84-027-Q1-E1-B7
Method	BLASTX
NCBI GI	g4056433
BLAST score	164
E value	2.0e-11
Match length	119
% identity	32
NCBI Description	(AC005990) Similar to anter-specific proline-rich protein (CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]
Seq. No.	301058
Seq. ID	LIB84-027-Q1-E1-D7
Method	BLASTN
NCBI GI	g4165327
BLAST score	52
E value	2.0e-20
Match length	80
% identity	91
NCBI Description	Oryza sativa 3-hydroxy-3-methylglutaryl-CoA reductase gene, promoter region and complete cds
Seq. No.	301059
Seq. ID	LIB84-027-Q1-E1-E6
Method	BLASTX
NCBI GI	g4512663
BLAST score	249
E value	2.0e-21
Match length	100
% identity	23
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4544470_gb_AAD22377.1_AC006580_9 (AC006580) hypothetical protein [Arabidopsis thaliana]
Seq. No.	301060
Seq. ID	LIB84-027-Q1-E1-F1
Method	BLASTX
NCBI GI	g4584524
BLAST score	183
E value	1.0e-13
Match length	95
% identity	41
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]
Seq. No.	301061
Seq. ID	LIB84-027-Q1-E1-H10
Method	BLASTX
NCBI GI	g2244926

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BLAST score 178
E value 5.0e-13
Match length 95
% identity 42
NCBI Description (Z97339) glutaredoxin [Arabidopsis thaliana]

Seq. No. 301062
Seq. ID LIB84-027-Q1-E1-H11
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 301063
Seq. ID LIB84-028-Q1-E1-A11
Method BLASTX
NCBI GI g4262236
BLAST score 242
E value 1.0e-20
Match length 70
% identity 67
NCBI Description (AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No. 301064
Seq. ID LIB84-028-Q1-E1-C1
Method BLASTX
NCBI GI g100878
BLAST score 420
E value 1.0e-41
Match length 87
% identity 91
NCBI Description glutamate--ammonia ligase (EC 6.3.1.2) - maize

Seq. No. 301065
Seq. ID LIB84-028-Q1-E1-C10
Method BLASTX
NCBI GI g4585882
BLAST score 271
E value 6.0e-24
Match length 54
% identity 96
NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 301066
Seq. ID LIB84-028-Q1-E1-C2
Method BLASTX
NCBI GI g3004555
BLAST score 372
E value 6.0e-36
Match length 98
% identity 66
NCBI Description (AC003673) similar to salt inducible protein [Arabidopsis

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Seq. No. 301067
Seq. ID LIB84-028-Q1-E1-C9
Method BLASTN
NCBI GI g2062705
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 301068
Seq. ID LIB84-028-Q1-E1-E1
Method BLASTX
NCBI GI g3063710
BLAST score 262
E value 7.0e-23
Match length 123
% identity 48
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 301069
Seq. ID LIB84-028-Q1-E1-E5
Method BLASTX
NCBI GI g1835731
BLAST score 295
E value 8.0e-27
Match length 81
% identity 72
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 301070
Seq. ID LIB84-028-Q1-E1-F1
Method BLASTX
NCBI GI g4582488
BLAST score 504
E value 3.0e-51
Match length 110
% identity 88
NCBI Description (AL021768) putative protein [Arabidopsis thaliana]

Seq. No. 301071
Seq. ID LIB84-028-Q1-E1-F5
Method BLASTX
NCBI GI g3413699
BLAST score 184
E value 9.0e-14
Match length 122
% identity 43
NCBI Description (AC004747) putative heat shock protein [Arabidopsis thaliana]

Seq. No. 301072
Seq. ID LIB84-028-Q1-E1-H7
Method BLASTX
NCBI GI g1352200

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BLAST score	460
E value	4.0e-46
Match length	92
% identity	100
NCBI Description	CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) >gi_480909_pir_S37497 triose phosphate/3-phosphoglycerate/phosphate translocator - maize >gi_405635_emb_CAA81349_ (Z26595) triose phosphate/phosphate translocator [Zea mays]
Seq. No.	301073
Seq. ID	LIB84-029-Q1-E1-A12
Method	BLASTX
NCBI GI	g2501296
BLAST score	174
E value	1.0e-12
Match length	61
% identity	54
NCBI Description	DNA GYRASE SUBUNIT B >gi_1652801_dbj_BAA17720_ (D90908) DNA gyrase B subunit [Synechocystis sp.]
Seq. No.	301074
Seq. ID	LIB84-029-Q1-E1-B8
Method	BLASTN
NCBI GI	g2832242
BLAST score	203
E value	1.0e-110
Match length	329
% identity	91
NCBI Description	Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.	301075
Seq. ID	LIB84-029-Q1-E1-D6
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	4.0e-11
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	301076
Seq. ID	LIB84-029-Q1-E1-D7
Method	BLASTX
NCBI GI	g531829
BLAST score	153
E value	4.0e-10
Match length	45
% identity	67
NCBI Description	(U12390) beta-galactosidase alpha peptide [cloning vector pSport1]
Seq. No.	301077
Seq. ID	LIB84-029-Q1-E1-E3
Method	BLASTX
NCBI GI	g2624328
BLAST score	279

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E value 7.0e-25
Match length 81
% identity 67
NCBI Description (AJ002894) OsGRP2 [Oryza sativa]

Seq. No. 301078
Seq. ID LIB84-029-Q1-E1-F2
Method BLASTX
NCBI GI g2494034
BLAST score 375
E value 4.0e-36
Match length 97
% identity 69
NCBI Description DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi_2129573_pir_S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787) diacylglycerol kinase [Arabidopsis thaliana]

Seq. No. 301079
Seq. ID LIB84-030-Q1-E1-A6
Method BLASTN
NCBI GI g3821780
BLAST score 37
E value 2.0e-11
Match length 37
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 301080
Seq. ID LIB84-030-Q1-E1-B6
Method BLASTX
NCBI GI g4510347
BLAST score 170
E value 5.0e-12
Match length 44
% identity 70
NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301081
Seq. ID LIB84-030-Q1-E1-C12
Method BLASTX
NCBI GI g1835731
BLAST score 244
E value 7.0e-21
Match length 61
% identity 72
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 301082
Seq. ID LIB84-030-Q1-E1-E5
Method BLASTN
NCBI GI g22356
BLAST score 60
E value 2.0e-25
Match length 166
% identity 84
NCBI Description Maize mRNA for light-harvesting chlorophyll a/b binding

protein LHCP

Seq. No. 301083
Seq. ID LIB84-030-Q1-E1-F7
Method BLASTX
NCBI GI g4006848
BLAST score 175
E value 3.0e-13
Match length 48
% identity 62
NCBI Description (AJ131433) selenocysteine methyltransferase [Astragalus bisulcatus]

Seq. No. 301084
Seq. ID LIB84-030-Q1-E1-F9
Method BLASTX
NCBI GI g4586259
BLAST score 462
E value 3.0e-46
Match length 134
% identity 62
NCBI Description (AL049640) hydrolase-like protein [Arabidopsis thaliana]

Seq. No. 301085
Seq. ID LIB84-030-Q1-E1-H12
Method BLASTX
NCBI GI g2501189
BLAST score 141
E value 3.0e-09
Match length 57
% identity 51
NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
>gi_2130146_pir_S61419 thiamine biosynthetic enzyme thi1-1
- maize >gi_596078 (U17350) thiamine biosynthetic enzyme
[Zea mays]

Seq. No. 301086
Seq. ID LIB84-030-Q1-E1-H4
Method BLASTX
NCBI GI g283038
BLAST score 269
E value 1.0e-23
Match length 119
% identity 58
NCBI Description chlorophyll a/b-binding protein (cab-m7) precursor - maize
>gi_22230_emb_CAA37474_(X53398) light harvesting
chlorophyll a /b binding protein [Zea mays]

Seq. No. 301087
Seq. ID LIB84-030-Q1-E1-H5
Method BLASTX
NCBI GI g3269296
BLAST score 419
E value 3.0e-41
Match length 126
% identity 58
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 301088
Seq. ID LIB84-030-Q1-E1-H6
Method BLASTX
NCBI GI g476418
BLAST score 550
E value 1.0e-56
Match length 106
% identity 94
NCBI Description cytochrome c - maize

Seq. No. 301089
Seq. ID LIB84-030-Q1-E1-H8
Method BLASTX
NCBI GI g4490722
BLAST score 178
E value 5.0e-13
Match length 54
% identity 54
NCBI Description (AL035709) 1-aminocyclopropane-1-carboxylate synthase [Arabidopsis thaliana]

Seq. No. 301090
Seq. ID afb700380804.h1
Method BLASTN
NCBI GI g488500
BLAST score 200
E value 1.0e-109
Match length 287
% identity 93
NCBI Description Human mRNA for KIAA0049 gene, complete cds

Seq. No. 301091
Seq. ID afb700380809.h1
Method BLASTN
NCBI GI g3004572
BLAST score 167
E value 5.0e-89
Match length 294
% identity 94
NCBI Description Homo sapiens BAC clone RG119C02 from 7p15, complete sequence [Homo sapiens]

Seq. No. 301092
Seq. ID afb700380822.h1
Method BLASTX
NCBI GI g3098603
BLAST score 376
E value 2.0e-36
Match length 93
% identity 75
NCBI Description (AF052191) katanin p60 subunit [Strongylocentrotus purpuratus]

Seq. No. 301093
Seq. ID afb700380846.h1
Method BLASTX

NCBI GI g4240321
BLAST score 372
E value 5.0e-36
Match length 96
% identity 77
NCBI Description (AB020723) KIAA0916 protein [Homo sapiens]

Seq. No. 301094
Seq. ID afb700380857.h1
Method BLASTX
NCBI GI g4559304
BLAST score 548
E value 1.0e-56
Match length 102
% identity 100
NCBI Description (AF127021) T7-like RNA polymerase [Zea mays]

Seq. No. 301095
Seq. ID afb700380901.h1
Method BLASTX
NCBI GI g2829208
BLAST score 144
E value 3.0e-09
Match length 28
% identity 93
NCBI Description (AF044076) candidate tumor suppressor p33ING1 [Homo sapiens]

Seq. No. 301096
Seq. ID afb700380906.h1
Method BLASTN
NCBI GI g887356
BLAST score 105
E value 2.0e-52
Match length 138
% identity 94
NCBI Description Homo sapiens (clone s153) mRNA fragment

Seq. No. 301097
Seq. ID afb700380989.h1
Method BLASTX
NCBI GI g4262224
BLAST score 278
E value 6.0e-25
Match length 79
% identity 63
NCBI Description (AC006200) putative amino acid or GABA permease [Arabidopsis thaliana]

Seq. No. 301098
Seq. ID afb700380994.h1
Method BLASTX
NCBI GI g133820
BLAST score 150
E value 3.0e-10
Match length 30
% identity 97

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NCBI Description 40S RIBOSOMAL PROTEIN S17 >gi_304526 (M13933) ribosomal protein S17 [Cricetulus griseus] >gi_1526555 dbj_BAA04943_ (D25213) ribosomal protein S17 [Mus musculus]

Seq. No. 301099
Seq. ID afb700381015.h1
Method BLASTN
NCBI GI g4505760
BLAST score 229
E value 1.0e-126
Match length 301
% identity 95
NCBI Description Homo sapiens placental growth factor, vascular endothelial growth factor-related protein (PGF) mRNA >gi_35521_emb_X54936_HSPLGF H.sapiens mRNA for placenta growth factor (PlGF) >gi_512448_emb_A18411.1_A18411 PlGF gene seq ID No:1

Seq. No. 301100
Seq. ID afb700381017.h1
Method BLASTN
NCBI GI g4416300
BLAST score 36
E value 5.0e-11
Match length 44
% identity 48
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No. 301101
Seq. ID afb700381056.h1
Method BLASTN
NCBI GI g4416300
BLAST score 79
E value 2.0e-36
Match length 159
% identity 87
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No. 301102
Seq. ID afb700381068.h1
Method BLASTX
NCBI GI g3176726
BLAST score 224
E value 6.0e-19
Match length 56
% identity 71
NCBI Description (AC002392) putative serine proteinase [Arabidopsis thaliana]

Seq. No. 301103
Seq. ID afb700381113.h1
Method BLASTX
NCBI GI g1710756
BLAST score 188
E value 2.0e-14

Match length 46
% identity 80
NCBI Description 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)

Seq. No. 301104
Seq. ID afb700381116.h1
Method BLASTN
NCBI GI g4507580
BLAST score 194
E value 1.0e-105
Match length 238
% identity 96
NCBI Description Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA >gi_29850_emb_X60592_HSCDW40 Human CDw40 mRNA for nerve growth factor receptor-related B-lymphocyte activation molecule >gi_590074_gb_I07284_Sequence 31 from Patent EP

Seq. No. 301105
Seq. ID afb700381138.h1
Method BLASTN
NCBI GI g4102714
BLAST score 117
E value 3.0e-59
Match length 276
% identity 86
NCBI Description Homo sapiens serine protease mRNA, complete cds

Seq. No. 301106
Seq. ID afb700381156.h1
Method BLASTX
NCBI GI g3661529
BLAST score 262
E value 5.0e-23
Match length 52
% identity 96
NCBI Description (AF089814) growth suppressor related [Homo sapiens]

Seq. No. 301107
Seq. ID afb700381157.h1
Method BLASTN
NCBI GI g1617516
BLAST score 171
E value 1.0e-91
Match length 227
% identity 94
NCBI Description Human orphan G protein-coupled receptor (RDC1) mRNA, partial cds

Seq. No. 301108
Seq. ID afb700381181.h1
Method BLASTN
NCBI GI g1698488
BLAST score 37
E value 1.0e-11
Match length 78
% identity 88

NCBI Description Peltoboykinia tellimoides 18S ribosomal RNA, complete sequence

Seq. No. 301109
Seq. ID afb700381189.h1
Method BLASTN
NCBI GI g2281061
BLAST score 79
E value 1.0e-36
Match length 171
% identity 87
NCBI Description Human Chromosome 11 Cosmid cSRL16b6, complete sequence [Homo sapiens]

Seq. No. 301110
Seq. ID afb700381218.h1
Method BLASTX
NCBI GI g2501624
BLAST score 381
E value 5.0e-37
Match length 97
% identity 79
NCBI Description UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)
>gi_1652159_dbj_BAA17083_ (D90903) urease alpha subunit [Synechocystis sp.]

Seq. No. 301111
Seq. ID afb700381224.h1
Method BLASTX
NCBI GI g899254
BLAST score 153
E value 3.0e-10
Match length 40
% identity 65
NCBI Description (Z50038) predicted trithorax protein [Drosophila virilis]

Seq. No. 301112
Seq. ID afb700381226.h1
Method BLASTX
NCBI GI g2984709
BLAST score 227
E value 5.0e-23
Match length 68
% identity 85
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 301113
Seq. ID afb700381301.h1
Method BLASTX
NCBI GI g4056615
BLAST score 154
E value 2.0e-10
Match length 39
% identity 74
NCBI Description (AF067401) Scl1 protein [Oryza sativa]

Seq. No. 301114

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Seq. ID afb700381303.h1
Method BLASTX
NCBI GI g3025299
BLAST score 395
E value 1.0e-38
Match length 100
% identity 72
NCBI Description HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi_2088660
(AF002109) ABC1 isolog [Arabidopsis thaliana]

Seq. No. 301115
Seq. ID afb700381326.h1
Method BLASTN
NCBI GI g3549156
BLAST score 172
E value 4.0e-92
Match length 264
% identity 92
NCBI Description Homo sapiens chromosome 19, cosmid R30017, complete
sequence [Homo sapiens]

Seq. No. 301116
Seq. ID afb700381330.h1
Method BLASTX
NCBI GI g1717793
BLAST score 151
E value 4.0e-10
Match length 91
% identity 38
NCBI Description PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR)
>gi_1083553_pir_A55117_tsg24 protein - mouse
>gi_642252_emb_CAA56450_ (X80169) tsg24 [Mus musculus]

Seq. No. 301117
Seq. ID afb700381357.h1
Method BLASTX
NCBI GI g3080424
BLAST score 214
E value 2.0e-17
Match length 100
% identity 53
NCBI Description (AL022604) NAD⁺ dependent isocitrate dehydrogenase subunit
1 [Arabidopsis thaliana]

Seq. No. 301118
Seq. ID afb700381361.h1
Method BLASTX
NCBI GI g2911056
BLAST score 170
E value 3.0e-12
Match length 76
% identity 45
NCBI Description (AL021961) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301119
Seq. ID afb700381372.h1
Method BLASTX

NCBI GI g2978255
BLAST score 153
E value 1.0e-10
Match length 35
% identity 83
NCBI Description (AB007407) myeloid zinc finger protein-2 [Mus musculus]

Seq. No. 301120
Seq. ID afb700381414.h1
Method BLASTX
NCBI GI g2498329
BLAST score 384
E value 2.0e-37
Match length 100
% identity 74
NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir_S65571
pattern-formation protein GNOM - Arabidopsis thaliana
>gi_1209633 (U36433) GNOM gene product [Arabidopsis
thaliana] >gi_1335997 (U56140) similar to the Saccharomyces
cerevisiae Sec7 protein, GenBank Accession Number J03918
[Arabidopsis thaliana] >gi_1335999 (U56141) similar to the
Saccharomyces cerevisiae Sec7 protein, GenBank Accession
Number J03918 [Arabidopsis thaliana]

Seq. No. 301121
Seq. ID afb700381428.h1
Method BLASTN
NCBI GI g3789930
BLAST score 156
E value 2.0e-82
Match length 288
% identity 89
NCBI Description Homo sapiens H19 gene, complete sequence

Seq. No. 301122
Seq. ID afb700381439.h1
Method BLASTX
NCBI GI g3043415
BLAST score 324
E value 2.0e-30
Match length 62
% identity 98
NCBI Description (Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No. 301123
Seq. ID afb700381471.h1
Method BLASTX
NCBI GI g4538911
BLAST score 182
E value 7.0e-14
Match length 42
% identity 83
NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301124
Seq. ID afb700381501.h1
Method BLASTN

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NCBI GI g3417305
BLAST score 244
E value 1.0e-135
Match length 304
% identity 95
NCBI Description Homo sapiens chromosome 17, clone hRPC1107_A_17, complete sequence [Homo sapiens]

Seq. No. 301125
Seq. ID afb700381513.h1
Method BLASTN
NCBI GI g4335966
BLAST score 226
E value 1.0e-124
Match length 290
% identity 95
NCBI Description Homo sapiens cell adhesion molecule (BL1A) mRNA, complete cds

Seq. No. 301126
Seq. ID afb700381522.h1
Method BLASTN
NCBI GI g558364
BLAST score 96
E value 1.0e-46
Match length 96
% identity 100
NCBI Description Z.mays mRNA for ADP-glucose pyrophosphorylase

Seq. No. 301127
Seq. ID afb700381529.h1
Method BLASTX
NCBI GI g4586036
BLAST score 203
E value 4.0e-16
Match length 96
% identity 41
NCBI Description (AC007109) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301128
Seq. ID afb700381530.h1
Method BLASTN
NCBI GI g181962
BLAST score 133
E value 7.0e-69
Match length 181
% identity 93
NCBI Description Human elongation factor EF-1-alpha gene, complete cds.
>gi_2170857_dbj_E02629_E02629 DNA of human polypeptide chain elongation factor-1 alpha

Seq. No. 301129
Seq. ID afb700381590.h1
Method BLASTN
NCBI GI g577824
BLAST score 46
E value 5.0e-17

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Match length 58
% identity 95
NCBI Description Z.mays gene for H2B histone (gH2B3)

Seq. No. 301130
Seq. ID afb700381593.h1
Method BLASTN
NCBI GI g22487
BLAST score 34
E value 4.0e-10
Match length 38
% identity 97
NCBI Description Maize gene for sucrose synthase

Seq. No. 301131
Seq. ID afb700381620.h1
Method BLASTX
NCBI GI g88969
BLAST score 252
E value 1.0e-41
Match length 103
% identity 85
NCBI Description ubiquitin--protein ligase (EC 6.3.2.19) E1 - human
>gi_340072 (M58028) ubiquitin-activating enzyme E1 [Homo sapiens]

Seq. No. 301132
Seq. ID afb700381624.h1
Method BLASTX
NCBI GI g4309738
BLAST score 175
E value 8.0e-13
Match length 52
% identity 54
NCBI Description (AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No. 301133
Seq. ID afb700381625.h1
Method BLASTN
NCBI GI g2576343
BLAST score 48
E value 5.0e-18
Match length 92
% identity 88
NCBI Description Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence [Homo sapiens]

Seq. No. 301134
Seq. ID afb700381648.h1
Method BLASTX
NCBI GI g183613
BLAST score 212
E value 2.0e-17
Match length 45
% identity 84
NCBI Description (M75161) granulin [Homo sapiens]

Seq. No. 301135
Seq. ID afb700381654.h1
Method BLASTN
NCBI GI g2098573
BLAST score 36
E value 7.0e-11
Match length 48
% identity 94
NCBI Description Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence [Homo sapiens]

Seq. No. 301136
Seq. ID afb700381687.h1
Method BLASTX
NCBI GI g2833293
BLAST score 166
E value 7.0e-12
Match length 84
% identity 40
NCBI Description PROBABLE ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC)
>gi_2146865_pir_S72578 gene C35D10.1 protein -
Caenorhabditis elegans >gi_687880 (U21324) similar to S.
cerevisiae hypothetical protein YKL166 [Caenorhabditis
elegans]

Seq. No. 301137
Seq. ID afb700381693.h1
Method BLASTX
NCBI GI g4502193
BLAST score 350
E value 1.0e-40
Match length 94
% identity 94
NCBI Description v-raf murine sarcoma 3611 viral oncogene homolog 1
>gi_1730068_sp_P10398_KRAA HUMAN A-RAF PROTO-ONCOGENE
SERINE/THREONINE-PROTEIN KINASE (ONCOGENE PKS2)
>gi_625217_pir_TVHUAF protein kinase A-raf-1 (EC 2.7.1.-)
- human >gi_780127 (L24038) ARAF1 [Homo sapiens]
>gi_1405977 (U01337) Ser/Thr protein kinase [Homo sapiens]

Seq. No. 301138
Seq. ID afb700381694.h1
Method BLASTN
NCBI GI g1596166
BLAST score 205
E value 1.0e-112
Match length 277
% identity 94
NCBI Description Human mRNA for RTP, complete cds

Seq. No. 301139
Seq. ID afb700381736.h1
Method BLASTN
NCBI GI g307374
BLAST score 209
E value 1.0e-114

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Match length	255
% identity	96
NCBI Description	Homo sapiens RHOA proto-oncogene multi-drug-resistance protein mRNA, 3' end
Seq. No.	301140
Seq. ID	afb700381831.h1
Method	BLASTX
NCBI GI	g3360291
BLAST score	168
E value	3.0e-12
Match length	52
% identity	63
NCBI Description	(AF023165) leucine-rich repeat transmembrane protein kinase 2 [Zea mays]
Seq. No.	301141
Seq. ID	afb700381832.h1
Method	BLASTN
NCBI GI	g6249668
BLAST score	57
E value	1.0e-23
Match length	148
% identity	85
NCBI Description	Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence [Homo sapiens]
Seq. No.	301142
Seq. ID	afb700381837.h1
Method	BLASTX
NCBI GI	g2984709
BLAST score	143
E value	3.0e-09
Match length	39
% identity	74
NCBI Description	(AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.	301143
Seq. ID	afb700381851.h1
Method	BLASTX
NCBI GI	g312179
BLAST score	457
E value	7.0e-46
Match length	90
% identity	97
NCBI Description	(X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.	301144
Seq. ID	afb700381860.h1
Method	BLASTX
NCBI GI	g4007113
BLAST score	487
E value	2.0e-49

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Match length 102
% identity 92
NCBI Description (AL022237) bK1191B2.3.1 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (isoform 1) [Homo sapiens]

Seq. No. 301145
Seq. ID afb700381862.h1
Method BLASTX
NCBI GI g3785977
BLAST score 441
E value 5.0e-44
Match length 103
% identity 81
NCBI Description (AC005560) putative growth regulator protein [Arabidopsis thaliana]

Seq. No. 301146
Seq. ID afb700381882.h1
Method BLASTX
NCBI GI g4506285
BLAST score 340
E value 2.0e-37
Match length 86
% identity 92
NCBI Description Protein tyrosine phosphatase IVA2 >gi_894159 (U14603) protein-tyrosine phosphatase [Homo sapiens] >gi_1777757 (U48297) protein tyrosine phosphatase PTPCAAX2 [Homo sapiens] >gi_1817730 (L48723) protein tyrosine phosphatase [Homo sapiens] >gi_2992630 (AF035644) mPRL-2 [Mus musculus]

Seq. No. 301147
Seq. ID afb700381915.h1
Method BLASTN
NCBI GI g4504864
BLAST score 86
E value 1.0e-40
Match length 196
% identity 92
NCBI Description Homo sapiens KH-type splicing regulatory protein (KHSRP) mRNA, and translated products >gi_2055426_gb_U94832_HSU94832 Human KH type splicing regulatory protein KSRP mRNA, complete cds

Seq. No. 301148
Seq. ID afb700381949.h1
Method BLASTN
NCBI GI g507770
BLAST score 65
E value 3.0e-28
Match length 137
% identity 88
NCBI Description Zea mays D3L H(+) -transporting ATPase (Mhal) gene, complete cds

Seq. No. 301149
Seq. ID afb700381966.h1
Method BLASTX

NCBI GI g3914019
 BLAST score 293
 E value 7.0e-27
 Match length 76
 % identity 80
 NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
 ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_2305014
 (AF004317) S-adenosyl-L-methionine synthetase homolog [Musa
 acuminata]

Seq. No. 301150
 Seq. ID afb700381967.h1
 Method BLASTX
 NCBI GI g3289993
 BLAST score 376
 E value 2.0e-36
 Match length 81
 % identity 91
 NCBI Description (AC005258) R30783_1 [Homo sapiens]

Seq. No. 301151
 Seq. ID afb700381976.h1
 Method BLASTX
 NCBI GI g399144
 BLAST score 182
 E value 6.0e-14
 Match length 53
 % identity 66
 NCBI Description COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR
 >gi_2144887_pir_C1HUQC complement subcomponent C1q chain C
 precursor - human

Seq. No. 301152
 Seq. ID arm700460708.h1
 Method BLASTX
 NCBI GI g3929647
 BLAST score 150
 E value 2.0e-22
 Match length 75
 % identity 63
 NCBI Description (AJ004881) Immutans protein [Arabidopsis thaliana]

Seq. No. 301153
 Seq. ID arm700460849.h1
 Method BLASTN
 NCBI GI g532624
 BLAST score 65
 E value 1.0e-28
 Match length 117
 % identity 90
 NCBI Description Zea mays malate synthase (MS) mRNA, complete cds

Seq. No. 301154
 Seq. ID arm700460850.h1
 Method BLASTN
 NCBI GI g168584
 BLAST score 58

E value 2.0e-24
Match length 118
% identity 88
NCBI Description Corn pyruvate,orthophosphate dikinase gene, exons 2-19

Seq. No. 301155
Seq. ID arm700460852.h1
Method BLASTN
NCBI GI g2282583
BLAST score 55
E value 1.0e-22
Match length 103
% identity 88
NCBI Description Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete cds

Seq. No. 301156
Seq. ID arm700460870.h1
Method BLASTN
NCBI GI g1632767
BLAST score 81
E value 3.0e-38
Match length 89
% identity 98
NCBI Description Maize mRNA for calcium dependent protein kinase, complete cds

Seq. No. 301157
Seq. ID bdu700382077.h1
Method BLASTN
NCBI GI g433043
BLAST score 35
E value 3.0e-10
Match length 51
% identity 92
NCBI Description Zea mays W-22 clone PREM-1E retroelement PREM-1, partial sequence

Seq. No. 301158
Seq. ID bdu700382215.h1
Method BLASTX
NCBI GI g2911052
BLAST score 245
E value 2.0e-21
Match length 65
% identity 69
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 301159
Seq. ID bdu700382237.h1
Method BLASTX
NCBI GI g1076758
BLAST score 176
E value 6.0e-13
Match length 43
% identity 72
NCBI Description heat-shock protein precursor - rye >gi_2130093_pir_S65776

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heat-shock protein, 82K, precursor - rye
>gi_556673_emb_CAA82945_ (Z30243) heat-shock protein
[Secale cereale]

Seq. No. 301160
Seq. ID bdu700382269.h1
Method BLASTX
NCBI GI g218179
BLAST score 448
E value 7.0e-45
Match length 98
% identity 90
NCBI Description (D10207) H-ATPase [Oryza sativa] >gi_444339_prf_1906387A H
ATPase [Oryza sativa]

Seq. No. 301161
Seq. ID bdu700382287.h1
Method BLASTN
NCBI GI g3283878
BLAST score 63
E value 4.0e-27
Match length 163
% identity 87
NCBI Description Homo sapiens clone 24732 unknown mRNA, partial cds

Seq. No. 301162
Seq. ID bdu700382306.h1
Method BLASTX
NCBI GI g4539662
BLAST score 339
E value 4.0e-32
Match length 98
% identity 60
NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 301163
Seq. ID bdu700382321.h1
Method BLASTN
NCBI GI g4309811
BLAST score 255
E value 1.0e-141
Match length 287
% identity 97
NCBI Description Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1,
complete sequence [Homo sapiens]

Seq. No. 301164
Seq. ID bdu700382376.h1
Method BLASTX
NCBI GI g1064931
BLAST score 165
E value 1.0e-11
Match length 45
% identity 71
NCBI Description (X92965) cyclin A-like protein [Nicotiana tabacum]

Seq. No. 301165

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Seq. ID bdu700382380.h1
Method BLASTX
NCBI GI g2213594
BLAST score 355
E value 6.0e-34
Match length 86
% identity 76
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No. 301166
Seq. ID bdu700382422.h1
Method BLASTX
NCBI GI g117478
BLAST score 195
E value 1.0e-15
Match length 67
% identity 57
NCBI Description CROOKED NECK PROTEIN

Seq. No. 301167
Seq. ID bdu700382427.h1
Method BLASTX
NCBI GI g126047
BLAST score 198
E value 7.0e-16
Match length 40
% identity 97
NCBI Description L-LACTATE DEHYDROGENASE M CHAIN (LDH-A)
>gi_65922_pir_DEHULM L-lactate dehydrogenase (EC 1.1.1.27)
chain M - human >gi_34313_emb_CAA26088 (X02152) lactate
dehydrogenase-A [Homo sapiens] >gi_780261_emb_CAA26879
(X03077) lactate dehydrogenase-A [Homo sapiens]

Seq. No. 301168
Seq. ID bdu700382431.h1
Method BLASTN
NCBI GI g4506860
BLAST score 126
E value 5.0e-65
Match length 126
% identity 100
NCBI Description Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA
>gi_28679_emb_X67016_HSAMPH H.sapiens mRNA for amphiglycan

Seq. No. 301169
Seq. ID bdu700382462.h1
Method BLASTX
NCBI GI g2462732
BLAST score 170
E value 2.0e-26
Match length 90
% identity 63
NCBI Description (AC002292) Hypothetical Protein [Arabidopsis thaliana]

Seq. No. 301170
Seq. ID bdu700382474.h1
Method BLASTN

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NCBI GI	g4416300
BLAST score	55
E value	3.0e-22
Match length	87
% identity	45
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence
Seq. No.	301171
Seq. ID	bdu700382478.h1
Method	BLASTN
NCBI GI	g6683125
BLAST score	107
E value	1.0e-53
Match length	115
% identity	98
NCBI Description	Human mRNA for KIAA0339 gene, complete cds
Seq. No.	301172
Seq. ID	bdu700382489.h1
Method	BLASTX
NCBI GI	g3170741
BLAST score	407
E value	4.0e-42
Match length	94
% identity	90
NCBI Description	(AF062139) immunoglobulin heavy chain variable region [Homo sapiens] >gi_3170743 (AF062140) immunoglobulin heavy chain variable region [Homo sapiens]
Seq. No.	301173
Seq. ID	bdu700382560.h1
Method	BLASTX
NCBI GI	g1184776
BLAST score	158
E value	2.0e-12
Match length	49
% identity	84
NCBI Description	(U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC4 [Zea mays]
Seq. No.	301174
Seq. ID	bdu700382617.h1
Method	BLASTN
NCBI GI	g22458
BLAST score	294
E value	1.0e-165
Match length	309
% identity	99
NCBI Description	Z.mays pollen specific mRNA C-terminal (clone 4H7)
Seq. No.	301175
Seq. ID	bdu700382660.h1
Method	BLASTN
NCBI GI	g4506044
BLAST score	92
E value	9.0e-45

Match length 112
% identity 96
NCBI Description Homo sapiens proteoglycan 1, secretory granule (PRG1) mRNA
>gi_32432_emb_X17042_HSHPCP Human mRNA for hematopoetic
proteoglycan core protein

Seq. No. 301176
Seq. ID bdu700382741.h1
Method BLASTX
NCBI GI g123648
BLAST score 235
E value 1.0e-24
Match length 72
% identity 82
NCBI Description HEAT SHOCK COGNATE 71 KD PROTEIN >gi_87625_pir_A27077 heat
shock cognate protein 70 - human >gi_32467_emb_CAA68445
(Y00371) 71 Kd heat shock cognate protein [Homo sapiens]

Seq. No. 301177
Seq. ID bdu700382770.h1
Method BLASTX
NCBI GI g2245020
BLAST score 236
E value 2.0e-20
Match length 58
% identity 71
NCBI Description (Z97341) growth regulator homolog [Arabidopsis thaliana]

Seq. No. 301178
Seq. ID bdu700382785.h1
Method BLASTX
NCBI GI g2462753
BLAST score 151
E value 2.0e-10
Match length 41
% identity 59
NCBI Description (AC002292) putative polygalacturonase [Arabidopsis
thaliana]

Seq. No. 301179
Seq. ID bdu700382801.h1
Method BLASTN
NCBI GI g455025
BLAST score 55
E value 1.0e-22
Match length 79
% identity 46
NCBI Description Human beta globin region on chromosome 11

Seq. No. 301180
Seq. ID bdu700382804.h1
Method BLASTX
NCBI GI g548493
BLAST score 229
E value 1.0e-19
Match length 68
% identity 71

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NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
(GALACTURAN 1, 4-ALPHA-GALACTURONIDASE)
>gi_629854_pir_S30067 polygalacturonase - maize
>gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea mays]

Seq. No. 301181
Seq. ID bdu700382862.h1
Method BLASTX
NCBI GI g3643593
BLAST score 158
E value 6.0e-11
Match length 57
% identity 61
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301182
Seq. ID bdu700382886.h1
Method BLASTX
NCBI GI g283050
BLAST score 214
E value 7.0e-33
Match length 88
% identity 81
NCBI Description polygalacturonase (EC 3.2.1.15) precursor (clone W2265) - maize (fragment) >gi_22428_emb_CAA44247_ (X62383) polygalacturonase [Zea mays]

Seq. No. 301183
Seq. ID bdu700382895.h1
Method BLASTX
NCBI GI g1839188
BLAST score 268
E value 4.0e-24
Match length 70
% identity 66
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 301184
Seq. ID bdu700382901.h1
Method BLASTN
NCBI GI g2984708
BLAST score 112
E value 2.0e-56
Match length 131
% identity 97
NCBI Description Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete cds

Seq. No. 301185
Seq. ID bdu700382914.h1
Method BLASTX
NCBI GI g3176674
BLAST score 226
E value 6.0e-19
Match length 83
% identity 57

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NCBI Description (AC003671) Contains similarity to Ste20-like kinase homolog from A. thaliana chromosome 4 contig gb_Z97336.
[Arabidopsis thaliana]

Seq. No. 301186
Seq. ID bdu700382917.h1
Method BLASTX
NCBI GI g280401
BLAST score 146
E value 2.0e-15
Match length 57
% identity 68

NCBI Description H+-transporting ATPase (EC 3.6.1.35) - curled-leaved tobacco >gi_170206 (M27888) H+-translocating ATPase [Nicotiana plumbaginifolia]

Seq. No. 301187
Seq. ID bdu700382927.h1
Method BLASTX
NCBI GI g2316016
BLAST score 194
E value 2.0e-15
Match length 60
% identity 65

NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No. 301188
Seq. ID bdu700382930.h1
Method BLASTX
NCBI GI g3236353
BLAST score 333
E value 1.0e-31
Match length 86
% identity 73

NCBI Description (AF033664) cbp146 [Mus musculus]

Seq. No. 301189
Seq. ID bdu700382966.h1
Method BLASTX
NCBI GI g2832632
BLAST score 280
E value 2.0e-27
Match length 72
% identity 81

NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301190
Seq. ID bdu700382977.h1
Method BLASTN
NCBI GI g22458
BLAST score 72
E value 2.0e-32
Match length 181
% identity 92

NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)

Seq. No. 301191

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Seq. ID bdu700382992.h1
Method BLASTN
NCBI GI g643596
BLAST score 147
E value 2.0e-77
Match length 179
% identity 96
NCBI Description Corn mRNA for cysteine proteinase, clone CCP, complete cds

Seq. No. 301192
Seq. ID bdu700383027.h1
Method BLASTN
NCBI GI g995938
BLAST score 70
E value 3.0e-31
Match length 118
% identity 89
NCBI Description Human 13kD differentiation-associated protein mRNA, partial cds

Seq. No. 301193
Seq. ID bdu700383036.h1
Method BLASTX
NCBI GI g3935168
BLAST score 350
E value 2.0e-33
Match length 85
% identity 76
NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No. 301194
Seq. ID bdu700383041.h1
Method BLASTX
NCBI GI g2120736
BLAST score 149
E value 8.0e-10
Match length 89
% identity 36
NCBI Description X-Pro dipeptidyl-peptidase (EC 3.4.14.11) - Xanthomonas maltophilia >gi_1753197_dbj_BAA11872_ (D83263) dipeptidyl peptidase IV [Stenotrophomonas maltophilia]

Seq. No. 301195
Seq. ID bdu700383058.h1
Method BLASTX
NCBI GI g4218991
BLAST score 347
E value 5.0e-33
Match length 95
% identity 65
NCBI Description (AF098632) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 301196
Seq. ID bdu700383070.h1
Method BLASTX
NCBI GI g4262162
BLAST score 161

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E value 3.0e-11
Match length 94
% identity 37
NCBI Description (AC005275) putative glycosylation enzyme [Arabidopsis thaliana]

Seq. No. 301197
Seq. ID bdu700383111.h1
Method BLASTX
NCBI GI g3646451
BLAST score 163
E value 1.0e-11
Match length 87
% identity 40
NCBI Description (AL031603) mRNA cap methyltransferase [Schizosaccharomyces pombe]

Seq. No. 301198
Seq. ID bdu700383114.h1
Method BLASTX
NCBI GI g283049
BLAST score 486
E value 2.0e-49
Match length 93
% identity 100
NCBI Description polygalacturonase (EC 3.2.1.15) precursor (clone W2247) - maize (fragment) >gi_481079_pir_S37718 polygalacturonase - maize >gi_22426_emb_CAA44248_(X62384) polygalacturonase [Zea mays] >gi_287830_emb_CAA47234_(X66692) polygalacturonase [Zea mays]

Seq. No. 301199
Seq. ID bdu700383135.h1
Method BLASTX
NCBI GI g4038030
BLAST score 309
E value 1.0e-28
Match length 94
% identity 62
NCBI Description (AC005936) putative protein kinase, 5' partial [Arabidopsis thaliana]

Seq. No. 301200
Seq. ID bdu700383193.h1
Method BLASTX
NCBI GI g416731
BLAST score 203
E value 3.0e-16
Match length 40
% identity 100
NCBI Description POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi_82655_pir_JQ1107 18.3K protein precursor, pollen - maize
>gi_255569_bbs_113677 (S44171) pollen specific protein [Zea mays=corn, Peptide, 170 aa] [Zea mays]
>gi_1588669_prf_2209273A Zm13 [Zea mays]

Seq. No. 301201

Seq. ID cat700016008.rl
Method BLASTX
NCBI GI g1362108
BLAST score 169
E value 2.0e-12
Match length 54
% identity 69
NCBI Description histone H3 homolog - common tobacco

Seq. No. 301202
Seq. ID cat700016084.rl
Method BLASTN
NCBI GI g18266
BLAST score 44
E value 8.0e-16
Match length 56
% identity 95
NCBI Description C.stellata mRNA for ribosomal protein L27

Seq. No. 301203
Seq. ID cat700016209.rl
Method BLASTX
NCBI GI g3687249
BLAST score 160
E value 3.0e-11
Match length 44
% identity 66
NCBI Description (AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No. 301204
Seq. ID cat700016243.rl
Method BLASTX
NCBI GI g4262228
BLAST score 341
E value 2.0e-32
Match length 85
% identity 71
NCBI Description (AC006200) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 301205
Seq. ID cat700016271.rl
Method BLASTN
NCBI GI g1314406
BLAST score 145
E value 5.0e-76
Match length 145
% identity 100
NCBI Description Zea mays ssp. parviglumis Doebley M106 ITS1, 5.8S ribosomal RNA, ITS2

Seq. No. 301206
Seq. ID cat700016327.rl
Method BLASTX
NCBI GI g3004950
BLAST score 224

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E value 6.0e-19
Match length 44
% identity 100
NCBI Description (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]

Seq. No. 301207
Seq. ID cat700016372.rl
Method BLASTX
NCBI GI g4539660
BLAST score 238
E value 1.0e-20
Match length 57
% identity 72
NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 301208
Seq. ID cat700016375.rl
Method BLASTN
NCBI GI g2723470
BLAST score 56
E value 6.0e-23
Match length 120
% identity 87
NCBI Description Oryza sativa mRNA for sucrose transporter, complete cds

Seq. No. 301209
Seq. ID cat700016453.rl
Method BLASTX
NCBI GI g2245123
BLAST score 275
E value 7.0e-25
Match length 69
% identity 71
NCBI Description (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No. 301210
Seq. ID cat700016454.rl
Method BLASTN
NCBI GI g1657760
BLAST score 57
E value 1.0e-23
Match length 176
% identity 84
NCBI Description Zea mays retrotransposon Cinful 5' LTR and and primer binding site DNA sequence

Seq. No. 301211
Seq. ID cat700016510.rl
Method BLASTX
NCBI GI g4585979
BLAST score 207
E value 5.0e-17
Match length 72
% identity 60
NCBI Description (AC005287) Similar to ABC-transporter atp-binding protein [Arabidopsis thaliana]

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Seq. No.	301212
Seq. ID	cat700016585.r1
Method	BLASTX
NCBI GI	g2130141
BLAST score	163
E value	8.0e-12
Match length	68
% identity	46
NCBI Description	mudrA protein - maize transposon MuDR >gi_540581 (M76978) mudrA [Zea mays] >gi_595816 (U14597) mudrA gene product [Zea mays]
Seq. No.	301213
Seq. ID	cat700016592.r1
Method	BLASTX
NCBI GI	g586021
BLAST score	174
E value	4.0e-13
Match length	69
% identity	49
NCBI Description	PROBABLE PEPTIDYL-TRNA HYDROLASE (PTH) (STAGE V SPORULATION PROTEIN C) >gi_2127242_pir_S66083 stage V sporulation protein - Bacillus subtilis >gi_467442_dbj_BAA05288_ (D26185) stage V sporulation [Bacillus subtilis] >gi_2632320_emb_CAB11829_ (Z99104) thermosensitive mutant blocks spore coat formation (stage V sporulation) [Bacillus subtilis]
Seq. No.	301214
Seq. ID	cat700016744.r1
Method	BLASTX
NCBI GI	g2088647
BLAST score	261
E value	3.0e-23
Match length	71
% identity	72
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]
Seq. No.	301215
Seq. ID	cat700016764.r1
Method	BLASTX
NCBI GI	g3860263
BLAST score	224
E value	6.0e-19
Match length	71
% identity	61
NCBI Description	(AC005824) putative cytochrome p450 protein [Arabidopsis thaliana]
Seq. No.	301216
Seq. ID	cat700016831.r2
Method	BLASTX
NCBI GI	g462234
BLAST score	186
E value	3.0e-14

Match length 40
% identity 90
NCBI Description HISTONE H2A >gi_419741_pir_S30155 histone H2A - Norway spruce >gi_297871_emb_CAA48030_ (X67819) histone H2A [Picea abies]

Seq. No. 301217
Seq. ID cat700016835.r2
Method BLASTX
NCBI GI g3786009
BLAST score 203
E value 2.0e-16
Match length 64
% identity 61
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 301218
Seq. ID cat700016883.rl
Method BLASTN
NCBI GI g1185553
BLAST score 86
E value 7.0e-41
Match length 99
% identity 53
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2) gene, complete cds

Seq. No. 301219
Seq. ID cat700017172.rl
Method BLASTX
NCBI GI g2462763
BLAST score 282
E value 9.0e-26
Match length 65
% identity 78
NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 301220
Seq. ID cat700017201.rl
Method BLASTX
NCBI GI g3702341
BLAST score 197
E value 1.0e-15
Match length 70
% identity 50
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301221
Seq. ID cat700017234.rl
Method BLASTX
NCBI GI g4530595
BLAST score 155
E value 7.0e-11
Match length 47
% identity 62
NCBI Description (AF132477) heme oxygenase 2 [Arabidopsis thaliana]

Seq. No. 301222
Seq. ID cat700017238.rl
Method BLASTX
NCBI GI g4056502
BLAST score 199
E value 5.0e-16
Match length 64
% identity 61
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No. 301223
Seq. ID cat700017249.rl
Method BLASTX
NCBI GI g585963
BLAST score 172
E value 8.0e-13
Match length 48
% identity 75
NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No. 301224
Seq. ID cat700017326.rl
Method BLASTX
NCBI GI g3928519
BLAST score 379
E value 5.0e-37
Match length 78
% identity 85
NCBI Description (AB011670) wpk4 protein kinase [Triticum aestivum]

Seq. No. 301225
Seq. ID cat700017338.rl
Method BLASTX
NCBI GI g416922
BLAST score 268
E value 4.0e-24
Match length 70
% identity 73
NCBI Description DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE)
(DUTP PYROPHOSPHATASE) (P18) >gi_282947_pir_JQ1599 dUTP
pyrophosphatase (EC 3.6.1.23) - tomato
>gi_251897_bbs_109276 (S40549) deoxyuridine triphosphatase,
dUTPase, P18 {EC 3.6.1.23} [tomatoes, Tint Tim cultivar
LA154, Peptide, 169 aa] [Lycopersicon esculentum]

Seq. No. 301226
Seq. ID cat700017371.rl
Method BLASTX
NCBI GI g1705463
BLAST score 363
E value 4.0e-35
Match length 77
% identity 92
NCBI Description BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547_pir_S71201
biotin synthase - Arabidopsis thaliana >gi_1045316 (U24147)
biotin synthase [Arabidopsis thaliana] >gi_1403662 (U31806)

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BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413)
biotin synthase [Arabidopsis thaliana] >gi_2288983
(AC002335) biotin synthase (Bio B) [Arabidopsis thaliana]
>gi_1589016_prf_2209438A biotin synthase [Arabidopsis thaliana]

Seq. No. 301227
Seq. ID cat700017381.rl
Method BLASTX
NCBI GI g4559334
BLAST score 219
E value 2.0e-18
Match length 56
% identity 68
NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 301228
Seq. ID cat700017562.rl
Method BLASTN
NCBI GI g3747043
BLAST score 73
E value 4.0e-33
Match length 77
% identity 99
NCBI Description Zea mays blue copper protein mRNA, partial cds

Seq. No. 301229
Seq. ID cat700017669.rl
Method BLASTN
NCBI GI g22292
BLAST score 70
E value 3.0e-31
Match length 70
% identity 100
NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 301230
Seq. ID cat700017758.rl
Method BLASTX
NCBI GI g3513727
BLAST score 260
E value 3.0e-23
Match length 72
% identity 67
NCBI Description (AF080118) contains similarity to TPR domains (Pfam:
TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:
kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 301231
Seq. ID cat700017884.rl
Method BLASTX
NCBI GI g3393018
BLAST score 161
E value 1.0e-11
Match length 67

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% identity 49
NCBI Description (AL031174) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 301232
Seq. ID cat700017912.rl
Method BLASTX
NCBI GI g1172977
BLAST score 271
E value 2.0e-24
Match length 63
% identity 84
NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 301233
Seq. ID cat700018032.rl
Method BLASTX
NCBI GI g4467125
BLAST score 284
E value 7.0e-26
Match length 64
% identity 78
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 301234
Seq. ID cat700018050.rl
Method BLASTX
NCBI GI g322752
BLAST score 262
E value 2.0e-23
Match length 73
% identity 60
NCBI Description auxin-independent growth promoter - Nicotiana tabacum >gi_559921_emb_CAA56570_ (X80301) axi 1 [Nicotiana tabacum]

Seq. No. 301235
Seq. ID cat700018068.rl
Method BLASTX
NCBI GI g4093155
BLAST score 197
E value 8.0e-16
Match length 71
% identity 58
NCBI Description (AF088281) phytochrome-associated protein 1 [Arabidopsis thaliana]

Seq. No. 301236
Seq. ID cat700018158.rl
Method BLASTX
NCBI GI g112994
BLAST score 239
E value 1.0e-20
Match length 54
% identity 91
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN >gi_82685_pir_S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 301237
Seq. ID cat700018189.rl
Method BLASTX
NCBI GI g3269285
BLAST score 144
E value 1.0e-09
Match length 60
% identity 53
NCBI Description (AL030978) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301238
Seq. ID cat700018373.rl
Method BLASTX
NCBI GI g1706956
BLAST score 166
E value 4.0e-12
Match length 70
% identity 41
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]

Seq. No. 301239
Seq. ID cat700018510.rl
Method BLASTX
NCBI GI g70774
BLAST score 385
E value 1.0e-37
Match length 78
% identity 100
NCBI Description histone H4 (TH091) - wheat >gi_170747 (M12277) histone H4 [Triticum aestivum]

Seq. No. 301240
Seq. ID cat700018543.rl
Method BLASTX
NCBI GI g4539452
BLAST score 346
E value 3.0e-33
Match length 70
% identity 84
NCBI Description (AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No. 301241
Seq. ID cat700018555.rl
Method BLASTX
NCBI GI g3152566
BLAST score 159
E value 3.0e-11
Match length 77
% identity 45
NCBI Description (AC002986) Similar to hypothetical protein YLR002c, gb_Z7314 from S. cerevisiae. [Arabidopsis thaliana]

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Seq. No. 301242
Seq. ID cat700018762.rl
Method BLASTX
NCBI GI g2281090
BLAST score 203
E value 2.0e-16
Match length 72
% identity 58
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301243
Seq. ID cat700018814.rl
Method BLASTX
NCBI GI g584825
BLAST score 310
E value 5.0e-29
Match length 67
% identity 85
NCBI Description B2 PROTEIN >gi_322726_pir_S32124 B2 protein - carrot
>gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus carota]

Seq. No. 301244
Seq. ID cat700018855.rl
Method BLASTX
NCBI GI g2290400
BLAST score 244
E value 3.0e-21
Match length 70
% identity 69
NCBI Description (U91339) stearoyl-ACP desaturase [Helianthus annuus]

Seq. No. 301245
Seq. ID cat700018911.rl
Method BLASTX
NCBI GI g2499477
BLAST score 161
E value 2.0e-11
Match length 29
% identity 97
NCBI Description 2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_861010_emb_CAA84396_ (Z34917) bas1 protein [Hordeum vulgare]

Seq. No. 301246
Seq. ID cat700019030.rl
Method BLASTN
NCBI GI g22322
BLAST score 82
E value 2.0e-38
Match length 165
% identity 88
NCBI Description Z.mays mRNA for H2B histone (clone cH2B214)

Seq. No. 301247
Seq. ID cat700019045.rl
Method BLASTX

NCBI GI g134946
BLAST score 277
E value 5.0e-25
Match length 79
% identity 65
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
(STEAROYL-ACP DESATURASE) >gi_66361_pir_OHSPAD
acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6)
precursor - spinach >gi_21230_emb_CAA44687_ (X62898)
stearoyl-acyl-[acyl-carrier-protein] desaturase [Spinacia
oleracea]

Seq. No. 301248
Seq. ID cat700019120.rl
Method BLASTX
NCBI GI g4262240
BLAST score 209
E value 4.0e-17
Match length 49
% identity 73
NCBI Description (AC006200) putative stress protein [Arabidopsis thaliana]

Seq. No. 301249
Seq. ID cat700019139.rl
Method BLASTX
NCBI GI g595295
BLAST score 199
E value 7.0e-16
Match length 80
% identity 50
NCBI Description (U09269) delta6-palmitoyl-acyl carrier protein desaturase
precursor [Thunbergia alata]

Seq. No. 301250
Seq. ID cat700019151.rl
Method BLASTX
NCBI GI g3786011
BLAST score 309
E value 8.0e-29
Match length 72
% identity 78
NCBI Description (AC005499) putative elongation factor [Arabidopsis
thaliana]

Seq. No. 301251
Seq. ID cat700019203.rl
Method BLASTN
NCBI GI g22292
BLAST score 87
E value 2.0e-41
Match length 175
% identity 87
NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 301252
Seq. ID cat700019228.rl
Method BLASTX

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NCBI GI g542157
BLAST score 177
E value 2.0e-13
Match length 66
% identity 58
NCBI Description ribosomal 5S RNA-binding protein - Rice

Seq. No. 301253
Seq. ID cat700019237.r1
Method BLASTX
NCBI GI g3219858
BLAST score 194
E value 2.0e-15
Match length 43
% identity 86
NCBI Description DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE
>gi_2129724_pir_S71204 RNA polymerase II 13.6 kDa chain -
Arabidopsis thaliana >gi_881501 (U28048) RNA polymerase II
13.6 kDa subunit [Arabidopsis thaliana]

Seq. No. 301254
Seq. ID cat700019241.r1
Method BLASTX
NCBI GI g2706450
BLAST score 181
E value 1.0e-13
Match length 69
% identity 58
NCBI Description (AJ225172) magnesium dependent soluble inorganic
pyrophosphatase [Solanum tuberosum]

Seq. No. 301255
Seq. ID cat700019270.r1
Method BLASTX
NCBI GI g2832661
BLAST score 232
E value 1.0e-19
Match length 80
% identity 60
NCBI Description (AL021710) pherophorin - like protein [Arabidopsis
thaliana]

Seq. No. 301256
Seq. ID cat700019281.r1
Method BLASTX
NCBI GI g2347207
BLAST score 140
E value 6.0e-09
Match length 57
% identity 40
NCBI Description (AC002338) APG protein isolog [Arabidopsis thaliana]
>gi_3150400 (AC004165) putative APG-like protein
[Arabidopsis thaliana]

Seq. No. 301257
Seq. ID cat700019338.r1
Method BLASTX

NCBI GI g2505874
BLAST score 176
E value 2.0e-13
Match length 69
% identity 48
NCBI Description (Y12776) putative kinase [Arabidopsis thaliana]

Seq. No. 301258
Seq. ID cat700019396.rl
Method BLASTX
NCBI GI g1524383
BLAST score 152
E value 2.0e-10
Match length 47
% identity 68
NCBI Description (X63374) 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]

Seq. No. 301259
Seq. ID cat700019404.rl
Method BLASTX
NCBI GI g1206013
BLAST score 262
E value 3.0e-23
Match length 61
% identity 77
NCBI Description (U44087) beta-D-glucosidase precursor [Zea mays]

Seq. No. 301260
Seq. ID cat700019425.rl
Method BLASTX
NCBI GI g3128195
BLAST score 320
E value 4.0e-30
Match length 77
% identity 79
NCBI Description (AC004521) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] >gi_3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana]

Seq. No. 301261
Seq. ID cat700019446.rl
Method BLASTX
NCBI GI g3935181
BLAST score 187
E value 2.0e-14
Match length 46
% identity 70
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No. 301262
Seq. ID cat700019462.rl
Method BLASTX
NCBI GI g4165488
BLAST score 257
E value 8.0e-23

Match length 60
% identity 83
NCBI Description (AJ132399) alpha-tubulin 3 [Hordeum vulgare]

Seq. No. 301263
Seq. ID cat700019515.rl
Method BLASTX
NCBI GI g404688
BLAST score 220
E value 2.0e-18
Match length 75
% identity 55
NCBI Description (L19074) cytochrome P450 [Catharanthus roseus]

Seq. No. 301264
Seq. ID cat700019575.rl
Method BLASTX
NCBI GI g2130003
BLAST score 196
E value 3.0e-21
Match length 64
% identity 81
NCBI Description squamosa-promoter binding protein 1 - garden snapdragon
>gi_1183866_emb_CAA63113_ (X92369) squamosa-promoter
binding protein 1 [Antirrhinum majus]

Seq. No. 301265
Seq. ID cat700019675.rl
Method BLASTX
NCBI GI g1174745
BLAST score 149
E value 5.0e-10
Match length 49
% identity 76
NCBI Description TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
>gi_1363523_pir_S53761 triose-phosphate isomerase (EC
5.3.1.1) precursor, chloroplast - rye
>gi_609262_emb_CAA83533_ (Z32521) triosephosphate isomerase
[Secale cereale] >gi_1095494_prf_2109226B triosephosphate
isomerase [Secale cereale]

Seq. No. 301266
Seq. ID cat700019710.rl
Method BLASTN
NCBI GI g168500
BLAST score 49
E value 9.0e-19
Match length 164
% identity 83
NCBI Description Maize (Zea mays) histone H4 gene (H4C14), complete cds

Seq. No. 301267
Seq. ID cat700019715.rl
Method BLASTX
NCBI GI g2511531
BLAST score 409
E value 2.0e-40

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Match length 78
% identity 100
NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]
>gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
[Eleusine indica]

Seq. No. 301268
Seq. ID cat700019756.rl
Method BLASTX
NCBI GI g2344901
BLAST score 144
E value 2.0e-09
Match length 31
% identity 84
NCBI Description (AC002388) serine/threonine protein kinase isolog
[Arabidopsis thaliana]

Seq. No. 301269
Seq. ID cat700019764.rl
Method BLASTX
NCBI GI g4586246
BLAST score 143
E value 2.0e-09
Match length 39
% identity 67
NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 301270
Seq. ID cat700019795.rl
Method BLASTX
NCBI GI g2058313
BLAST score 137
E value 9.0e-09
Match length 45
% identity 51
NCBI Description (X97433) cinnamoyl-CoA reductase [Eucalyptus gunnii]

Seq. No. 301271
Seq. ID cat700019839.rl
Method BLASTX
NCBI GI g1619297
BLAST score 389
E value 3.0e-38
Match length 73
% identity 100
NCBI Description (Y08490) alpha-tubulin 2 [Hordeum vulgare]

Seq. No. 301272
Seq. ID cat700020112.rl
Method BLASTX
NCBI GI g4587607
BLAST score 221
E value 2.0e-18
Match length 75
% identity 53
NCBI Description (AC006951) putative antisense basic fibroblast growth
factor [Arabidopsis thaliana]

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Seq. No. 301273
Seq. ID cat700020186.rl
Method BLASTX
NCBI GI g4567209
BLAST score 168
E value 3.0e-12
Match length 79
% identity 47
NCBI Description (AC007168) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301274
Seq. ID cat700020314.rl
Method BLASTN
NCBI GI g22378
BLAST score 35
E value 2.0e-10
Match length 43
% identity 95
NCBI Description Z.mays gene for nucleic acid binding protein

Seq. No. 301275
Seq. ID cat700020344.rl
Method BLASTX
NCBI GI g1172633
BLAST score 186
E value 2.0e-14
Match length 42
% identity 86
NCBI Description PROLIFERA PROTEIN >gi_675491 (L39954) contains MCM2/3/5 family signature; PROSITE; PS00847; disruption leads to early lethal phenotype; similar to MCM2/3/5 family, most similar to YBR1441 [Arabidopsis thaliana]

Seq. No. 301276
Seq. ID cat700020388.rl
Method BLASTX
NCBI GI g1405353
BLAST score 170
E value 2.0e-12
Match length 62
% identity 56
NCBI Description (D86086) canalicular multispecific organic anion transporter [Rattus norvegicus]

Seq. No. 301277
Seq. ID cat700020406.rl
Method BLASTX
NCBI GI g166384
BLAST score 163
E value 9.0e-12
Match length 33
% identity 94
NCBI Description (M35867) histone H3 (H3-1.1) [Medicago sativa]

Seq. No. 301278
Seq. ID cat700020418.rl

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Method BLASTN
NCBI GI g575730
BLAST score 187
E value 1.0e-101
Match length 187
% identity 100
NCBI Description Z.mays mRNA for transmembrane protein

Seq. No. 301279
Seq. ID cat700020521.rl
Method BLASTX
NCBI GI g4584545
BLAST score 190
E value 8.0e-15
Match length 65
% identity 55
NCBI Description (AL049608) putative protein [Arabidopsis thaliana]

Seq. No. 301280
Seq. ID cat700020544.rl
Method BLASTN
NCBI GI g22292
BLAST score 88
E value 4.0e-42
Match length 116
% identity 94
NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 301281
Seq. ID cat700020547.rl
Method BLASTX
NCBI GI g2832644
BLAST score 150
E value 3.0e-10
Match length 44
% identity 70
NCBI Description (AL021710) teosinte branched1 - like protein [Arabidopsis thaliana]

Seq. No. 301282
Seq. ID cat700020591.rl
Method BLASTX
NCBI GI g3687243
BLAST score 205
E value 1.0e-16
Match length 44
% identity 89
NCBI Description (AC005169) putative ribosomal protein [Arabidopsis thaliana]

Seq. No. 301283
Seq. ID cat700020621.rl
Method BLASTX
NCBI GI g4585875
BLAST score 220
E value 2.0e-18
Match length 58

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% identity 69
NCBI Description (AC005850) Unknown protein [Arabidopsis thaliana]

Seq. No. 301284
Seq. ID cat700020642.r1
Method BLASTX
NCBI GI g2662341
BLAST score 383
E value 1.0e-37
Match length 73
% identity 97
NCBI Description (D63580) EF-1 alpha [Oryza sativa]
>gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
[Oryza sativa]

Seq. No. 301285
Seq. ID cat700020659.r1
Method BLASTX
NCBI GI g3236252
BLAST score 145
E value 1.0e-09
Match length 56
% identity 55
NCBI Description (AC004684) CER1-like protein [Arabidopsis thaliana]

Seq. No. 301286
Seq. ID cat700020669.r1
Method BLASTX
NCBI GI g729671
BLAST score 151
E value 2.0e-10
Match length 32
% identity 94
NCBI Description HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]

Seq. No. 301287
Seq. ID cat700020717.r1
Method BLASTX
NCBI GI g1362086
BLAST score 405
E value 6.0e-40
Match length 83
% identity 94
NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine
S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
>gi_2129919_pir_S65957
5-methyltetrahydropteroyltriglutamate--homocysteine
S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
>gi_886471_emb_CAA58474_ (X83499) methionine synthase
[Catharanthus roseus]

Seq. No. 301288
Seq. ID cat700020833.r1
Method BLASTX
NCBI GI g135398
BLAST score 415

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E value 3.0e-41
Match length 77
% identity 100
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir_S15773 tubulin alpha-1 chain - maize >gi_22147_emb_CAA33734_ (X15704)
alpha1-tubulin [Zea mays]

Seq. No. 301289
Seq. ID cat700020905.rl
Method BLASTX
NCBI GI g82733
BLAST score 291
E value 1.0e-26
Match length 83
% identity 72
NCBI Description ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937)
ubiquitin fusion protein [Zea mays] >gi_902527 (U29161)
ubiquitin fusion protein [Zea mays]
>gi_1589388_prf_2211240B ubiquitin fusion protein [Zea mays]

Seq. No. 301290
Seq. ID cat700020907.rl
Method BLASTX
NCBI GI g4115386
BLAST score 144
E value 1.0e-09
Match length 72
% identity 47
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 301291
Seq. ID cat700020950.rl
Method BLASTX
NCBI GI g2624328
BLAST score 195
E value 2.0e-15
Match length 60
% identity 60
NCBI Description (AJ002894) OsGRP2 [Oryza sativa]

Seq. No. 301292
Seq. ID cat700021164.rl
Method BLASTX
NCBI GI g121982
BLAST score 168
E value 3.0e-12
Match length 36
% identity 92
NCBI Description HISTONE H2A.2.2

Seq. No. 301293
Seq. ID cat700021167.rl
Method BLASTX
NCBI GI g886740
BLAST score 232
E value 7.0e-20

Match length 56
% identity 86
NCBI Description (X84376) histone 4 [Zea mays]

Seq. No. 301294
Seq. ID cat700021185.rl
Method BLASTX
NCBI GI g3142295
BLAST score 179
E value 1.0e-13
Match length 70
% identity 51
NCBI Description (AC002411) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. [Arabidopsis thaliana]

Seq. No. 301295
Seq. ID cat700021266.rl
Method BLASTX
NCBI GI g2191187
BLAST score 161
E value 1.0e-11
Match length 52
% identity 62
NCBI Description (AF007271) contains similarity to a DNAJ-like domain [Arabidopsis thaliana]

Seq. No. 301296
Seq. ID cat700021355.rl
Method BLASTX
NCBI GI g2274859
BLAST score 168
E value 3.0e-12
Match length 32
% identity 97
NCBI Description (AJ000016) Cks1 protein [Arabidopsis thaliana]
>gi_4510420_gb_AAD21506.1 (AC006929) putative cyclin-dependent kinase regulatory subunit [Arabidopsis thaliana]

Seq. No. 301297
Seq. ID cat700021473.rl
Method BLASTX
NCBI GI g4539671
BLAST score 169
E value 2.0e-12
Match length 53
% identity 68
NCBI Description (AF061282) serine carboxypeptidase [Sorghum bicolor]

Seq. No. 301298
Seq. ID cat700021486.rl
Method BLASTN
NCBI GI g22320
BLAST score 34
E value 8.0e-10
Match length 64

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% identity 89
NCBI Description Maize H1 mRNA for H1 histone

Seq. No. 301299
Seq. ID cat700021541.rl
Method BLASTX
NCBI GI g4038471
BLAST score 228
E value 3.0e-19
Match length 52
% identity 83
NCBI Description (AF111029) 40S ribosomal protein S27 homolog [Zea mays]

Seq. No. 301300
Seq. ID cat700021543.rl
Method BLASTN
NCBI GI g662931
BLAST score 41
E value 6.0e-14
Match length 61
% identity 92
NCBI Description G. max mRNA for heat shock transcription factor

Seq. No. 301301
Seq. ID cat700021548.rl
Method BLASTX
NCBI GI g1304409
BLAST score 162
E value 1.0e-11
Match length 61
% identity 52
NCBI Description (U40344) myristyl-ACP desaturase [Pelargonium hortorum]

Seq. No. 301302
Seq. ID cat700021636.rl
Method BLASTN
NCBI GI g2645165
BLAST score 69
E value 1.0e-30
Match length 85
% identity 95
NCBI Description Oryza sativa mRNA, similar to ribosomal protein

Seq. No. 301303
Seq. ID cat700021704.rl
Method BLASTX
NCBI GI g3152596
BLAST score 156
E value 6.0e-11
Match length 75
% identity 56
NCBI Description (AC002986) YUP8H12R.36 [Arabidopsis thaliana]

Seq. No. 301304
Seq. ID cat700021768.rl
Method BLASTX
NCBI GI g4006878

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BLAST score 183
E value 5.0e-14
Match length 60
% identity 53
NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No. 301305
Seq. ID cat700021776.rl
Method BLASTN
NCBI GI g1906603
BLAST score 48
E value 2.0e-18
Match length 64
% identity 94
NCBI Description Zea mays ACCase gene, intron containing colonist1 and colonist2 retrotransposons and reverse transcriptase pseudogene, complete sequence

Seq. No. 301306
Seq. ID cat700021789.rl
Method BLASTX
NCBI GI g498931
BLAST score 205
E value 1.0e-16
Match length 70
% identity 63
NCBI Description (Z12825) ORF167; homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]

Seq. No. 301307
Seq. ID cat700021845.rl
Method BLASTN
NCBI GI g312178
BLAST score 71
E value 4.0e-32
Match length 75
% identity 49
NCBI Description Z.mays GapC2 gene

Seq. No. 301308
Seq. ID cat700021935.rl
Method BLASTX
NCBI GI g3335363
BLAST score 155
E value 9.0e-11
Match length 72
% identity 40
NCBI Description (AC003028) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301309
Seq. ID cat700022019.rl
Method BLASTX
NCBI GI g2583135
BLAST score 319
E value 5.0e-30
Match length 67

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% identity 87
NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]
>gi_3822216 (AF074948) FIL [Arabidopsis thaliana]
>gi_4322477_gb_AAD16053_ (AF087015) abnormal floral organs
protein [Arabidopsis thaliana]

Seq. No. 301310
Seq. ID ceu700421522.h1
Method BLASTX
NCBI GI g462195
BLAST score 436
E value 2.0e-43
Match length 93
% identity 89
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
>gi_100682_pir_S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza
sativa]

Seq. No. 301311
Seq. ID ceu700421529.h1
Method BLASTX
NCBI GI g2244989
BLAST score 223
E value 1.0e-18
Match length 71
% identity 62
NCBI Description (Z97340) strong similarity to naringenin 3-dioxygenase
[Arabidopsis thaliana]

Seq. No. 301312
Seq. ID ceu700421531.h1
Method BLASTX
NCBI GI g3292817
BLAST score 244
E value 6.0e-21
Match length 95
% identity 55
NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301313
Seq. ID ceu700421571.h1
Method BLASTX
NCBI GI g3721836
BLAST score 202
E value 4.0e-16
Match length 59
% identity 75
NCBI Description (AB013384) HIP3 [Homo sapiens]

Seq. No. 301314
Seq. ID ceu700421578.h1
Method BLASTX
NCBI GI g3269291
BLAST score 190
E value 1.0e-14

CDS/EST/CDNA

Match length 76
% identity 57
NCBI Description (AL030978) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 301315
Seq. ID ceu700421596.h1
Method BLASTX
NCBI GI g4210948
BLAST score 257
E value 1.0e-22
Match length 50
% identity 96
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 301316
Seq. ID ceu700421675.h1
Method BLASTN
NCBI GI g4503730
BLAST score 78
E value 3.0e-36
Match length 98
% identity 95
NCBI Description Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products >gi_3319236_gb_AF038847_AF038847 Homo sapiens 36 kDa FK506 binding protein (FKBP36) mRNA, complete cds

Seq. No. 301317
Seq. ID ceu700421714.h1
Method BLASTN
NCBI GI g1657753
BLAST score 187
E value 1.0e-101
Match length 199
% identity 98
NCBI Description Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds

Seq. No. 301318
Seq. ID ceu700421719.h1
Method BLASTN
NCBI GI g22430
BLAST score 233
E value 1.0e-128
Match length 275
% identity 97
NCBI Description Maize pseudo-Gpa2 pseudogene for glyceraldehyde-3-phosphate dehydrogenase subunit A

Seq. No. 301319
Seq. ID ceu700421726.h1
Method BLASTN
NCBI GI g3413919
BLAST score 146
E value 8.0e-77
Match length 158

% identity 98
NCBI Description Homo sapiens mRNA for KIAA0479 protein, partial cds

Seq. No. 301320
Seq. ID ceu700421728.h1
Method BLASTX
NCBI GI g3292816
BLAST score 169
E value 3.0e-12
Match length 60
% identity 60
NCBI Description (AL031018) putative fizzy-related protein [Arabidopsis thaliana]

Seq. No. 301321
Seq. ID ceu700421730.h1
Method BLASTX
NCBI GI g4585897
BLAST score 189
E value 1.0e-14
Match length 55
% identity 64
NCBI Description (AC007133) hypothetical protein, 5' partial [Arabidopsis thaliana]

Seq. No. 301322
Seq. ID ceu700421753.h1
Method BLASTN
NCBI GI g22221
BLAST score 44
E value 1.0e-15
Match length 60
% identity 93
NCBI Description Z.mays ZSF4C3 gene for zein

Seq. No. 301323
Seq. ID ceu700421774.h1
Method BLASTN
NCBI GI g4454705
BLAST score 146
E value 7.0e-77
Match length 150
% identity 99
NCBI Description Homo sapiens chromosome 17 HSPC009 mRNA, complete cds

Seq. No. 301324
Seq. ID ceu700421787.h1
Method BLASTX
NCBI GI g1709848
BLAST score 191
E value 7.0e-15
Match length 78
% identity 53
NCBI Description PHOTOSYSTEM II REACTION CENTRE W PROTEIN
>gi_2147936_pir_S73268 photosystem II protein W - Porphyra purpurea chloroplast >gi_1276813 (U38804) Photosystem II protein W [Porphyra purpurea]

Seq. No. 301325
Seq. ID ceu700421808.h1
Method BLASTX
NCBI GI g2393722
BLAST score 180
E value 9.0e-14
Match length 36
% identity 97
NCBI Description (U90313) glutathione-S-transferase homolog [Homo sapiens]

Seq. No. 301326
Seq. ID ceu700421842.h1
Method BLASTN
NCBI GI g3342001
BLAST score 134
E value 1.0e-69
Match length 183
% identity 94
NCBI Description Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds

Seq. No. 301327
Seq. ID ceu700421848.h1
Method BLASTX
NCBI GI g4263831
BLAST score 140
E value 6.0e-09
Match length 78
% identity 44
NCBI Description (AC006067) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No. 301328
Seq. ID ceu700421861.h1
Method BLASTX
NCBI GI g4512018
BLAST score 306
E value 2.0e-28
Match length 71
% identity 82
NCBI Description (AF106660) mRNA binding protein precursor [Lycopersicon esculentum]

Seq. No. 301329
Seq. ID ceu700421876.h1
Method BLASTN
NCBI GI g3043569
BLAST score 125
E value 3.0e-64
Match length 154
% identity 94
NCBI Description Homo sapiens mRNA for KIAA0523 protein, partial cds

Seq. No. 301330
Seq. ID ceu700421973.h1
Method BLASTX

NCBI GI g3641252
BLAST score 281
E value 1.0e-25
Match length 57
% identity 86
NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No. 301331
Seq. ID ceu700422069.h1
Method BLASTX
NCBI GI g1001257
BLAST score 235
E value 5.0e-20
Match length 84
% identity 51
NCBI Description (D64003) hypothetical protein [Synechocystis sp.]

Seq. No. 301332
Seq. ID ceu700422087.h1
Method BLASTX
NCBI GI g4506883
BLAST score 186
E value 2.0e-14
Match length 39
% identity 97
NCBI Description semenogelin I >gi_134426 sp_P04279 SEM1_HUMAN SEMENOGENIN I PROTEIN PRECURSOR (SGI) [CONTAINS: SEMINAL BASIC PROTEIN; ALPHA-INHIBIN-92; ALPHA-INHIBIN-31] >gi_338019 (J04440) semenogelin [Homo sapiens]

Seq. No. 301333
Seq. ID ceu700422091.h1
Method BLASTN
NCBI GI g2411434
BLAST score 243
E value 1.0e-134
Match length 251
% identity 99
NCBI Description Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence [Homo sapiens]

Seq. No. 301334
Seq. ID ceu700422165.h1
Method BLASTX
NCBI GI g4539355
BLAST score 139
E value 9.0e-09
Match length 68
% identity 46
NCBI Description (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 301335
Seq. ID ceu700422192.h1
Method BLASTX
NCBI GI g4432825

BLAST score 292
E value 1.0e-26
Match length 83
% identity 61
NCBI Description (AC006593) putative SOP2p protein [Arabidopsis thaliana]

Seq. No. 301336
Seq. ID ceu700422230.h1
Method BLASTX
NCBI GI g3212861
BLAST score 195
E value 2.0e-15
Match length 46
% identity 78
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 301337
Seq. ID ceu700422244.h1
Method BLASTN
NCBI GI g452340
BLAST score 79
E value 7.0e-37
Match length 95
% identity 96
NCBI Description Z.mays mRNA for type II light-harvesting chlorophyll a/b-binding protein

Seq. No. 301338
Seq. ID ceu700422316.h1
Method BLASTN
NCBI GI g1684871
BLAST score 159
E value 1.0e-84
Match length 163
% identity 99
NCBI Description Homo sapiens LPS-Induced TNF-Alpha Factor (LITAF) mRNA, complete cds

Seq. No. 301339
Seq. ID ceu700422377.h1
Method BLASTX
NCBI GI g82733
BLAST score 190
E value 6.0e-15
Match length 39
% identity 90
NCBI Description ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937)
ubiquitin fusion protein [Zea mays] >gi_902527 (U29161)
ubiquitin fusion protein [Zea mays]
>gi_1589388_prf_2211240B ubiquitin fusion protein [Zea mays]

Seq. No. 301340
Seq. ID ceu700422385.h1
Method BLASTX
NCBI GI g99758
BLAST score 159

E value 3.0e-11
Match length 37
% identity 76
NCBI Description monosaccharid transport protein STP4 - Arabidopsis thaliana
>gi_16524_emb_CAA47325_(X66857) sugar transport protein
[Arabidopsis thaliana]

Seq. No. 301341
Seq. ID ceu700422424.h1
Method BLASTN
NCBI GI g4567173
BLAST score 107
E value 1.0e-53
Match length 123
% identity 97
NCBI Description Homo sapiens chromosome 19, cosmid R34187, complete sequence

Seq. No. 301342
Seq. ID ceu700422426.h1
Method BLASTX
NCBI GI g3914555
BLAST score 234
E value 4.0e-20
Match length 71
% identity 68
NCBI Description PUTATIVE RIBOSOME-BINDING FACTOR A, CHLOROPLAST PRECURSOR
>gi_3096942_emb_CAA18852.1_(AL023094) putative protein
[Arabidopsis thaliana]

Seq. No. 301343
Seq. ID ceu700422519.h1
Method BLASTX
NCBI GI g3941468
BLAST score 259
E value 8.0e-23
Match length 55
% identity 78
NCBI Description (AF062888) putative transcription factor [Arabidopsis thaliana]

Seq. No. 301344
Seq. ID ceu700422540.h1
Method BLASTX
NCBI GI g1747296
BLAST score 330
E value 4.0e-31
Match length 70
% identity 97
NCBI Description (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
>gi_3298476_dbj_BAA31524_(AB012766) ovp2 [Oryza sativa]

Seq. No. 301345
Seq. ID ceu700422613.h1
Method BLASTN
NCBI GI g405634
BLAST score 85

E value 2.0e-40
Match length 180
% identity 88
NCBI Description Z.mays zmcpt mRNA triose phosphate/phosphate translocator

Seq. No. 301346
Seq. ID ceu700422631.h1
Method BLASTX
NCBI GI g2262136
BLAST score 159
E value 2.0e-11
Match length 31
% identity 94
NCBI Description (AC002330) predicted protein of unknown function [Arabidopsis thaliana] >gi_4263520_gb_AAD15346_ (AC004044) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No. 301347
Seq. ID ceu700422639.h1
Method BLASTX
NCBI GI g4506885
BLAST score 227
E value 3.0e-19
Match length 58
% identity 79
NCBI Description semenogelin II >gi_401079_sp_Q02383_SEM2_HUMAN SEMENOGENLIN II PRECURSOR (SGII) >gi_346359_pir_A43412 semenogelin II precursor - human >gi_307418 (M81651) semenogelin II [Homo sapiens] >gi_338239 (M81652) semenogelin II [Homo sapiens] >gi_1147570_emb_CAA87637_ (Z47556) semenogelin II [Homo sapiens]

Seq. No. 301348
Seq. ID ceu700422736.h1
Method BLASTX
NCBI GI g2832677
BLAST score 154
E value 2.0e-10
Match length 82
% identity 38
NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301349
Seq. ID ceu700422775.h1
Method BLASTN
NCBI GI g2984582
BLAST score 120
E value 4.0e-61
Match length 268
% identity 95
NCBI Description Homo sapiens chromosome 9, P1 clone 11659, complete sequence [Homo sapiens]

Seq. No. 301350
Seq. ID ceu700422887.h1
Method BLASTX

NCBI GI g4455271
BLAST score 240
E value 1.0e-20
Match length 81
% identity 56
NCBI Description (AL035527) serine protease-like protein [Arabidopsis thaliana]

Seq. No. 301351
Seq. ID ceu700422908.h1
Method BLASTX
NCBI GI g2244940
BLAST score 161
E value 3.0e-11
Match length 47
% identity 64
NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301352
Seq. ID ceu700422974.h1
Method BLASTN
NCBI GI g1663516
BLAST score 172
E value 4.0e-92
Match length 234
% identity 94
NCBI Description Homo sapiens mRNA for membrane glycoprotein M6, complete cds

Seq. No. 301353
Seq. ID ceu700423143.h1
Method BLASTN
NCBI GI g2898171
BLAST score 103
E value 2.0e-51
Match length 115
% identity 97
NCBI Description Homo sapiens microtubule-associated protein tau (tau) gene, alternatively spliced products, exon 13/14 and complete cds

Seq. No. 301354
Seq. ID ceu700423146.h1
Method BLASTX
NCBI GI g3293031
BLAST score 320
E value 6.0e-30
Match length 90
% identity 67
NCBI Description (AJ007574) amino acid carrier [Ricinus communis]

Seq. No. 301355
Seq. ID ceu700423150.h1
Method BLASTX
NCBI GI g2494275
BLAST score 253
E value 4.0e-22
Match length 88

% identity 55
NCBI Description ELONGATION FACTOR P (EF-P) >gi_1399829 (U59235) elongation factor P [Synechococcus PCC7942]

Seq. No. 301356
Seq. ID ceu700423233.h1
Method BLASTX
NCBI GI g2760327
BLAST score 246
E value 4.0e-21
Match length 58
% identity 79
NCBI Description (AC002130) F1N21.12 [Arabidopsis thaliana]

Seq. No. 301357
Seq. ID ceu700423234.h1
Method BLASTX
NCBI GI g1279876
BLAST score 148
E value 2.0e-14
Match length 61
% identity 61
NCBI Description (U52867) high affinity sulfate transporter HVST1 [Hordeum vulgare]

Seq. No. 301358
Seq. ID ceu700423243.h1
Method BLASTN
NCBI GI g1213279
BLAST score 54
E value 1.0e-21
Match length 54
% identity 100
NCBI Description Z.mays ZEMc gene

Seq. No. 301359
Seq. ID ceu700423301.h1
Method BLASTX
NCBI GI g231654
BLAST score 157
E value 5.0e-11
Match length 33
% identity 88
NCBI Description BRITTLE-1 PROTEIN PRECURSOR >gi_82676_pir_JQ1459 Bt1 protein precursor - maize >gi_168426 (M79333) brittle-1 protein [Zea mays]

Seq. No. 301360
Seq. ID ceu700423456.h1
Method BLASTX
NCBI GI g3193328
BLAST score 296
E value 4.0e-27
Match length 76
% identity 67
NCBI Description (AF069299) No definition line found [Arabidopsis thaliana]

Seq. No. 301361
Seq. ID ceu700423471.h1
Method BLASTN
NCBI GI g4240320
BLAST score 275
E value 1.0e-153
Match length 287
% identity 99
NCBI Description Homo sapiens mRNA for KIAA0916 protein, partial cds

Seq. No. 301362
Seq. ID ceu700423583.h1
Method BLASTN
NCBI GI g4503872
BLAST score 83
E value 2.0e-39
Match length 99
% identity 96
NCBI Description Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1)
mRNA >gi_182935_gb_M81883 HUMGAD67A Human glutamate
decarboxylase (GAD67) mRNA, complete cds.
>gi_1408341_gb_G28526_G28526 human STS SHGC-31511

Seq. No. 301363
Seq. ID ceu700423665.h1
Method BLASTX
NCBI GI g3522947
BLAST score 179
E value 2.0e-13
Match length 52
% identity 62
NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301364
Seq. ID ceu700423670.h1
Method BLASTX
NCBI GI g4510348
BLAST score 148
E value 8.0e-10
Match length 57
% identity 60
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 301365
Seq. ID ceu700423689.h1
Method BLASTX
NCBI GI g419792
BLAST score 419
E value 1.0e-41
Match length 84
% identity 94
NCBI Description alternative oxidase - voodoo lily >gi_21216_emb_CAA78823_
(Z15117) salicylic acid-inducible alternative oxidase
[Sauromatum guttatum]

Seq. No. 301366
Seq. ID ceu700423711.h1

Method BLASTN
NCBI GI g733457
BLAST score 84
E value 6.0e-40
Match length 127
% identity 94
NCBI Description Zea mays chlorophyll a/b-binding apoprotein CP24 (Lhcb6-1) mRNA, complete cds

Seq. No. 301367
Seq. ID ceu700423717.h1
Method BLASTX
NCBI GI g2129628
BLAST score 154
E value 2.0e-10
Match length 92
% identity 43
NCBI Description ketoconazole resistant protein - Arabidopsis thaliana >gi_928938_emb_CAA61433_ (X89036) ketoconazole resistant protein [Arabidopsis thaliana]

Seq. No. 301368
Seq. ID ceu700423838.h1
Method BLASTX
NCBI GI g4206306
BLAST score 289
E value 2.0e-41
Match length 89
% identity 95
NCBI Description (AF049110) prpol [Zea mays]

Seq. No. 301369
Seq. ID ceu700423847.h1
Method BLASTN
NCBI GI g387670
BLAST score 135
E value 2.0e-70
Match length 139
% identity 99
NCBI Description Human MG61 mRNA, partial cds

Seq. No. 301370
Seq. ID ceu700423863.h1
Method BLASTN
NCBI GI g4507098
BLAST score 59
E value 8.0e-25
Match length 132
% identity 95
NCBI Description Homo sapiens synaptosomal-associated protein, 25kD (SNAP25) mRNA >gi_2373387_dbj_D21267_D21267 Homo sapiens mRNA, complete cds

Seq. No. 301371
Seq. ID ceu700423877.h1
Method BLASTX
NCBI GI g4467125

BLAST score 208
E value 8.0e-17
Match length 88
% identity 53
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 301372
Seq. ID ceu700423958.h1
Method BLASTN
NCBI GI g2668747
BLAST score 61
E value 7.0e-26
Match length 61
% identity 100
NCBI Description Zea mays ribosomal protein L17 (rpl17) mRNA, complete cds

Seq. No. 301373
Seq. ID ceu700423967.h1
Method BLASTN
NCBI GI g3360421
BLAST score 223
E value 1.0e-122
Match length 243
% identity 98
NCBI Description Homo sapiens clone 23887 mRNA sequence

Seq. No. 301374
Seq. ID ceu700424002.h1
Method BLASTX
NCBI GI g585574
BLAST score 234
E value 4.0e-20
Match length 52
% identity 85
NCBI Description NEURONAL PROTEIN NP25 >gi_2119343_pir_I52644 neuronal protein - rat >gi_205755 (M84725) neuronal protein [Rattus norvegicus]

Seq. No. 301375
Seq. ID ceu700424010.h1
Method BLASTN
NCBI GI g3097872
BLAST score 120
E value 4.0e-61
Match length 245
% identity 97
NCBI Description Homo sapiens chromosome 17, clone HCIT305D20, complete sequence [Homo sapiens]

Seq. No. 301376
Seq. ID ceu700424017.h1
Method BLASTN
NCBI GI g1835730
BLAST score 33
E value 4.0e-09
Match length 33
% identity 100

NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA,
complete cds

Seq. No. 301377
Seq. ID ceu700424046.h1
Method BLASTX
NCBI GI g2286121
BLAST score 144
E value 2.0e-09
Match length 42
% identity 69
NCBI Description (U88068) sec14 like protein [Oryza sativa]

Seq. No. 301378
Seq. ID ceu700424085.h1
Method BLASTN
NCBI GI g37967
BLAST score 198
E value 1.0e-107
Match length 254
% identity 94
NCBI Description H.sapiens WRS gene for tryptophanyl-tRNA synthetase, exon

Seq. No. 301379
Seq. ID ceu700424116.h1
Method BLASTN
NCBI GI g3413869
BLAST score 120
E value 5.0e-61
Match length 252
% identity 91
NCBI Description Homo sapiens mRNA for KIAA0454 protein, partial cds

Seq. No. 301380
Seq. ID ceu700424174.h1
Method BLASTX
NCBI GI g2815606
BLAST score 140
E value 1.0e-13
Match length 56
% identity 76
NCBI Description (AF025439) Opa-interacting protein OIP3 [Homo sapiens]

Seq. No. 301381
Seq. ID ceu700424195.h1
Method BLASTX
NCBI GI g461999
BLAST score 166
E value 1.0e-20
Match length 82
% identity 67
NCBI Description ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)

Seq. No. 301382
Seq. ID ceu700424281.h1
Method BLASTX
NCBI GI g4510348

BLAST score 158
E value 3.0e-11
Match length 60
% identity 70
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 301383
Seq. ID ceu700424324.h1
Method BLASTX
NCBI GI g540450
BLAST score 152
E value 3.0e-10
Match length 53
% identity 62
NCBI Description (M28584) MHC class II DR-beta [Homo sapiens]

Seq. No. 301384
Seq. ID ceu700424327.h1
Method BLASTX
NCBI GI g4508068
BLAST score 162
E value 2.0e-11
Match length 63
% identity 57
NCBI Description (AC005882) 3063 [Arabidopsis thaliana]

Seq. No. 301385
Seq. ID ceu700424345.h1
Method BLASTX
NCBI GI g466160
BLAST score 230
E value 2.0e-19
Match length 58
% identity 76
NCBI Description HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
>gi_630771_pir_S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis elegans]

Seq. No. 301386
Seq. ID ceu700424359.h1
Method BLASTX
NCBI GI g2494849
BLAST score 287
E value 3.0e-26
Match length 77
% identity 69
NCBI Description HYDROXYACYLGLUTATHIONE HYDROLASE (GLYOXALASE II) (GLX II)
>gi_1237213_emb_CAA62483_ (X90999) glyoxalase II [Homo sapiens]

Seq. No. 301387
Seq. ID ceu700424413.h1
Method BLASTN
NCBI GI g3582311
BLAST score 63
E value 2.0e-27

Match length 87
% identity 93
NCBI Description Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence [Homo sapiens]

Seq. No. 301388
Seq. ID ceu700424487.h1
Method BLASTN
NCBI GI g3005598
BLAST score 79
E value 5.0e-37
Match length 87
% identity 98
NCBI Description Homo sapiens katanin p80 subunit mRNA, complete cds

Seq. No. 301389
Seq. ID ceu700424502.h1
Method BLASTX
NCBI GI g133978
BLAST score 255
E value 2.0e-22
Match length 75
% identity 73
NCBI Description 40S RIBOSOMAL PROTEIN S6 (PHOSPHOPROTEIN NP33)
>gi_70932_pir_R3RTS6 ribosomal protein S6 - rat
>gi_70933_pir_R3MS6 ribosomal protein S6 - mouse
>gi_319910_pir_R3HU6 ribosomal protein S6 - human
>gi_36148_emb_CAA47719_ (X67309) ribosomal protein S6 [Homo sapiens] >gi_54010_emb_CAA68430_ (Y00348) ribosomal protein S6 [Mus musculus] >gi_206747 (M29358) ribosomal protein S6 [Rattus norvegicus] >gi_307393 (M77232) ribosomal protein S6 [Homo sapiens] >gi_1177549_emb_CAA90936_ (Z54209) rpS6 [Mus musculus]

Seq. No. 301390
Seq. ID ceu700424520.h1
Method BLASTX
NCBI GI g3288881
BLAST score 292
E value 1.0e-26
Match length 88
% identity 77
NCBI Description (AF073839) bithoraxoid-like protein [Rattus norvegicus]

Seq. No. 301391
Seq. ID ceu700424560.h1
Method BLASTX
NCBI GI g4468986
BLAST score 176
E value 4.0e-13
Match length 66
% identity 44
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 301392
Seq. ID ceu700424624.h1
Method BLASTN

NCBI GI g4506044
 BLAST score 105
 E value 3.0e-52
 Match length 173
 % identity 88
 NCBI Description Homo sapiens proteoglycan 1, secretory granule (PRG1) mRNA
 >gi_32432_emb_X17042_HSHPCP Human mRNA for hematopoetic
 proteoglycan core protein

Seq. No. 301393
 Seq. ID ceu700424638.h1
 Method BLASTN
 NCBI GI g4090180
 BLAST score 85
 E value 2.0e-40
 Match length 120
 % identity 93
 NCBI Description Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human
 BAC Library) complete sequence [Homo sapiens]

Seq. No. 301394
 Seq. ID ceu700424641.h1
 Method BLASTN
 NCBI GI g181207
 BLAST score 142
 E value 2.0e-74
 Match length 178
 % identity 97
 NCBI Description Human Cu/Zn superoxide dismutase gene

Seq. No. 301395
 Seq. ID ceu700424686.h1
 Method BLASTX
 NCBI GI g3287688
 BLAST score 148
 E value 5.0e-10
 Match length 40
 % identity 72
 NCBI Description (AC003979) Contains similarity to ycf37 gene product
 gb_1001425 from Synechocystis sp. genome gb_D63999. ESTs
 gb_T43026, gb_R64902, gb_Z18169 and gb_N37374 come from
 this gene. [Arabidopsis thaliana]

Seq. No. 301396
 Seq. ID ceu700424714.h1
 Method BLASTX
 NCBI GI g3006143
 BLAST score 164
 E value 1.0e-11
 Match length 42
 % identity 69
 NCBI Description (AL022299) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 301397
 Seq. ID ceu700424732.h1
 Method BLASTX
 NCBI GI g2244816

BLAST score 162
E value 2.0e-11
Match length 67
% identity 40
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301398
Seq. ID ceu700424769.h1
Method BLASTX
NCBI GI g4115559
BLAST score 238
E value 2.0e-20
Match length 82
% identity 50
NCBI Description (AB013596) UDP-glucose:anthocyanin 5-O-glucosyltransferase [Perilla frutescens]

Seq. No. 301399
Seq. ID ceu700424933.h1
Method BLASTX
NCBI GI g3779218
BLAST score 142
E value 3.0e-09
Match length 36
% identity 72
NCBI Description (AF030879) protein kinase CPK1 [Solanum tuberosum]

Seq. No. 301400
Seq. ID ceu700424993.h1
Method BLASTX
NCBI GI g1806192
BLAST score 164
E value 9.0e-12
Match length 84
% identity 40
NCBI Description (Z84395) sppA [Mycobacterium tuberculosis]

Seq. No. 301401
Seq. ID ceu700424996.h1
Method BLASTN
NCBI GI g3036778
BLAST score 121
E value 5.0e-62
Match length 129
% identity 98
NCBI Description Human DNA sequence from cosmid 398G5 from a region of the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains RAR (RAS like GTPASE) like gene, an anonymous gene and ESTs. Contains CpG island

Seq. No. 301402
Seq. ID ceu700425005.h1
Method BLASTX
NCBI GI g295855
BLAST score 313
E value 3.0e-29
Match length 64

09684016-202000

% identity 97
NCBI Description (X15642) P-pyruvate carboxylase [Zea mays]

Seq. No. 301403
Seq. ID ceu700425034.h1
Method BLASTX
NCBI GI g2979544
BLAST score 320
E value 7.0e-30
Match length 93
% identity 60
NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No. 301404
Seq. ID ceu700425066.h1
Method BLASTX
NCBI GI g4507065
BLAST score 440
E value 5.0e-44
Match length 92
% identity 83
NCBI Description secretory leukocyte protease inhibitor
(antileukoproteinase) >gi_113636_sp_P03973_ALK1_HUMAN
ANTILEUKOPROTEINASE 1 PRECURSOR (ALP) (HUSI-1) (SEMINAL
PROTEINASE INHIBITOR) (SECRETORY LEUKOCYTE PROTEASE
INHIBITOR) (BLPI) (MUCUS PROTEINASE INHIBITOR) (MPI)
>gi_1070529_pir_TIHUSP antileukoproteinase 1 precursor -
human >gi_28639_emb_CAA28158 (X04470) precursor ALP [Homo
sapiens] >gi_36491_emb_CAA28188 (X04503) SLPI-precursor
[Homo sapiens] >gi_758101_emb_CAA28187 (X04502) secretory
leukocyte protease inhibitor (SLPI) [Homo sapiens]
>gi_4378759_gb_AAD19661 (AF114471) secretory leukocyte
proteinase inhibitor precursor [Homo sapiens]

Seq. No. 301405
Seq. ID ceu700425119.h1
Method BLASTN
NCBI GI g3176654
BLAST score 70
E value 1.0e-31
Match length 123
% identity 96
NCBI Description Homo sapiens chromosome 16, cosmid clone RT140 (LANL),
complete sequence [Homo sapiens]

Seq. No. 301406
Seq. ID ceu700425120.h1
Method BLASTX
NCBI GI g4102582
BLAST score 163
E value 2.0e-11
Match length 63
% identity 52
NCBI Description (AF013115) CAO [Arabidopsis thaliana]

Seq. No. 301407
Seq. ID ceu700425135.h1

Method BLASTN
NCBI GI g687589
BLAST score 163
E value 7.0e-87
Match length 187
% identity 97
NCBI Description Human (AF1q) mRNA, complete cds

Seq. No. 301408
Seq. ID ceu700425136.h1
Method BLASTN
NCBI GI g285909
BLAST score 177
E value 4.0e-95
Match length 212
% identity 97
NCBI Description Homo sapiens P2 mRNA for ATP synthase subunit c, complete cds

Seq. No. 301409
Seq. ID ceu700425224.h1
Method BLASTX
NCBI GI g4262242
BLAST score 148
E value 1.0e-16
Match length 52
% identity 84
NCBI Description (AC006200) NADC homolog [Arabidopsis thaliana]

Seq. No. 301410
Seq. ID ceu700425227.h1
Method BLASTN
NCBI GI g3550039
BLAST score 114
E value 7.0e-58
Match length 121
% identity 99
NCBI Description Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B

Seq. No. 301411
Seq. ID ceu700425273.h1
Method BLASTN
NCBI GI g3281967
BLAST score 142
E value 2.0e-74
Match length 169
% identity 96
NCBI Description Human DNA sequence from clone 425C14 on chromosome 6q22. Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein DIFF33 gene. Contains

Seq. No. 301412
Seq. ID ceu700425274.h1

Method BLASTN
NCBI GI g1633547
BLAST score 101
E value 6.0e-50
Match length 167
% identity 98
NCBI Description Human chromosome 12p13 sequence, complete sequence [Homo sapiens]

Seq. No. 301413
Seq. ID ceu700425276.h1
Method BLASTN
NCBI GI g3582736
BLAST score 98
E value 4.0e-48
Match length 105
% identity 99
NCBI Description Homo sapiens putative holocytochrome c-type synthetase (HCCS) gene, nuclear gene encoding mitochondrial protein, exon

Seq. No. 301414
Seq. ID ceu700425315.h1
Method BLASTX
NCBI GI g3800742
BLAST score 140
E value 4.0e-09
Match length 35
% identity 80
NCBI Description (AF036548) RGC-32 [Rattus norvegicus]

Seq. No. 301415
Seq. ID ceu700425331.h1
Method BLASTN
NCBI GI g533965
BLAST score 134
E value 1.0e-69
Match length 188
% identity 93
NCBI Description H.sapiens (xs99) mRNA, 344bp

Seq. No. 301416
Seq. ID ceu700425370.h1
Method BLASTX
NCBI GI g3287693
BLAST score 210
E value 2.0e-22
Match length 62
% identity 87
NCBI Description (AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No. 301417
Seq. ID ceu700425446.h1
Method BLASTN
NCBI GI g1228046

BLAST score 130
E value 3.0e-67
Match length 150
% identity 97
NCBI Description Human mRNA for KIAA0199 gene, partial cds

Seq. No. 301418
Seq. ID ceu700425609.h1
Method BLASTX
NCBI GI g2832692
BLAST score 239
E value 2.0e-20
Match length 63
% identity 68
NCBI Description (AL021713) putative protein [Arabidopsis thaliana]

Seq. No. 301419
Seq. ID ceu700425688.h1
Method BLASTN
NCBI GI g4503012
BLAST score 195
E value 1.0e-106
Match length 218
% identity 97
NCBI Description Homo sapiens copine I (CPNE1) mRNA
>gi_1791256_gb_U83246_HSU83246 Homo sapiens copine I mRNA,
complete cds

Seq. No. 301420
Seq. ID ceu700425793.h2
Method BLASTX
NCBI GI g2244965
BLAST score 245
E value 3.0e-21
Match length 79
% identity 57
NCBI Description (Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No. 301421
Seq. ID ceu700425940.h1
Method BLASTN
NCBI GI g4185579
BLAST score 103
E value 3.0e-51
Match length 119
% identity 97
NCBI Description Homo sapiens p120E4F transcription factor mRNA, complete
cds

Seq. No. 301422
Seq. ID ceu700426046.h1
Method BLASTX
NCBI GI g282748
BLAST score 182
E value 9.0e-14
Match length 80
% identity 42

NCBI Description gene coxII intron 2 protein - liverwort (*Marchantia polymorpha*) mitochondrion >gi_786218 (M68929) coxII intron2 ORF [*Marchantia polymorpha*]

Seq. No. 301423
Seq. ID ceu700426114.h1
Method BLASTN
NCBI GI g3851004
BLAST score 36
E value 2.0e-11
Match length 52
% identity 92

NCBI Description Zea mays pyruvate dehydrogenase E1 alpha subunit RNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 301424
Seq. ID ceu700426128.h1
Method BLASTX
NCBI GI g3402713
BLAST score 175
E value 3.0e-13
Match length 67
% identity 55

NCBI Description (AC004261) hypothetical protein [*Arabidopsis thaliana*]

Seq. No. 301425
Seq. ID ceu700426176.h1
Method BLASTN
NCBI GI g4062855
BLAST score 99
E value 7.0e-49
Match length 135
% identity 93

NCBI Description Homo sapiens mRNA for HIS1 protein, complete cds

Seq. No. 301426
Seq. ID ceu700426183.h1
Method BLASTX
NCBI GI g1154954
BLAST score 173
E value 1.0e-12
Match length 52
% identity 75

NCBI Description (X94693) histone H2A [*Triticum aestivum*]

Seq. No. 301427
Seq. ID ceu700426184.h1
Method BLASTX
NCBI GI g82466
BLAST score 160
E value 3.0e-11
Match length 49
% identity 61

NCBI Description probable ferredoxin--NADP+ reductase (EC 1.18.1.2) - rice >gi_218163_dbj_BAA02248_(D12815) ferredoxin-NADP+ reductase enzyme [*Oryza sativa*]

Seq. No. 301428
Seq. ID ceu700426186.h1
Method BLASTX
NCBI GI g2129698
BLAST score 158
E value 3.0e-11
Match length 53
% identity 64
NCBI Description protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
>gi_1054633_emb_CAA63387_ (X92728) protein kinase
[Arabidopsis thaliana]

Seq. No. 301429
Seq. ID ceu700426245.h1
Method BLASTX
NCBI GI g4263714
BLAST score 404
E value 1.0e-39
Match length 96
% identity 83
NCBI Description (AC006223) putative integral membrane protein [Arabidopsis thaliana]

Seq. No. 301430
Seq. ID ceu700426343.h1
Method BLASTX
NCBI GI g115771
BLAST score 292
E value 1.0e-26
Match length 55
% identity 100
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll a/b-binding protein precursor - maize
>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

Seq. No. 301431
Seq. ID ceu700426425.h1
Method BLASTN
NCBI GI g3108052
BLAST score 58
E value 2.0e-24
Match length 106
% identity 89
NCBI Description Zea mays myo-inositol 1-phosphate synthase mRNA, complete cds

Seq. No. 301432
Seq. ID ceu700426431.h1
Method BLASTN
NCBI GI g22396
BLAST score 43
E value 1.0e-15
Match length 107
% identity 85
NCBI Description Z.mays gene for phosphoenolpyruvate carboxylase (EC

4.1.1.31)

Seq. No. 301433
Seq. ID ceu700426494.h1
Method BLASTX
NCBI GI g1086147
BLAST score 153
E value 1.0e-10
Match length 31
% identity 90
NCBI Description protein S2 - Phalaris coerulescens >gi_556833_emb_CAA57520_(X81992) S2 [Phalaris coerulescens]

Seq. No. 301434
Seq. ID ceu700426584.h1
Method BLASTX
NCBI GI g2144902
BLAST score 190
E value 6.0e-15
Match length 39
% identity 100
NCBI Description semenogelin I precursor - human >gi_487420 (M81650) SEMGI [Homo sapiens] >gi_1147569_emb_CAA87636_ (Z47556) semenogelin I [Homo sapiens]

Seq. No. 301435
Seq. ID ceu700426592.h1
Method BLASTN
NCBI GI g4416300
BLAST score 51
E value 5.0e-20
Match length 63
% identity 32
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No. 301436
Seq. ID ceu700426733.h1
Method BLASTX
NCBI GI g3402751
BLAST score 149
E value 1.0e-13
Match length 88
% identity 27
NCBI Description (AL031187) putative protein [Arabidopsis thaliana]

Seq. No. 301437
Seq. ID ceu700426758.h1
Method BLASTN
NCBI GI g495268
BLAST score 92
E value 9.0e-45
Match length 112
% identity 96
NCBI Description R.norvegicus cox VIa gene (heart)

Seq. No. 301438

Seq. ID ceu700426791.h1
Method BLASTN
NCBI GI g168436
BLAST score 33
E value 1.0e-09
Match length 33
% identity 100
NCBI Description Zea mays catalase (Cat3) gene, complete cds

Seq. No. 301439
Seq. ID ceu700426834.h1
Method BLASTN
NCBI GI g56669
BLAST score 133
E value 5.0e-69
Match length 185
% identity 93
NCBI Description Rat mRNA for ventricular myosin light chain

Seq. No. 301440
Seq. ID ceu700426943.h1
Method BLASTX
NCBI GI g4567228
BLAST score 143
E value 3.0e-09
Match length 40
% identity 62
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 301441
Seq. ID ceu700426963.h1
Method BLASTX
NCBI GI g4503479
BLAST score 201
E value 3.0e-16
Match length 40
% identity 97
NCBI Description eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
>gi_461994_sp_P29692_EF1D_HUMAN_ELONGATION FACTOR 1-DELTA (EF-1-DELTA) >gi_1085404_pir_S34626 translation elongation factor eEF-1 delta chain - human >gi_38522_emb_CAA79716_(Z21507) human elongation factor-1-delta [Homo sapiens]

Seq. No. 301442
Seq. ID ceu700426984.h1
Method BLASTX
NCBI GI g559371
BLAST score 210
E value 3.0e-17
Match length 45
% identity 96
NCBI Description (D29766) Crk-associated substrate, p130 [Rattus norvegicus]

Seq. No. 301443
Seq. ID ceu700427158.h1
Method BLASTX

NCBI GI g4105794
BLAST score 155
E value 1.0e-10
Match length 54
% identity 50
NCBI Description (AF049928) PGP224 [Petunia x hybrida]

Seq. No. 301444
Seq. ID ceu700427161.h1
Method BLASTX
NCBI GI g3047114
BLAST score 287
E value 5.0e-26
Match length 73
% identity 70
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 301445
Seq. ID ceu700427201.h1
Method BLASTX
NCBI GI g2385369
BLAST score 376
E value 2.0e-36
Match length 73
% identity 97
NCBI Description (AJ001421) Rer1 protein [Homo sapiens]

Seq. No. 301446
Seq. ID ceu700427203.h1
Method BLASTN
NCBI GI g203477
BLAST score 213
E value 1.0e-116
Match length 255
% identity 96
NCBI Description Rat skeletal muscle creatine kinase composite mRNA, complete cds

Seq. No. 301447
Seq. ID ceu700427219.h1
Method BLASTX
NCBI GI g4406818
BLAST score 189
E value 1.0e-14
Match length 56
% identity 61
NCBI Description (AC006201) putative transcription factor-like protein [Arabidopsis thaliana]

Seq. No. 301448
Seq. ID ceu700427241.h1
Method BLASTX
NCBI GI g115793
BLAST score 172
E value 1.0e-12
Match length 33
% identity 94

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR (CAB) >gi_72749_pir_CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881 (X63197) type III LHCII CAB precursor protein [Hordeum vulgare]

Seq. No. 301449
Seq. ID ceu700427273.h1
Method BLASTN
NCBI GI g20276
BLAST score 51
E value 7.0e-20
Match length 85
% identity 91
NCBI Description O.sativa oryzacystatin-II gene

Seq. No. 301450
Seq. ID ceu700427302.h1
Method BLASTN
NCBI GI g203477
BLAST score 104
E value 5.0e-52
Match length 104
% identity 100
NCBI Description Rat skeletal muscle creatine kinase composite mRNA, complete cds

Seq. No. 301451
Seq. ID ceu700427325.h1
Method BLASTX
NCBI GI g3688576
BLAST score 200
E value 4.0e-16
Match length 43
% identity 93
NCBI Description (D00512) mitochondrial acetoacetyl-CoA thiolase precursor [Rattus sp.]

Seq. No. 301452
Seq. ID ceu700427336.h1
Method BLASTX
NCBI GI g4522011
BLAST score 194
E value 2.0e-15
Match length 59
% identity 54
NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301453
Seq. ID ceu700427394.h1
Method BLASTX
NCBI GI g2493493
BLAST score 147
E value 7.0e-10
Match length 32
% identity 78
NCBI Description SERINE CARBOXYPEPTIDASE II-1 PRECURSOR (CP-MII.1)

>gi_619352_bbs_153538 CP-MII.1=serine carboxypeptidase
[Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 324
aa]

Seq. No. 301454
Seq. ID ceu700427416.h1
Method BLASTN
NCBI GI g1906603
BLAST score 54
E value 6.0e-22
Match length 54
% identity 100
NCBI Description Zea mays ACCase gene, intron containing colonist1 and
colonist2 retrotransposons and reverse transcriptase
pseudogene, complete sequence

Seq. No. 301455
Seq. ID ceu700427482.h1
Method BLASTX
NCBI GI g4102839
BLAST score 139
E value 9.0e-09
Match length 72
% identity 42
NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No. 301456
Seq. ID ceu700427617.h1
Method BLASTX
NCBI GI g4512624
BLAST score 259
E value 9.0e-23
Match length 66
% identity 67
NCBI Description (AC004793) Strong similarity to gi_3033401 F19I3.29
putative potassium transporter from Arabidopsis thaliana
BAC gb_AC004238

Seq. No. 301457
Seq. ID ceu700427634.h1
Method BLASTX
NCBI GI g3461821
BLAST score 153
E value 3.0e-10
Match length 82
% identity 44
NCBI Description (AC004138) putative nucleoside triphosphatase [Arabidopsis
thaliana]

Seq. No. 301458
Seq. ID ceu700427648.h1
Method BLASTN
NCBI GI g168508
BLAST score 110
E value 4.0e-55
Match length 203
% identity 94

NCBI Description Maize oleosin KD18 (KD18; L2) gene, complete cds

Seq. No. 301459
Seq. ID ceu700427766.h1
Method BLASTX
NCBI GI g3746903
BLAST score 155
E value 8.0e-11
Match length 36
% identity 86
NCBI Description (AF089724) signal recognition particle 54 kDa subunit precursor [Pisum sativum]

Seq. No. 301460
Seq. ID ceu700428036.h1
Method BLASTX
NCBI GI g4586260
BLAST score 158
E value 3.0e-11
Match length 45
% identity 67
NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 301461
Seq. ID ceu700428060.h1
Method BLASTN
NCBI GI g4506236
BLAST score 88
E value 2.0e-42
Match length 100
% identity 98
NCBI Description Homo sapiens proteasome (prosome, macropain) activator subunit 2 (PA28 beta) (PSME2) mRNA
>gi_1008914_dbj_D45248_HUMPHPA28A Human mRNA for proteasome activator hPA28 subunit beta, complete cds

Seq. No. 301462
Seq. ID ceu700428122.h1
Method BLASTX
NCBI GI g557474
BLAST score 143
E value 3.0e-09
Match length 74
% identity 41
NCBI Description (U15179) ORF1 [Bacteroides ovatus]

Seq. No. 301463
Seq. ID ceu700428144.h1
Method BLASTX
NCBI GI g1352410
BLAST score 157
E value 6.0e-11
Match length 45
% identity 62
NCBI Description ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR
>gi_484645_pir_JS0738 ATPase inhibitor protein precursor, mitochondrial - rat >gi_286198_dbj_BAA02424_ (D13122)

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ATPase inhibitor protein precursor [Rattus norvegicus]
>gi_517226 (U12250) mitochondrial ATPase inhibitor [Rattus norvegicus]

Seq. No. 301464
Seq. ID ceu700428190.h1
Method BLASTN
NCBI GI g3150014
BLAST score 231
E value 1.0e-127
Match length 255
% identity 98
NCBI Description Human Chromosome 15q26.1 PAC clone pDJ443n8, complete sequence [Homo sapiens]

Seq. No. 301465
Seq. ID ceu700428285.h1
Method BLASTX
NCBI GI g168586
BLAST score 248
E value 1.0e-21
Match length 79
% identity 98
NCBI Description (M58656) pyruvate,orthophosphate dikinase [Zea mays]

Seq. No. 301466
Seq. ID ceu700428329.h1
Method BLASTX
NCBI GI g133863
BLAST score 158
E value 4.0e-11
Match length 31
% identity 100
NCBI Description 40S RIBOSOMAL PROTEIN S24 (S19) >gi_71037_pir_R3XL19
ribosomal protein S24 - African clawed frog
>gi_65054_emb_CAA24704_ (V01443) ribsomal protein S19
[Xenopus laevis]

Seq. No. 301467
Seq. ID ceu700428531.h1
Method BLASTX
NCBI GI g2997589
BLAST score 154
E value 1.0e-10
Match length 40
% identity 75
NCBI Description (AF020813) glucose-6-phosphate/phosphate-translocator precursor [Zea mays]

Seq. No. 301468
Seq. ID ceu700428610.h1
Method BLASTN
NCBI GI g8051606
BLAST score 112
E value 2.0e-56
Match length 210
% identity 88

SEARCHED

NCBI Description Homo sapiens glycophorin C (Gerbich blood group) (GYPC)
mRNA >gi_36459_emb_X12496_HSSIALOB Human mRNA for
erythrocyte membrane sialoglycoprotein beta (glycophorin C)

Seq. No. 301469
Seq. ID ceu700428741.h1
Method BLASTN
NCBI GI g576644
BLAST score 249
E value 1.0e-138
Match length 269
% identity 98
NCBI Description Human calmodulin-I (CALM1) mRNA, 3'UTR, partial sequence

Seq. No. 301470
Seq. ID ceu700428751.h1
Method BLASTX
NCBI GI g1168329
BLAST score 162
E value 7.0e-25
Match length 80
% identity 60
NCBI Description ACTIN-LIKE PROTEIN 3 (ACTIN-LIKE PROTEIN 66B) (ACTIN-2)
>gi_558568_emb_CAA50674_(X71789) actin related protein
[Drosophila melanogaster] >gi_1096138_prf_2111232A
actin-related protein [Drosophila melanogaster]

Seq. No. 301471
Seq. ID ceu700428768.h1
Method BLASTX
NCBI GI g3250693
BLAST score 223
E value 1.0e-18
Match length 88
% identity 45
NCBI Description (AL024486) lectin like protein [Arabidopsis thaliana]

Seq. No. 301472
Seq. ID ceu700428793.h1
Method BLASTX
NCBI GI g4544383
BLAST score 168
E value 4.0e-12
Match length 84
% identity 42
NCBI Description (AC007047) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301473
Seq. ID ceu700428822.h1
Method BLASTX
NCBI GI g3309565
BLAST score 315
E value 2.0e-29
Match length 83
% identity 78
NCBI Description (AF049460) nuclear DEAF-1 related transcriptional regulator
protein 8 [Homo sapiens]

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Seq. No.	301474
Seq. ID	ceu700428830.h1
Method	BLASTN
NCBI GI	g2588612
BLAST score	34
E value	1.0e-09
Match length	38
% identity	97
NCBI Description	Human BAC clone RG326G04 from 7p21, complete sequence [Homo sapiens]
Seq. No.	301475
Seq. ID	ceu700428854.h1
Method	BLASTN
NCBI GI	g4508148
BLAST score	137
E value	2.0e-71
Match length	205
% identity	91
NCBI Description	Homo sapiens clone DJ0747G18, complete sequence
Seq. No.	301476
Seq. ID	ceu700428927.h1
Method	BLASTN
NCBI GI	g3095110
BLAST score	222
E value	1.0e-122
Match length	250
% identity	98
NCBI Description	Homo sapiens 15 kDa selenoprotein mRNA, complete cds
Seq. No.	301477
Seq. ID	ceu700429017.h1
Method	BLASTX
NCBI GI	g4506679
BLAST score	150
E value	3.0e-10
Match length	33
% identity	88
NCBI Description	ribosomal protein S10 >gi_1173177_sp_P46783_RS10_HUMAN 40S RIBOSOMAL PROTEIN S10 >gi_1362933_pir_S55918 ribosomal protein S10 - human >gi_550025 (U14972) ribosomal protein S10 [Homo sapiens] >gi_1096944_prf_2113200G ribosomal protein S10 [Homo sapiens]
Seq. No.	301478
Seq. ID	ceu700429031.h1
Method	BLASTX
NCBI GI	g2760834
BLAST score	252
E value	6.0e-22
Match length	84
% identity	64
NCBI Description	(AC003105) putative nitrate transporter [Arabidopsis thaliana]

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Seq. No.	301479
Seq. ID	ceu700429060.h1
Method	BLASTN
NCBI GI	g2055391
BLAST score	54
E value	4.0e-22
Match length	98
% identity	89
NCBI Description	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
Seq. No.	301480
Seq. ID	ceu700429079.h1
Method	BLASTN
NCBI GI	g4416300
BLAST score	109
E value	2.0e-54
Match length	263
% identity	86
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence
Seq. No.	301481
Seq. ID	ceu700429156.h1
Method	BLASTN
NCBI GI	g2326946
BLAST score	97
E value	2.0e-47
Match length	204
% identity	89
NCBI Description	Z. mays mRNA for chlorophyll a/b-binding protein CP29
Seq. No.	301482
Seq. ID	ceu700429190.h1
Method	BLASTX
NCBI GI	g1592832
BLAST score	233
E value	9.0e-20
Match length	50
% identity	86
NCBI Description	(L36095) mipA [Mesembryanthemum crystallinum]
Seq. No.	301483
Seq. ID	ceu700429194.h1
Method	BLASTN
NCBI GI	g3777601
BLAST score	43
E value	4.0e-15
Match length	139
% identity	83
NCBI Description	Oryza sativa clone LS195 50S ribosomal protein L10 (rpl10) mRNA, nuclear gene encoding chloroplast protein, complete cds
Seq. No.	301484
Seq. ID	ceu700429206.h1
Method	BLASTX

NCBI GI g2088647
BLAST score 220
E value 6.0e-22
Match length 95
% identity 59
NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]
>gi_3158394 (AF036340) LRR-containing F-box protein
[Arabidopsis thaliana]

Seq. No. 301485
Seq. ID ceu700429287.h1
Method BLASTX
NCBI GI g4580468
BLAST score 150
E value 5.0e-10
Match length 36
% identity 75
NCBI Description (AC006081) putative protein kinase; similar to human PKX1
and Drosophila DC2 [Arabidopsis thaliana]

Seq. No. 301486
Seq. ID ceu700429293.h1
Method BLASTX
NCBI GI g3421413
BLAST score 229
E value 3.0e-19
Match length 80
% identity 53
NCBI Description (AF081922) protein phosphatase 2A 55 kDa B regulatory
subunit [Oryza sativa] >gi_3421415 (AF081923) protein
phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

Seq. No. 301487
Seq. ID ceu700429295.h1
Method BLASTX
NCBI GI g3287696
BLAST score 326
E value 1.0e-30
Match length 78
% identity 76
NCBI Description (AC003979) Strong similarity to phosphoribosylanthranilate
transferase gb_D86180 from Pisum sativum. This ORF may be
part of a larger gene that lies in the overlapping region.
[Arabidopsis thaliana]

Seq. No. 301488
Seq. ID ceu700429329.h1
Method BLASTX
NCBI GI g3337367
BLAST score 151
E value 4.0e-13
Match length 86
% identity 51
NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301489
Seq. ID ceu700429388.h1

Method BLASTN
NCBI GI g3132309
BLAST score 47
E value 1.0e-17
Match length 82
% identity 90
NCBI Description Zea mays mRNA for phosphoenolpyruvate carboxylase, complete cds

Seq. No. 301490
Seq. ID ceu700429408.h1
Method BLASTN
NCBI GI g452340
BLAST score 69
E value 4.0e-31
Match length 77
% identity 99
NCBI Description Z. mays mRNA for type II light-harvesting chlorophyll a/b-binding protein

Seq. No. 301491
Seq. ID ceu700429511.h1
Method BLASTX
NCBI GI g2499987
BLAST score 147
E value 6.0e-10
Match length 54
% identity 56
NCBI Description PEPTIDYL-TRNA HYDROLASE (PTH) >gi_1870014_emb_CAB06865_(Z92539) pth [Mycobacterium tuberculosis]

Seq. No. 301492
Seq. ID ceu700429666.h1
Method BLASTX
NCBI GI g3057120
BLAST score 294
E value 7.0e-27
Match length 64
% identity 78
NCBI Description (AF023159) starch synthase DULL1 [Zea mays]

Seq. No. 301493
Seq. ID ceu700429691.h1
Method BLASTX
NCBI GI g3510374
BLAST score 269
E value 5.0e-24
Match length 81
% identity 69
NCBI Description (AB017188) antisecretory factor [Rattus norvegicus]

Seq. No. 301494
Seq. ID ceu700429707.h1
Method BLASTN
NCBI GI g4416300
BLAST score 178
E value 7.0e-96

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Match length 182
% identity 99
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No. 301495
Seq. ID ceu700429724.h1
Method BLASTN
NCBI GI g3256174
BLAST score 58
E value 3.0e-24
Match length 74
% identity 95
NCBI Description Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence [Homo sapiens]

Seq. No. 301496
Seq. ID ceu700429786.h1
Method BLASTX
NCBI GI g2213558
BLAST score 137
E value 1.0e-08
Match length 51
% identity 47
NCBI Description (Z97052) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 301497
Seq. ID ceu700429931.h1
Method BLASTX
NCBI GI g1658315
BLAST score 268
E value 7.0e-24
Match length 47
% identity 94
NCBI Description (Y08988) osr40g3 [Oryza sativa]

Seq. No. 301498
Seq. ID ceu700429978.h1
Method BLASTX
NCBI GI g3386565
BLAST score 277
E value 6.0e-25
Match length 62
% identity 85
NCBI Description (AF079588) 1-aminocyclopropane-1-carboxylate oxidase [Sorghum bicolor]

Seq. No. 301499
Seq. ID ceu700430011.h1
Method BLASTX
NCBI GI g3157946
BLAST score 228
E value 4.0e-19
Match length 92
% identity 53
NCBI Description (AC002131) Similar to salt-inducible membrane protein

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gb_U08285 from Nicotiana tabacum. EST gb_F14010 comes from
this gene. [Arabidopsis thaliana]

Seq. No. 301500
Seq. ID ceu700430046.h1
Method BLASTX
NCBI GI g951112
BLAST score 178
E value 3.0e-13
Match length 79
% identity 43
NCBI Description (U22470) galactose-binding lectin precursor [Arachis hypogaea]

Seq. No. 301501
Seq. ID ceu700430049.h1
Method BLASTX
NCBI GI g2500139
BLAST score 231
E value 2.0e-19
Match length 74
% identity 58
NCBI Description PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1)
>gi_1653916_dbj_BAA18826 (D90917) peptide chain release factor [Synechocystis sp.]

Seq. No. 301502
Seq. ID ceu700430064.h1
Method BLASTX
NCBI GI g4544418
BLAST score 150
E value 3.0e-10
Match length 55
% identity 56
NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301503
Seq. ID ceu700430093.h1
Method BLASTX
NCBI GI g2055273
BLAST score 156
E value 9.0e-11
Match length 43
% identity 60
NCBI Description (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No. 301504
Seq. ID ceu700430292.h1
Method BLASTX
NCBI GI g3790581
BLAST score 196
E value 2.0e-15
Match length 54
% identity 50
NCBI Description (AF079179) RING-H2 finger protein RHB1a [Arabidopsis thaliana]

DRAFT

Seq. No. 301505
Seq. ID ceu700430339.h1
Method BLASTN
NCBI GI g3947780
BLAST score 42
E value 2.0e-14
Match length 169
% identity 82
NCBI Description Human DNA sequence from clone 1118D24 on chromosome 1p36.11-36.33. Contains part of a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo)gene and two 3' exons of the

Seq. No. 301506
Seq. ID ceu700430501.h1
Method BLASTX
NCBI GI g4210330
BLAST score 146
E value 2.0e-09
Match length 29
% identity 93
NCBI Description (AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No. 301507
Seq. ID ceu700430575.h1
Method BLASTX
NCBI GI g3329368
BLAST score 286
E value 8.0e-26
Match length 89
% identity 63
NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 301508
Seq. ID ceu700430656.h1
Method BLASTN
NCBI GI g4506882
BLAST score 69
E. value 4.0e-31
Match length 105
% identity 91
NCBI Description Homo sapiens semenogelin I (SEMG1) mRNA >gi_338018_gb_J04440_HUMSEM Homo sapiens semenogelin protein (SEMG) mRNA, complete cds

Seq. No. 301509
Seq. ID ceu700430776.h1
Method BLASTX
NCBI GI g3024122
BLAST score 373
E value 4.0e-36
Match length 94
% identity 81
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

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Seq. No.	301510
Seq. ID	ceu700430813.h1
Method	BLASTX
NCBI GI	g2766450
BLAST score	162
E value	1.0e-11
Match length	43
% identity	74
NCBI Description	(AF029857) cytochrome P450 CYP99A1 [Sorghum bicolor]
Seq. No.	301511
Seq. ID	ceu700430827.h1
Method	BLASTX
NCBI GI	g1805654
BLAST score	170
E value	4.0e-23
Match length	92
% identity	71
NCBI Description	(X99972) calmodulin-stimulated calcium-ATPase [Brassica oleracea]
Seq. No.	301512
Seq. ID	ceu700430866.h1
Method	BLASTX
NCBI GI	g3337389
BLAST score	292
E value	1.0e-26
Match length	95
% identity	56
NCBI Description	(AC004682) pre-mRNA splicing factor (PRP16) (KIAA0224) [Homo sapiens]
Seq. No.	301513
Seq. ID	ceu700430881.h1
Method	BLASTX
NCBI GI	g3342734
BLAST score	206
E value	8.0e-17
Match length	44
% identity	93
NCBI Description	(AC005329) NUKM_HUMAN, partial CDS; COMPLETE; CI-20KD; PSST SUBUNIT [Homo sapiens]
Seq. No.	301514
Seq. ID	ceu700431089.h1
Method	BLASTX
NCBI GI	g1938424
BLAST score	167
E value	3.0e-12
Match length	44
% identity	68
NCBI Description	(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]
Seq. No.	301515
Seq. ID	ceu700431138.h1

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Method	BLASTX
NCBI GI	g118104
BLAST score	325
E value	2.0e-30
Match length	66
% identity	92
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_68408_pir_CSZM peptidylprolyl isomerase (EC 5.2.1.8) - maize >gi_168461 (M55021) cyclophilin [Zea mays] >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
Seq. No.	301516
Seq. ID	ceu700431190.h1
Method	BLASTN
NCBI GI	g498145
BLAST score	98
E value	6.0e-48
Match length	255
% identity	92
NCBI Description	Human mRNA for HHR23A protein, complete cds >gi_1408335_gb_G28520_G28520 human STS SHGC-31478
Seq. No.	301517
Seq. ID	ceu700431325.h1
Method	BLASTN
NCBI GI	g4505884
BLAST score	116
E value	5.0e-59
Match length	120
% identity	99
NCBI Description	Homo sapiens perilipin (PLIN) mRNA >gi_3041770_dbj_AB005293_AB005293 Homo sapiens mRNA for perilipin, complete cds
Seq. No.	301518
Seq. ID	ceu700431403.h1
Method	BLASTN
NCBI GI	g2979600
BLAST score	67
E value	2.0e-29
Match length	165
% identity	86
NCBI Description	Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence [Homo sapiens]
Seq. No.	301519
Seq. ID	ceu700431404.h1
Method	BLASTN
NCBI GI	g433039
BLAST score	61
E value	4.0e-26
Match length	129
% identity	87
NCBI Description	Zea mays W-22 clone PREM-1 retroelement PREM-1, partial sequence

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Seq. No.	301520
Seq. ID	ceu700431413.h1
Method	BLASTX
NCBI GI	g3549669
BLAST score	195
E value	3.0e-15
Match length	61
% identity	64
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]
Seq. No.	301521
Seq. ID	ceu700431465.h1
Method	BLASTN
NCBI GI	g1098664
BLAST score	35
E value	2.0e-10
Match length	120
% identity	84
NCBI Description	Zea mays phytoene synthase (Y1) gene, complete cds
Seq. No.	301522
Seq. ID	ceu700431489.h1
Method	BLASTN
NCBI GI	g4505578
BLAST score	222
E value	1.0e-122
Match length	254
% identity	97
NCBI Description	Homo sapiens paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein) (PACE) mRNA >gi_31477_emb_X17094_HSFUR Human fur mRNA for furin
Seq. No.	301523
Seq. ID	ceu700431556.h1
Method	BLASTX
NCBI GI	g3769549
BLAST score	309
E value	3.0e-38
Match length	90
% identity	89
NCBI Description	(AF089812) ubiquitin-conjugating enzyme HR6A [Mus musculus]
Seq. No.	301524
Seq. ID	ceu700431616.h1
Method	BLASTN
NCBI GI	g1754648
BLAST score	48
E value	5.0e-18
Match length	60
% identity	95
NCBI Description	Homo sapiens mRNA for HSM-2, complete cds
Seq. No.	301525
Seq. ID	ceu700431677.h1
Method	BLASTX
NCBI GI	g4406764
BLAST score	171

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E value 4.0e-21
Match length 91
% identity 57
NCBI Description (AC006836) putative uridylyl transferase [Arabidopsis thaliana]

Seq. No. 301526
Seq. ID ceu700431728.h1
Method BLASTN
NCBI GI g22378
BLAST score 43
E value 4.0e-15
Match length 87
% identity 89
NCBI Description Z.mays gene for nucleic acid binding protein

Seq. No. 301527
Seq. ID ceu700431773.h1
Method BLASTX
NCBI GI g2465923
BLAST score 193
E value 5.0e-15
Match length 89
% identity 46
NCBI Description (AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 301528
Seq. ID ceu700431776.h1
Method BLASTX
NCBI GI g3935168
BLAST score 169
E value 3.0e-12
Match length 57
% identity 60
NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]

Seq. No. 301529
Seq. ID ceu700431783.h1
Method BLASTN
NCBI GI g3819359
BLAST score 53
E value 5.0e-21
Match length 85
% identity 91
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0829.uni

Seq. No. 301530
Seq. ID ceu700431831.h1
Method BLASTX
NCBI GI g1293835
BLAST score 150
E value 6.0e-12
Match length 72
% identity 47
NCBI Description (U56965) C15H9.5 gene product [Caenorhabditis elegans]

Seq. No. 301531
Seq. ID ceu700431853.h1
Method BLASTX
NCBI GI g2135819
BLAST score 233
E value 6.0e-20
Match length 43
% identity 100
NCBI Description neuropolypeptide h3, brain - human (fragment)
>gi_4261934_gb_AAD14234_S76773_1 (S76773) neuropolypeptide h3 [Homo sapiens]

Seq. No. 301532
Seq. ID ceu700431858.h1
Method BLASTN
NCBI GI g4557252
BLAST score 240
E value 1.0e-132
Match length 240
% identity 100
NCBI Description Homo sapiens disintegrin and metalloprotease domain 8 (ADAM8) mRNA >gi_1864004_dbj_D26579_D26579 Homo sapiens mRNA for transmembrane protein, complete cds

Seq. No. 301533
Seq. ID ceu700431906.h1
Method BLASTN
NCBI GI g950423
BLAST score 88
E value 2.0e-42
Match length 116
% identity 95
NCBI Description Homo sapiens splicing factor, arginine/serine-rich 7 (SFRS7) gene, complete cds

Seq. No. 301534
Seq. ID ceu700431946.h1
Method BLASTN
NCBI GI g285948
BLAST score 91
E value 4.0e-44
Match length 103
% identity 97
NCBI Description Human mRNA for KIAA0106 gene, complete cds

Seq. No. 301535
Seq. ID ceu700431967.h1
Method BLASTX
NCBI GI g1001355
BLAST score 203
E value 3.0e-16
Match length 83
% identity 52
NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]

Seq. No. 301536
Seq. ID ceu700431983.h1

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Method	BLASTN
NCBI GI	g3970875
BLAST score	217
E value	1.0e-119
Match length	273
% identity	95
NCBI Description	Homo sapiens HRIHFB2216 mRNA, partial cds
Seq. No.	301537
Seq. ID	ceu700432127.h1
Method	BLASTN
NCBI GI	g22239
BLAST score	150
E value	4.0e-79
Match length	181
% identity	96
NCBI Description	Maize cytosolic mRNA for subunit A of chloroplast GAPDH (GapA) glyceraldehyde-3-phosphate dehydrogenase
Seq. No.	301538
Seq. ID	ceu700432132.h1
Method	BLASTN
NCBI GI	g3599965
BLAST score	158
E value	7.0e-84
Match length	190
% identity	97
NCBI Description	Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds
Seq. No.	301539
Seq. ID	ceu700432229.h1
Method	BLASTN
NCBI GI	g809120
BLAST score	64
E value	6.0e-28
Match length	129
% identity	97
NCBI Description	Human DNA from cosmid DNA MMDB (f10080) and MMDC (f13544) from chromosome 19q13.3 (obtained by automated sequence analysis)
Seq. No.	301540
Seq. ID	ceu700432248.h1
Method	BLASTN
NCBI GI	g4507812
BLAST score	47
E value	7.0e-18
Match length	63
% identity	94
NCBI Description	Homo sapiens UDP-glucose dehydrogenase (UGDH) mRNA, and translated products >gi_3127126_gb_AF061016_AF061016 Homo sapiens UDP-glucose dehydrogenase (UGDH) mRNA, complete cds
Seq. No.	301541
Seq. ID	ceu700432264.h1
Method	BLASTX

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NCBI GI g3688172
BLAST score 204
E value 1.0e-16
Match length 60
% identity 63
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 301542
Seq. ID ceu700432286.h1
Method BLASTN
NCBI GI g4500013
BLAST score 104
E value 1.0e-51
Match length 188
% identity 88
NCBI Description Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053)

Seq. No. 301543
Seq. ID ceu700432287.h1
Method BLASTN
NCBI GI g4506606
BLAST score 80
E value 1.0e-37
Match length 100
% identity 95
NCBI Description Homo sapiens ribosomal protein L18 (RPL18) mRNA
>gi_337492_gb_L11566_HUMRPL18A Homo sapiens ribosomal protein L18 (RPL18) mRNA, complete cds

Seq. No. 301544
Seq. ID ceu700432339.h1
Method BLASTX
NCBI GI g3786011
BLAST score 147
E value 8.0e-10
Match length 51
% identity 67
NCBI Description (AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No. 301545
Seq. ID ceu700432432.h1
Method BLASTX
NCBI GI g3334667
BLAST score 264
E value 2.0e-23
Match length 83
% identity 59
NCBI Description (Y10493) putative cytochrome P450 [Glycine max]

Seq. No. 301546
Seq. ID ceu700432437.h1
Method BLASTN
NCBI GI g4416300
BLAST score 81
E value 8.0e-38

SCIENCE SOURCE

Match length 252
% identity 84.
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No. 301547
Seq. ID ceu700432474.h1
Method BLASTX
NCBI GI g4490314
BLAST score 361
E value 8.0e-35
Match length 82
% identity 78
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 301548
Seq. ID ceu700432509.h1
Method BLASTN
NCBI GI g2815550
BLAST score 241
E value 1.0e-133
Match length 273
% identity 97
NCBI Description Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence [Homo sapiens]

Seq. No. 301549
Seq. ID ceu700432533.h1
Method BLASTN
NCBI GI g3150016
BLAST score 76
E value 5.0e-35
Match length 160
% identity 87
NCBI Description Homo sapiens chromosome 7 clone NHGRI:yWSS1564 from 7p14-15, complete sequence [Homo sapiens]

Seq. No. 301550
Seq. ID ceu700432577.h1
Method BLASTX
NCBI GI g3406749
BLAST score 245
E value 2.0e-21
Match length 52
% identity 90
NCBI Description (AF068180) B cell linker protein BLNK [Homo sapiens]

Seq. No. 301551
Seq. ID ceu700432636.h1
Method BLASTX
NCBI GI g1076290
BLAST score 279
E value 4.0e-25
Match length 70
% identity 71
NCBI Description amino acid transporter AAP4 - Arabidopsis thaliana
>gi_608671_emb_CAA54631_ (X77500) amino acid transporter

[Arabidopsis thaliana]

Seq. No. 301552
Seq. ID ceu700432654.h1
Method BLASTX
NCBI GI g3252807
BLAST score 155
E value 8.0e-11
Match length 45
% identity 64
NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301553
Seq. ID ceu700432689.h1
Method BLASTN
NCBI GI g3135974
BLAST score 109
E value 7.0e-55
Match length 125
% identity 97
NCBI Description Homo sapiens DNA sequence from PAC 422H11 on chromosome 6p21.1-22.2. Contains the gene coding for two isoforms of a known Serine Kinase. Contains ESTs, STSs and a GSS, complete sequence [Homo sapiens]

Seq. No. 301554
Seq. ID ceu700432771.h1
Method BLASTX
NCBI GI g4510347
BLAST score 141
E value 5.0e-09
Match length 66
% identity 48
NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301555
Seq. ID ceu700432778.h1
Method BLASTX
NCBI GI g1911166
BLAST score 206
E value 1.0e-16
Match length 70
% identity 53
NCBI Description (X94400) soluble-starch-synthase [Solanum tuberosum]

Seq. No. 301556
Seq. ID ceu700432807.h1
Method BLASTX
NCBI GI g3776082
BLAST score 346
E value 5.0e-33
Match length 88
% identity 72
NCBI Description (Y18250) MtN30 [Medicago truncatula]

Seq. No. 301557
Seq. ID ceu700432943.h1

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Method	BLASTX
NCBI GI	g3088575
BLAST score	411
E value	1.0e-40
Match length	83
% identity	94
NCBI Description	(AF059531) protein arginine N-methyltransferase 3 [Homo sapiens]
Seq. No.	301558
Seq. ID	ceu700432978.h1
Method	BLASTN
NCBI GI	g1103627
BLAST score	124
E value	1.0e-63
Match length	139
% identity	98
NCBI Description	Z.mays Fer1 gene
Seq. No.	301559
Seq. ID	ceu700433004.h1
Method	BLASTX
NCBI GI	g3335345
BLAST score	412
E value	1.0e-40
Match length	91
% identity	87
NCBI Description	(AC004512) Contains similarity to ABC transporter gb_1651790 from Synechocystis sp. gb_D90900. [Arabidopsis thaliana]
Seq. No.	301560
Seq. ID	ceu700433048.h1
Method	BLASTX
NCBI GI	g4587568
BLAST score	206
E value	1.0e-16
Match length	51
% identity	69
NCBI Description	(AC006550) Contains PF_00637 Clathrin 7-fold repeat. EST gb_AA721862 comes from this gene. [Arabidopsis thaliana]
Seq. No.	301561
Seq. ID	ceu700433070.h1
Method	BLASTN
NCBI GI	g236729
BLAST score	80
E value	3.0e-37
Match length	243
% identity	86
NCBI Description	metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
Seq. No.	301562
Seq. ID	ceu700433077.h1
Method	BLASTX
NCBI GI	g3047119
BLAST score	235

E value 5.0e-20
Match length 86
% identity 49
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 301563
Seq. ID ceu700433173.h1
Method BLASTX
NCBI GI g1574938
BLAST score 244
E value 4.0e-21
Match length 47
% identity 100
NCBI Description (U34726) superoxide dismutase 4 [Zea mays]

Seq. No. 301564
Seq. ID ceu700433264.h1
Method BLASTX
NCBI GI g4580013
BLAST score 162
E value 1.0e-11
Match length 46
% identity 65
NCBI Description (U83194) TRAF4-associated factor 2 [Homo sapiens]

Seq. No. 301565
Seq. ID ceu700433458.h1
Method BLASTN
NCBI GI g606814
BLAST score 82
E value 7.0e-39
Match length 90
% identity 98
NCBI Description Zea mays Golden Bantam carbonic anhydrase mRNA, complete cds

Seq. No. 301566
Seq. ID ceu700433528.h1
Method BLASTN
NCBI GI g609287
BLAST score 51
E value 7.0e-20
Match length 262
% identity 81
NCBI Description Z.diploperennis Grandel gene

Seq. No. 301567
Seq. ID ceu700433555.h1
Method BLASTN
NCBI GI g56543
BLAST score 67
E value 2.0e-29
Match length 262
% identity 82
NCBI Description Rat mRNA for lactate dehydrogenase

Seq. No. 301568

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Seq. ID ceu700433588.h1
Method BLASTX
NCBI GI g4106342
BLAST score 371
E value 6.0e-36
Match length 85
% identity 87
NCBI Description (AF062076) palmitoylated serine/threonine kinase [Mus musculus]

Seq. No. 301569
Seq. ID ceu700433595.h1
Method BLASTX
NCBI GI g4538934
BLAST score 262
E value 4.0e-23
Match length 85
% identity 58
NCBI Description (AL049483) putative leucine-rich-repeat protein [Arabidopsis thaliana]

Seq. No. 301570
Seq. ID ceu700433642.h1
Method BLASTX
NCBI GI g4539009
BLAST score 228
E value 2.0e-19
Match length 55
% identity 75
NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 301571
Seq. ID ceu700433657.h1
Method BLASTX
NCBI GI g2773156
BLAST score 252
E value 1.0e-31
Match length 75
% identity 91
NCBI Description (AF039574) serine/threonine protein kinase [Mus musculus]

Seq. No. 301572
Seq. ID ceu700433658.h1
Method BLASTX
NCBI GI g1495804
BLAST score 164
E value 1.0e-11
Match length 33
% identity 85
NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No. 301573
Seq. ID ceu700433713.h1
Method BLASTX
NCBI GI g2618721
BLAST score 257
E value 2.0e-22

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Match length 76
% identity 70
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]

Seq. No. 301574
Seq. ID ceu700433813.h1
Method BLASTX
NCBI GI g3004565
BLAST score 336
E value 2.0e-32
Match length 87
% identity 74
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 301575
Seq. ID ceu700433822.h1
Method BLASTX
NCBI GI g4503155
BLAST score 452
E value 2.0e-45
Match length 89
% identity 93
NCBI Description cathepsin L >gi_115741_sp_P07711_CATL_HUMAN CATHEPSIN L
PRECURSOR (MAJOR EXCRETED PROTEIN) (MEP)
>gi_67649_pir_KHHUL cathepsin L (EC 3.4.22.15) precursor -
human >gi_29715_emb_CAA30981 (X12451) pro-(cathepsin L)
[Homo sapiens] >gi_190418 (M20496) preprocathepsin L
precursor [Homo sapiens]

Seq. No. 301576
Seq. ID ceu700433827.h1
Method BLASTX
NCBI GI g2058498
BLAST score 220
E value 3.0e-18
Match length 65
% identity 66
NCBI Description (U76029) hemoglobin 1 [Oryza sativa] >gi_2058500 (U76030)
hemoglobin 1 [Oryza sativa]

Seq. No. 301577
Seq. ID ceu700433829.h1
Method BLASTN
NCBI GI g2393736
BLAST score 38
E value 4.0e-12
Match length 38
% identity 100
NCBI Description Human BAC clone GS025M02 from 7q21-q22, complete sequence
[Homo sapiens]

Seq. No. 301578
Seq. ID ceu700433861.h1
Method BLASTX
NCBI GI g3395426
BLAST score 315
E value 2.0e-29

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Match length 86
% identity 64
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 301579
Seq. ID ceu700433918.h2
Method BLASTX
NCBI GI g629602
BLAST score 201
E value 3.0e-16
Match length 52
% identity 67
NCBI Description probable imbibition protein - wild cabbage
>gi_488787_emb_CAA55893_(X79330) putative imbibition
protein [Brassica oleracea]

Seq. No. 301580
Seq. ID ceu700433935.h2
Method BLASTX
NCBI GI g3176726
BLAST score 315
E value 2.0e-29
Match length 73
% identity 75
NCBI Description (AC002392) putative serine proteinase [Arabidopsis
thaliana]

Seq. No. 301581
Seq. ID ceu700433958.h2
Method BLASTN
NCBI GI g2121307
BLAST score 69
E value 1.0e-30
Match length 157
% identity 86
NCBI Description Human DNA sequence from 4PTEL, Huntington's Disease Region,
chromosome 4p16.3

Seq. No. 301582
Seq. ID ceu700434008.h1
Method BLASTN
NCBI GI g4240216
BLAST score 120
E value 5.0e-61
Match length 253
% identity 98
NCBI Description Homo sapiens mRNA for KIAA0864 protein, partial cds

Seq. No. 301583
Seq. ID ceu700434206.h1
Method BLASTX
NCBI GI g3128173
BLAST score 209
E value 7.0e-17
Match length 65
% identity 74
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

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Seq. No. 301584
Seq. ID ceu700434343.h1
Method BLASTN
NCBI GI g1835730
BLAST score 55
E value 2.0e-22
Match length 82
% identity 93
NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA, complete cds

Seq. No. 301585
Seq. ID ceu700434376.h1
Method BLASTX
NCBI GI g2501620
BLAST score 185
E value 2.0e-14
Match length 51
% identity 71
NCBI Description UREASE (UREA AMIDOHYDROLASE) >gi_1944148_dbj_BAA19550_(AB002590) Ure1p [Schizosaccharomyces pombe]

Seq. No. 301586
Seq. ID ceu700434382.h1
Method BLASTN
NCBI GI g2529562
BLAST score 135
E value 3.0e-70
Match length 175
% identity 94
NCBI Description Homo sapiens TRAIL receptor 2 mRNA, complete cds

Seq. No. 301587
Seq. ID ceu700434393.h1
Method BLASTX
NCBI GI g1076791
BLAST score 224
E value 6.0e-19
Match length 42
% identity 98
NCBI Description calcium-binding protein - maize >gi_2119370_pir_S58170
Calreticulin precursor - maize >gi_577612_emb_CAA86728_(Z46772)
calcium-binding protein [Zea mays]
>gi_927572_emb_CAA61939_(X89813) Calreticulin precursor
[Zea mays] >gi_1587033_prf_2205314A calreticulin [Zea mays]

Seq. No. 301588
Seq. ID ceu700434408.h1
Method BLASTN
NCBI GI g4503100
BLAST score 173
E value 7.0e-93
Match length 180
% identity 99
NCBI Description Homo sapiens cysteine and glycine-rich protein 2 (LIM

domain only, smooth muscle) (CSRP2) mRNA

Seq. No. 301589
Seq. ID ceu700434483.h1
Method BLASTN
NCBI GI g436123
BLAST score 100
E value 2.0e-49
Match length 147
% identity 93
NCBI Description M.musculus mRNA for phosphorylase kinase

Seq. No. 301590
Seq. ID ceu700434492.h1
Method BLASTX
NCBI GI g2459446
BLAST score 147
E value 6.0e-10
Match length 57
% identity 47
NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No. 301591
Seq. ID ceu700434619.h1
Method BLASTX
NCBI GI g4506655
BLAST score 315
E value 1.0e-35
Match length 90
% identity 90
NCBI Description ribosomal protein L5 >gi_1173054_sp_P46777_RL5_HUMAN 60S RIBOSOMAL PROTEIN L5 >gi_1362932_pir_S55912 ribosomal protein L5 - human >gi_550013 (U14966) ribosomal protein L5 [Homo sapiens] >gi_1096938_prf_2113200A ribosomal protein L5 [Homo sapiens]

Seq. No. 301592
Seq. ID ceu700434640.h1
Method BLASTX
NCBI GI g3063448
BLAST score 194
E value 3.0e-15
Match length 87
% identity 46
NCBI Description (AC003981) F22013.10 [Arabidopsis thaliana]

Seq. No. 301593
Seq. ID cjh700192904.h1
Method BLASTN
NCBI GI g168681
BLAST score 234
E value 1.0e-129
Match length 260
% identity 74
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
>gi_270686_gb_I03333_Sequence 8 from Patent US

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Seq. No. 301594
Seq. ID cjh700192964.h1
Method BLASTN
NCBI GI g3015620
BLAST score 101
E value 9.0e-50
Match length 101
% identity 100
NCBI Description Zea mays low molecular weight heat shock protein precursor (hsp22) mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No. 301595
Seq. ID cjh700193222.h1
Method BLASTX
NCBI GI g82654
BLAST score 208
E value 6.0e-17
Match length 55
% identity 69
NCBI Description 10K zein precursor - maize >gi_22541_emb_CAA30409_ (X07535)
10kDa zein (AA 1 - 150) [Zea mays]

Seq. No. 301596
Seq. ID cjh700193275.h1
Method BLASTX
NCBI GI g136757
BLAST score 252
E value 3.0e-36
Match length 81
% identity 100
NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
>gi_100881_pir_S07314 UDPglucose--starch
glucosyltransferase (EC 2.4.1.11) precursor - maize
>gi_168653 (M24258) amyloplast-specific transit protein
[Zea mays] >gi_1644339_emb_CAA27574_ (X03935) glucosyl
transferase [Zea mays]

Seq. No. 301597
Seq. ID cjh700193292.h1
Method BLASTX
NCBI GI g82660
BLAST score 211
E value 3.0e-17
Match length 58
% identity 76
NCBI Description 19K zein precursor (clone ZG31A) - maize (fragment)
>gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]

Seq. No. 301598
Seq. ID cjh700193306.h1
Method BLASTN
NCBI GI g22514
BLAST score 209
E value 1.0e-114
Match length 252

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% identity 96
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 301599
Seq. ID cjh700193374.h1
Method BLASTN
NCBI GI g340933
BLAST score 124
E value 1.0e-63
Match length 124
% identity 100
NCBI Description Zea mays 10-kDa zein gene, complete cds

Seq. No. 301600
Seq. ID cjh700193403.h1
Method BLASTN
NCBI GI g168669
BLAST score 88
E value 5.0e-42
Match length 100
% identity 97
NCBI Description Maize 19 kDa zein mRNA, clone cZ19A2, partial cds

Seq. No. 301601
Seq. ID cjh700193418.h1
Method BLASTN
NCBI GI g625147
BLAST score 128
E value 4.0e-66
Match length 148
% identity 97
NCBI Description Zea mays protein disulfide isomerase (pdi) mRNA, complete cds

Seq. No. 301602
Seq. ID cjh700193595.h1
Method BLASTX
NCBI GI g2832247
BLAST score 353
E value 7.0e-34
Match length 86
% identity 86
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 301603
Seq. ID cjh700193609.h1
Method BLASTX
NCBI GI g121472
BLAST score 139
E value 2.0e-12
Match length 77
% identity 61
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea

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mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

Seq. No. 301604
Seq. ID cjh700193621.h1
Method BLASTN
NCBI GI g463151
BLAST score 77
E value 2.0e-35
Match length 123
% identity 90
NCBI Description Zea mays high sulfur zein gene, complete cds

Seq. No. 301605
Seq. ID cjh700193677.h1
Method BLASTX
NCBI GI g224514
BLAST score 191
E value 6.0e-15
Match length 39
% identity 97
NCBI Description zein M8 [Zea mays]

Seq. No. 301606
Seq. ID cjh700193680.h1
Method BLASTN
NCBI GI g1864000
BLAST score 132
E value 2.0e-68
Match length 205
% identity 32
NCBI Description Maize DNA for Fd III, complete cds

Seq. No. 301607
Seq. ID cjh700193736.h1
Method BLASTN
NCBI GI g4416300
BLAST score 41
E value 6.0e-14
Match length 129
% identity 83
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence

Seq. No. 301608
Seq. ID cjh700193770.h1
Method BLASTN
NCBI GI g22100
BLAST score 33
E value 3.0e-09
Match length 61
% identity 89
NCBI Description Z.mays 27kDa zein locus DNA

Seq. No. 301609
Seq. ID cjh700193786.h1
Method BLASTN
NCBI GI g168398

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BLAST score	84
E value	1.0e-39
Match length	92
% identity	98
NCBI Description	Zea mays auxin-binding protein (abp4) gene, exons 1-5 and complete cds
Seq. No.	301610
Seq. ID	cjh700193992.h1
Method	BLASTN
NCBI GI	g1314391
BLAST score	77
E value	8.0e-36
Match length	116
% identity	93
NCBI Description	Zea mays ssp. mays USDA PI 214195 ITS1, 5.8S ribosomal RNA, ITS2
Seq. No.	301611
Seq. ID	cjh700194040.h1
Method	BLASTX
NCBI GI	g141616
BLAST score	264
E value	2.0e-23
Match length	57
% identity	88
NCBI Description	ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3) >gi_168662 (M12147) 15 kDa zein protein [Zea mays]
Seq. No.	301612
Seq. ID	cjh700194170.h1
Method	BLASTN
NCBI GI	g168681
BLAST score	186
E value	1.0e-100
Match length	220
% identity	54
NCBI Description	Maize 19 kDa zein mRNA, clone cZ19D1, complete cds. >gi_270686_gb_I03333_Sequence 8 from Patent US
Seq. No.	301613
Seq. ID	cjh700194189.h1
Method	BLASTN
NCBI GI	g3452306
BLAST score	38
E value	3.0e-12
Match length	66
% identity	91
NCBI Description	Zea mays retrotransposon Opie-3 5' LTR, partial sequence
Seq. No.	301614
Seq. ID	cjh700194192.h1
Method	BLASTX
NCBI GI	g1632831
BLAST score	141
E value	4.0e-09
Match length	54

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% identity 50
NCBI Description (Z49698) orf [Ricinus communis]

Seq. No. 301615
Seq. ID cjh700194216.h1
Method BLASTX
NCBI GI g2982289
BLAST score 469
E value 2.0e-47
Match length 91
% identity 99
NCBI Description (AF051229) 60S ribosomal protein L17 [Picea mariana]

Seq. No. 301616
Seq. ID cjh700194226.h1
Method BLASTX
NCBI GI g4206196
BLAST score 147
E value 1.0e-09
Match length 49
% identity 53
NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301617
Seq. ID cjh700194250.h1
Method BLASTX
NCBI GI g4325341
BLAST score 368
E value 1.0e-35
Match length 85
% identity 74
NCBI Description (AF128393) similar to the Drosophila DES-1 protein
(GB:X94180) [Arabidopsis thaliana]

Seq. No. 301618
Seq. ID cjh700194263.h1
Method BLASTX
NCBI GI g168701
BLAST score 336
E value 8.0e-32
Match length 91
% identity 76
NCBI Description (M60837) zein [Zea mays]

Seq. No. 301619
Seq. ID cjh700194320.h1
Method BLASTX
NCBI GI g509810
BLAST score 193
E value 4.0e-15
Match length 84
% identity 44
NCBI Description (L08468) envelope Ca²⁺-ATPase [Arabidopsis thaliana]

Seq. No. 301620
Seq. ID cjh700194440.h1
Method BLASTX

NCBI GI g2832247
BLAST score 322
E value 2.0e-30
Match length 83
% identity 83
NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 301621
Seq. ID cjh700194482.h1
Method BLASTN
NCBI GI g22548
BLAST score 76
E value 6.0e-35
Match length 76
% identity 100
NCBI Description Maize chimeric zein/beta-phaseolin gene 3'end region

Seq. No. 301622
Seq. ID cjh700194549.h1
Method BLASTX
NCBI GI g121472
BLAST score 154
E value 1.0e-16
Match length 86
% identity 60
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea
mays] >gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 301623
Seq. ID cjh700194632.h1
Method BLASTX
NCBI GI g4006921
BLAST score 367
E value 2.0e-35
Match length 84
% identity 83
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 301624
Seq. ID cjh700194690.h1
Method BLASTN
NCBI GI g287829
BLAST score 118
E value 6.0e-60
Match length 194
% identity 90
NCBI Description Z.mays gene for polygalacturonase

Seq. No. 301625
Seq. ID cjh700194701.h1
Method BLASTX
NCBI GI g121472
BLAST score 182

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E value	4.0e-25
Match length	85
% identity	81
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea mays] >gi_168485_(M16066) glutelin-2 [Zea mays]
Seq. No.	301626
Seq. ID	cjh700194747.h1
Method	BLASTX
NCBI GI	g141617
BLAST score	226
E value	5.0e-19
Match length	56
% identity	77
NCBI Description	ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) >gi_100941_pir_S12140 zein Zc1 - maize >gi_100945_pir_B29017 zein 2 - maize >gi_22515_emb_CAA37595_(X53515) zein Zc1 [Zea mays] >gi_168666_(M16460) 16-kDa zein protein [Zea mays]
Seq. No.	301627
Seq. ID	cjh700194753.h1
Method	BLASTX
NCBI GI	g2243118
BLAST score	257
E value	1.0e-22
Match length	71
% identity	68
NCBI Description	(Y10984) glutathione synthetase [Brassica juncea]
Seq. No.	301628
Seq. ID	cjh700194828.h1
Method	BLASTX
NCBI GI	g100812
BLAST score	245
E value	3.0e-21
Match length	48
% identity	100
NCBI Description	ubiquitin precursor - wheat (fragment) >gi_21816_emb_CAA40138_(X56803) ubiquitin [Triticum aestivum] >gi_21900_emb_CAA39938_(X56601) ubiquitin [Triticum aestivum]
Seq. No.	301629
Seq. ID	cjh700194857.h1
Method	BLASTX
NCBI GI	g4185308
BLAST score	185
E value	1.0e-22
Match length	82
% identity	70
NCBI Description	(AF090446) 22-kDa alpha zein protein 21 [Zea mays]

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Seq. No. 301630
Seq. ID cjh700194908.h1
Method BLASTX
NCBI GI g3560243
BLAST score 144
E value 2.0e-09
Match length 85
% identity 35
NCBI Description (AL031532) putative hydrolase [Schizosaccharomyces pombe]

Seq. No. 301631
Seq. ID cjh700195039.h1
Method BLASTX
NCBI GI g4581149
BLAST score 212
E value 2.0e-17
Match length 69
% identity 59
NCBI Description (AC006919) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301632
Seq. ID cjh700195051.h1
Method BLASTX
NCBI GI g511870
BLAST score 220
E value 3.0e-18
Match length 53
% identity 77
NCBI Description (M23537) zein protein [Zea mays]

Seq. No. 301633
Seq. ID cjh700195155.h1
Method BLASTN
NCBI GI g22514
BLAST score 146
E value 1.0e-76
Match length 245
% identity 90
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 301634
Seq. ID cjh700195156.h1
Method BLASTX
NCBI GI g3445212
BLAST score 315
E value 2.0e-29
Match length 80
% identity 78
NCBI Description (AC004786) putative chloroplast envelope Ca²⁺-ATPase [Arabidopsis thaliana]

Seq. No. 301635
Seq. ID cjh700195169.h1
Method BLASTX
NCBI GI g141616
BLAST score 161
E value 2.0e-11

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Match length 40
% identity 78
NCBI Description ZEIN-BETA PRECURSOR (16 KD) (ZEIN 2) (CLONE 15A3)
>gi_168662 (M12147) 15 kDa zein protein [Zea mays]

Seq. No. 301636
Seq. ID cjh700195179.h1
Method BLASTN
NCBI GI g1129085
BLAST score 33
E value 4.0e-09
Match length 53
% identity 91
NCBI Description Wheat mRNA for protein H2A, complete cds, clone wcH2A-9

Seq. No. 301637
Seq. ID cjh700195210.h1
Method BLASTX
NCBI GI g4544430
BLAST score 175
E value 3.0e-13
Match length 51
% identity 63
NCBI Description (AC006955) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No. 301638
Seq. ID cjh700195247.h1
Method BLASTN
NCBI GI g602605
BLAST score 37
E value 1.0e-11
Match length 64
% identity 91
NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin

Seq. No. 301639
Seq. ID cjh700195351.h1
Method BLASTN
NCBI GI g168681
BLAST score 128
E value 7.0e-66
Match length 260
% identity 72
NCBI Description Maize 19 kDa zein mRNA, clone cz19D1, complete cds.
>gi_270686_gb_I03333 Sequence 8 from Patent US

Seq. No. 301640
Seq. ID cjh700195381.h1
Method BLASTN
NCBI GI g1244652
BLAST score 171
E value 2.0e-91
Match length 243
% identity 93
NCBI Description Zea mays copia-type retroelement PREM-2 gag gene, complete cds

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Seq. No.	301641
Seq. ID	cjh700195392.h1
Method	BLASTN
NCBI GI	g168681
BLAST score	163
E value	9.0e-87
Match length	235
% identity	92
NCBI Description	Maize 19 kDa zein mRNA, clone cZ19D1, complete cds. >gi_270686_gb_I03333_Sequence 8 from Patent US
Seq. No.	301642
Seq. ID	cjh700195401.h1
Method	BLASTX
NCBI GI	g3914899
BLAST score	249
E value	7.0e-22
Match length	59
% identity	86
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal protein S4 type I [Zea mays]
Seq. No.	301643
Seq. ID	cjh700195522.h1
Method	BLASTN
NCBI GI	g4416300
BLAST score	47
E value	2.0e-17
Match length	71
% identity	54
NCBI Description	Zea mays chromosome 4 22 kDa zein-associated intercluster region, complete sequence
Seq. No.	301644
Seq. ID	cjh700195531.h1
Method	BLASTX
NCBI GI	g82654
BLAST score	208
E value	7.0e-17
Match length	55
% identity	69
NCBI Description	10K zein precursor - maize >gi_22541_emb_CAA30409_ (X07535) 10kDa zein (AA 1 - 150) [Zea mays]
Seq. No.	301645
Seq. ID	cjh700195562.h1
Method	BLASTN
NCBI GI	g432367
BLAST score	96
E value	9.0e-47
Match length	252
% identity	85
NCBI Description	Rice mRNA for elongation factor 1 beta, complete cds
Seq. No.	301646
Seq. ID	cjh700195573.h1

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Method BLASTX
NCBI GI g1685003
BLAST score 151
E value 3.0e-10
Match length 75
% identity 37
NCBI Description (U32643) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]

Seq. No. 301647
Seq. ID cjh700195582.h1
Method BLASTX
NCBI GI g322641
BLAST score 289
E value 3.0e-26
Match length 83
% identity 59
NCBI Description beta-1,3-glucanase homolog (clone A6) - rape (fragment)
>gi_17738_emb_CAA49513_ (X69887) beta-1,3-glucanase homologue [Brassica napus]

Seq. No. 301648
Seq. ID cjh700195669.h1
Method BLASTX
NCBI GI g1706327
BLAST score 252
E value 2.0e-31
Match length 81
% identity 89
NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
>gi_551261_emb_CAA57447_ (X81854) pyruvate decarboxylase [Nicotiana tabacum]

Seq. No. 301649
Seq. ID cjh700195717.h1
Method BLASTN
NCBI GI g507844
BLAST score 37
E value 1.0e-11
Match length 213
% identity 79
NCBI Description Zea mays A188 retrotransposon gag gene, complete cds

Seq. No. 301650
Seq. ID cjh700195786.h1
Method BLASTN
NCBI GI g3452299
BLAST score 69
E value 1.0e-30
Match length 159
% identity 94
NCBI Description Zea mays retrotransposon Ji-6 3' LTR, partial sequence

Seq. No. 301651
Seq. ID cjh700195788.h1
Method BLASTX
NCBI GI g2641619

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BLAST score 159
E value 4.0e-11
Match length 29
% identity 97
NCBI Description (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea mays]

Seq. No. 301652
Seq. ID cjh700195796.h1
Method BLASTX
NCBI GI g3738306
BLAST score 230
E value 2.0e-19
Match length 57
% identity 68
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 301653
Seq. ID cjh700195877.h1
Method BLASTX
NCBI GI g168703
BLAST score 381
E value 4.0e-37
Match length 85
% identity 91
NCBI Description (M86591) 22 kDa zein protein [Zea mays]

Seq. No. 301654
Seq. ID cjh700195921.h1
Method BLASTX
NCBI GI g4039155
BLAST score 158
E value 5.0e-11
Match length 80
% identity 41
NCBI Description (AF104258) putative copper-inducible 35.6 kDa protein [Festuca rubra]

Seq. No. 301655
Seq. ID cjh700196001.h1
Method BLASTX
NCBI GI g511870
BLAST score 225
E value 8.0e-19
Match length 54
% identity 78
NCBI Description (M23537) zein protein [Zea mays]

Seq. No. 301656
Seq. ID cjh700196114.h1
Method BLASTX
NCBI GI g4063760
BLAST score 208
E value 7.0e-17
Match length 57
% identity 67
NCBI Description (AC005561) putative POL3 protein [Arabidopsis thaliana]

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Seq. No. 301657
Seq. ID cjh700196130.h1
Method BLASTX
NCBI GI g3367520
BLAST score 214
E value 1.0e-17
Match length 77
% identity 55
NCBI Description (AC004392) Similar to protein kinase APK1A,
tyrosine-serine-threonine kinase gb_D12522 from A.
thaliana. [Arabidopsis thaliana]

Seq. No. 301658
Seq. ID cjh700196136.h1
Method BLASTX
NCBI GI g4574406
BLAST score 257
E value 1.0e-22
Match length 75
% identity 60
NCBI Description (AF121139) RIM2 protein [Oryza sativa]

Seq. No. 301659
Seq. ID cjh700196144.h1
Method BLASTX
NCBI GI g121472
BLAST score 142
E value 3.0e-12
Match length 50
% identity 75
NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
>gi_72326_pir_ZMZM19 glutelin 2 precursor (clone pME119) -
maize >gi_22289_emb_CAA26149_(X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_(X53514) zein Zc2 [Zea
mays] >gi_168485_(M16066) glutelin-2 [Zea mays]

Seq. No. 301660
Seq. ID cjh700196335.h1
Method BLASTN
NCBI GI g433044
BLAST score 69
E value 1.0e-30
Match length 97
% identity 93
NCBI Description Zea mays W-22 clone PREM-1D retroelement PREM-1, partial
sequence

Seq. No. 301661
Seq. ID cjh700196383.h1
Method BLASTX
NCBI GI g1076678
BLAST score 350
E value 1.0e-33
Match length 70
% identity 100

NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No. 301662
Seq. ID cjh700196412.h1
Method BLASTN
NCBI GI g22514
BLAST score 111
E value 8.0e-56
Match length 175
% identity 91
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 301663
Seq. ID cjh700196414.h1
Method BLASTX
NCBI GI g419803
BLAST score 154
E value 1.0e-10
Match length 75
% identity 49
NCBI Description zein protein - maize >gi_168705 (M72708) zein protein [Zea mays]

Seq. No. 301664
Seq. ID cjh700196449.h1
Method BLASTN
NCBI GI g22514
BLAST score 288
E value 1.0e-161
Match length 311
% identity 98
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 301665
Seq. ID cjh700196485.h1
Method BLASTX
NCBI GI g468516
BLAST score 246
E value 4.0e-21
Match length 108
% identity 56
NCBI Description (X55724) zein [Zea mays]

Seq. No. 301666
Seq. ID cjh700196511.h1
Method BLASTX
NCBI GI g4587589
BLAST score 271
E value 3.0e-24
Match length 80
% identity 65
NCBI Description (AC007232) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301667
Seq. ID cjh700196512.h1
Method BLASTX
NCBI GI g4582456

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BLAST score : 144
E value : 4.0e-10
Match length : 64
% identity : 55
NCBI Description : (AC007071) putative trithorax protein [Arabidopsis thaliana]

Seq. No. 301668
Seq. ID cjh700196515.h1
Method BLASTX
NCBI GI g511870
BLAST score 225
E value 8.0e-19
Match length 54
% identity 78
NCBI Description (M23537) zein protein [Zea mays]

Seq. No. 301669
Seq. ID cjh700196549.h1
Method BLASTX
NCBI GI q168586
BLAST score 228
E value 7.0e-27
Match length 67
% identity 94
NCBI Description (M58656) pyruvate,orthophosphate dikinase [Zea mays]

Seq. No. 301670
Seq. ID cjh700196620.h1
Method BLASTX
NCBI GI g511870
BLAST score 211
E value 3.0e-17
Match length 51
% identity 76
NCBI Description (M23537) zein protein [Zea mays]

Seq. No. 301671
Seq. ID cjh700196669.h1
Method BLASTX
NCBI GI g2842744
BLAST score 173
E value 9.0e-13
Match length 39
% identity 77
NCBI Description ENHANCER OF RUDIMENTARY HOMOLOG >gi_1595812 (U67398)
enhancer of rudimentary homolog ATER [Arabidopsis thaliana]

Seq. No. 301672
Seq. ID cjh700196675.h1
Method BLASTX
NCBI GI g4432861
BLAST score 237
E value 3.0e-20
Match length 68
% identity 63
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

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Seq. No.	301673
Seq. ID	cjh700196910.h1
Method	BLASTX
NCBI GI	g121472
BLAST score	142
E value	5.0e-25
Match length	84
% identity	80
NCBI Description	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi_72326_pir_ZM2M19 glutelin 2 precursor (clone pME119) - maize >gi_22289_emb_CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi_22517_emb_CAA37594 (X53514) zein Zc2 [Zea mays] >gi_168485 (M16066) glutelin-2 [Zea mays]
Seq. No.	301674
Seq. ID	cjh700196943.h1
Method	BLASTX
NCBI GI	g4206306
BLAST score	339
E value	3.0e-32
Match length	82
% identity	83
NCBI Description	(AF049110) prpol [Zea mays]
Seq. No.	301675
Seq. ID	cjh700196991.h1
Method	BLASTX
NCBI GI	g168703
BLAST score	219
E value	3.0e-18
Match length	50
% identity	90
NCBI Description	(M86591) 22 kDa zein protein [Zea mays]
Seq. No.	301676
Seq. ID	cjh700197014.h1
Method	BLASTX
NCBI GI	g1669599
BLAST score	196
E value	2.0e-15
Match length	87
% identity	43
NCBI Description	(D88746) AR791 [Arabidopsis thaliana]
Seq. No.	301677
Seq. ID	cjh700197143.h1
Method	BLASTX
NCBI GI	g4544383
BLAST score	192
E value	4.0e-15
Match length	64
% identity	61
NCBI Description	(AC007047) hypothetical protein [Arabidopsis thaliana]
Seq. No.	301678

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Seq. ID cjh700197152.h1
Method BLASTX
NCBI GI g4539460
BLAST score 172
E value 1.0e-12
Match length 85
% identity 20
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 301679
Seq. ID cjh700197248.h1
Method BLASTN
NCBI GI g4140643
BLAST score 53
E value 4.0e-21
Match length 93
% identity 89
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 301680
Seq. ID cjh700197404.h1
Method BLASTN
NCBI GI g3282440
BLAST score 220
E value 1.0e-120
Match length 261
% identity 96
NCBI Description Zea mays subsp. mexicana internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence

Seq. No. 301681
Seq. ID cjh700197413.h1
Method BLASTX
NCBI GI g1174780
BLAST score 254
E value 3.0e-22
Match length 51
% identity 94
NCBI Description TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR (ORANGE PERICARP 2) >gi_320135_pir_PQ0450 tryptophan synthase (EC 4.2.1.20) beta-2 chain precursor - maize (fragment) >gi_168574 (M76685) tryptophan synthase beta-subunit [Zea mays]

Seq. No. 301682
Seq. ID cjh700197414.h1
Method BLASTN
NCBI GI g169818
BLAST score 64
E value 1.0e-27
Match length 80
% identity 95
NCBI Description Rice 25S ribosomal RNA gene

Seq. No. 301683
Seq. ID cjh700197434.h1

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Method	BLASTN
NCBI GI	g168704
BLAST score	83
E value	5.0e-39
Match length	197
% identity	93
NCBI Description	Zea mays zein protein gene, complete cds
Seq. No.	301684
Seq. ID	cjh700197452.h1
Method	BLASTX
NCBI GI	g2829923
BLAST score	291
E value	1.0e-26
Match length	84
% identity	69
NCBI Description	(AC002291) Similar to uridylyl transferases [Arabidopsis thaliana]
Seq. No.	301685
Seq. ID	cjh700197463.h1
Method	BLASTX
NCBI GI	g4432825
BLAST score	141
E value	5.0e-09
Match length	58
% identity	57
NCBI Description	(AC006593) putative SOP2p protein [Arabidopsis thaliana]
Seq. No.	301686
Seq. ID	cjh700197482.h1
Method	BLASTX
NCBI GI	g1915974
BLAST score	147
E value	9.0e-10
Match length	57
% identity	47
NCBI Description	(U62329) fructokinase [Lycopersicon esculentum] >gi_2102693 (U64818) fructokinase [Lycopersicon esculentum]
Seq. No.	301687
Seq. ID	cjh700197611.h1
Method	BLASTN
NCBI GI	g168665
BLAST score	198
E value	1.0e-107
Match length	256
% identity	95
NCBI Description	Maize 16-kDa zein-2 mRNA, complete cds
Seq. No.	301688
Seq. ID	cjh700197639.h1
Method	BLASTX
NCBI GI	g141605
BLAST score	331
E value	3.0e-31
Match length	70

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% identity 93
NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
>gi_72312_pir_ZIZM92 19K zein precursor (clone cz19c2) -
maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]

Seq. No. 301689
Seq. ID cjh700197640.h1
Method BLASTX
NCBI GI g2832246
BLAST score 233
E value 8.0e-20
Match length 66
% identity 79
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]

Seq. No. 301690
Seq. ID cjh700197644.h1
Method BLASTN
NCBI GI g1244652
BLAST score 125
E value 4.0e-64
Match length 241
% identity 88
NCBI Description Zea mays copia-type retroelement PREM-2 gag gene, complete
cds

Seq. No. 301691
Seq. ID cjh700197646.h1
Method BLASTX
NCBI GI g4507857
BLAST score 155
E value 1.0e-10
Match length 75
% identity 43
NCBI Description Herpes virus-associated ubiquitin-specific protease
>gi_2501460_sp_Q93009_UPBH_HUMAN PROBABLE UBIQUITIN
CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE
HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP)
(DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED
UBIQUITIN-SPECIFIC PROTEASE) >gi_1545952_emb_CAA96580
(Z72499) herpesvirus associated ubiquitin-specific protease
(HAUSP) [Homo sapiens]

Seq. No. 301692
Seq. ID cjh700197716.h1
Method BLASTX
NCBI GI g3264767
BLAST score 237
E value 3.0e-20
Match length 68
% identity 63
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 301693
Seq. ID cjh700197718.h1
Method BLASTN
NCBI GI g22437

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BLAST score 44
E value 6.0e-16
Match length 71
% identity 92
NCBI Description Maize pML1 gene for zein

Seq. No. 301694
Seq. ID cjh700197723.h1
Method BLASTX
NCBI GI g2982459
BLAST score 255
E value 2.0e-22
Match length 80
% identity 66
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No. 301695
Seq. ID cjh700197738.h1
Method BLASTN
NCBI GI g22514
BLAST score 206
E value 1.0e-112
Match length 233
% identity 97
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)

Seq. No. 301696
Seq. ID cjh700197747.h1
Method BLASTX
NCBI GI g168701
BLAST score 187
E value 2.0e-14
Match length 62
% identity 68
NCBI Description (M60837) zein [Zea mays]

Seq. No. 301697
Seq. ID cjh700197752.h1
Method BLASTN
NCBI GI g1840117
BLAST score 311
E value 1.0e-175
Match length 334
% identity 99
NCBI Description Zea mays PIF-12 transposable element in r-1 (r-p) locus, complete sequence

Seq. No. 301698
Seq. ID cjh700197762.h1
Method BLASTX
NCBI GI g2642159
BLAST score 183
E value 5.0e-22
Match length 65
% identity 78
NCBI Description (AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose

pyrophosphorylase [Arabidopsis thaliana] >gi_4151925
(AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No. 301699
Seq. ID cjh700197860.h1
Method BLASTN
NCBI GI g793901
BLAST score 91
E value 9.0e-44
Match length 111
% identity 95
NCBI Description Z.mays mRNA for ZEM1 protein (ZEM1 gene)

Seq. No. 301700
Seq. ID ckd700461145.h1
Method BLASTX
NCBI GI g3135543
BLAST score 267
E value 9.0e-24
Match length 65
% identity 83
NCBI Description (AF062393) aquaporin [Oryza sativa]

Seq. No. 301701
Seq. ID ckd700461156.h1
Method BLASTX
NCBI GI g515377
BLAST score 251
E value 8.0e-22
Match length 51
% identity 100
NCBI Description (X79715) histone H4 [Lolium temulentum]

Seq. No. 301702
Seq. ID ckd700461234.h1
Method BLASTN
NCBI GI g473602
BLAST score 67
E value 2.0e-29
Match length 167
% identity 86
NCBI Description Zea mays W-22 histone H2A mRNA, complete cds

Seq. No. 301703
Seq. ID ckd700461283.h1
Method BLASTN
NCBI GI g168484
BLAST score 161
E value 2.0e-85
Match length 257
% identity 91
NCBI Description Maize endosperm glutelin-2 gene, complete cds

Seq. No. 301704
Seq. ID ckd700461290.h1
Method BLASTN
NCBI GI g22324

BLAST score 78
E value 5.0e-36
Match length 134
% identity 90
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No. 301705
Seq. ID clt700041505.f1
Method BLASTX
NCBI GI g3212861
BLAST score 381
E value 4.0e-37
Match length 90
% identity 78
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 301706
Seq. ID clt700041585.f1
Method BLASTN
NCBI GI g733457
BLAST score 85
E value 3.0e-40
Match length 169
% identity 96
NCBI Description Zea mays chlorophyll a/b-binding apoprotein CP24 (Lhcb6-1) mRNA, complete cds

Seq. No. 301707
Seq. ID clt700041682.f1
Method BLASTX
NCBI GI g543938
BLAST score 302
E value 7.0e-28
Match length 68
% identity 88
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB48) (LHCP) >gi_82681_pir_S22497 chlorophyll a/b-binding protein precursor (cab-48) - maize >gi_22228_emb_CAA44888_ (X63205) chlorophyll a /b binding protein [Zea mays]

Seq. No. 301708
Seq. ID clt700041776.f1
Method BLASTX
NCBI GI g3024871
BLAST score 234
E value 7.0e-20
Match length 86
% identity 59
NCBI Description HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No. 301709
Seq. ID clt700041813.f1
Method BLASTN
NCBI GI g22223

BLAST score 114
E value 1.0e-57
Match length 226
% identity 89
NCBI Description Maize cab-1 gene for chlorophyll a/b-binding protein

Seq. No. 301710
Seq. ID clt700041814.f1
Method BLASTX
NCBI GI g115771
BLAST score 257
E value 2.0e-26
Match length 66
% identity 89
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_82682_pir_S04453 chlorophyll a/b-binding protein precursor - maize >gi_22224_emb_CAA32900 (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

Seq. No. 301711
Seq. ID clt700041878.f1
Method BLASTX
NCBI GI g2275204
BLAST score 206
E value 1.0e-16
Match length 67
% identity 61
NCBI Description (AC002337) DNA binding protein isolog [Arabidopsis thaliana]

Seq. No. 301712
Seq. ID clt700041959.f1
Method BLASTX
NCBI GI g3618312
BLAST score 212
E value 3.0e-17
Match length 51
% identity 69
NCBI Description (AB001884) zinc finger protein [Oryza sativa]

Seq. No. 301713
Seq. ID clt700042043.f1
Method BLASTX
NCBI GI g115813
BLAST score 167
E value 5.0e-12
Match length 51
% identity 69
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR (CAB-8) >gi_19182_emb_CAA33330 (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]

Seq. No. 301714
Seq. ID clt700042078.f1
Method BLASTX
NCBI GI g1172704

BLAST score 160
E value 3.0e-11
Match length 66
% identity 50
NCBI Description PEPTIDE TRANSPORTER PTR2-B (HISTIDINE TRANSPORTING PROTEIN)
>gi_633940 (L39082) transport protein [Arabidopsis thaliana] >gi_4406786_gb_AAD20096_ (AC006532) histidine transport protein PTR2-B [Arabidopsis thaliana]

Seq. No. 301715
Seq. ID clt700042104.f1
Method BLASTX
NCBI GI g309673
BLAST score 141
E value 5.0e-09
Match length 43
% identity 65
NCBI Description (L19651) light harvesting protein [Pisum sativum]

Seq. No. 301716
Seq. ID clt700042105.f1
Method BLASTX
NCBI GI g4589961
BLAST score 292
E value 1.0e-26
Match length 88
% identity 61
NCBI Description (AC007169) unknown protein [Arabidopsis thaliana]

Seq. No. 301717
Seq. ID clt700042126.f1
Method BLASTX
NCBI GI g2864617
BLAST score 160
E value 3.0e-11
Match length 45
% identity 71
NCBI Description (AL021811) H+-transporting ATP synthase chain9 - like protein [Arabidopsis thaliana]

Seq. No. 301718
Seq. ID clt700042138.f1
Method BLASTX
NCBI GI g1063400
BLAST score 211
E value 3.0e-17
Match length 51
% identity 82
NCBI Description (X92888) glycolate oxidase [Lycopersicon esculentum]

Seq. No. 301719
Seq. ID clt700042166.f1
Method BLASTX
NCBI GI g2655098
BLAST score 201
E value 6.0e-16
Match length 69

% identity 55
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 301720
Seq. ID clt700042248.f1
Method BLASTX
NCBI GI g4567248
BLAST score 294
E value 6.0e-27
Match length 84
% identity 61
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

Seq. No. 301721
Seq. ID clt700042302.f1
Method BLASTX
NCBI GI g168586
BLAST score 201
E value 3.0e-34
Match length 81
% identity 98
NCBI Description (M58656) pyruvate,orthophosphate dikinase [Zea mays]

Seq. No. 301722
Seq. ID clt700042339.f1
Method BLASTN
NCBI GI g4160401
BLAST score 85
E value 3.0e-40
Match length 133
% identity 91
NCBI Description Zea mays eIF-5 gene, exons 1-2

Seq. No. 301723
Seq. ID clt700042342.f1
Method BLASTX
NCBI GI g4006855
BLAST score 282
E value 2.0e-25
Match length 87
% identity 62
NCBI Description (Z99707) Cu²⁺-transporting ATPase-like protein [Arabidopsis thaliana]

Seq. No. 301724
Seq. ID clt700042415.f1
Method BLASTX
NCBI GI g3641252
BLAST score 201
E value 6.0e-16
Match length 78
% identity 51
NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No. 301725
Seq. ID clt700042425.f1

Method BLASTX
NCBI GI g4115388
BLAST score 297
E value 3.0e-27
Match length 92
% identity 59
NCBI Description (AC005967) putative prolylcarboxypeptidase [Arabidopsis thaliana]

Seq. No. 301726
Seq. ID clt700042433.f1
Method BLASTX
NCBI GI g2984709
BLAST score 311
E value 7.0e-29
Match length 87
% identity 71
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 301727
Seq. ID clt700042435.f1
Method BLASTN
NCBI GI g168527
BLAST score 61
E value 8.0e-26
Match length 81
% identity 94
NCBI Description Maize NADP-dependent malic enzyme (Me1) mRNA, complete cds

Seq. No. 301728
Seq. ID clt700042440.f1
Method BLASTX
NCBI GI g482445
BLAST score 216
E value 5.0e-18
Match length 61
% identity 69
NCBI Description chlorophyll a/b-binding protein precursor - swollen duckweed >gi_168296 (M29334) light-harvesting chlorophyll a/b protein precursor [Lemna gibba]

Seq. No. 301729
Seq. ID clt700042446.f1
Method BLASTX
NCBI GI g606815
BLAST score 199
E value 9.0e-16
Match length 88
% identity 56
NCBI Description (U08403) carbonic anhydrase [Zea mays]

Seq. No. 301730
Seq. ID clt700042486.f1
Method BLASTN
NCBI GI g3450841
BLAST score 103
E value 6.0e-51

Match length 135
% identity 94
NCBI Description Oryza sativa mitogen activated protein kinase kinase (MEK1)
mRNA, complete cds

Seq. No. 301731
Seq. ID clt700042501.f1
Method BLASTX
NCBI GI g1154889
BLAST score 351
E value 1.0e-33
Match length 72
% identity 94
NCBI Description (Z68504) 3-hydroxy-3-methylglutaryl-CoA reductase [Oryza
sativa] >gi_1171364 (U43961) 3-hydroxy-3-methylglutaryl-CoA
reductase [Oryza sativa]

Seq. No. 301732
Seq. ID clt700042502.f1
Method BLASTX
NCBI GI g3402713
BLAST score 249
E value 1.0e-21
Match length 84
% identity 55
NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301733
Seq. ID clt700042578.f1
Method BLASTX
NCBI GI g3914465
BLAST score 143
E value 8.0e-17
Match length 50
% identity 98
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
(LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
>gi_2981207 (AF052076) photosystem I complex PsaH subunit
precursor [Zea mays]

Seq. No. 301734
Seq. ID clt700042586.f1
Method BLASTX
NCBI GI g120657
BLAST score 198
E value 2.0e-20
Match length 56
% identity 95
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
CHLOROPLAST >gi_66024_pir_DEZMG3
glyceraldehyde-3-phosphate dehydrogenase (NADP+)
(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
maize >gi_168479 (M18976) glyceraldehyde-3-phosphate
dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_(X15408)
glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 301735

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Seq. ID	clt700042626.f1
Method	BLASTX
NCBI GI	g2130042
BLAST score	286
E value	6.0e-26
Match length	92
% identity	72
NCBI Description	Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916) protoporphyrin IX Mg-chelatase subunit precursor [Hordeum vulgare]
Seq. No.	301736
Seq. ID	clt700042631.f1
Method	BLASTX
NCBI GI	g4099835
BLAST score	162
E value	2.0e-11
Match length	58
% identity	52
NCBI Description	(U90266) bifunctional nuclease [Zinnia elegans]
Seq. No.	301737
Seq. ID	clt700042682.f1
Method	BLASTN
NCBI GI	g3955064
BLAST score	65
E value	2.0e-28
Match length	191
% identity	85
NCBI Description	Zea mays PHYT I gene for acidic phytase
Seq. No.	301738
Seq. ID	clt700042683.f1
Method	BLASTN
NCBI GI	g733457
BLAST score	52
E value	1.0e-20
Match length	117
% identity	97
NCBI Description	Zea mays chlorophyll a/b-binding apoprotein CP24 (Lhcb6-1) mRNA, complete cds
Seq. No.	301739
Seq. ID	clt700042768.f1
Method	BLASTX
NCBI GI	g4455331
BLAST score	222
E value	2.0e-18
Match length	68
% identity	56
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]
Seq. No.	301740
Seq. ID	clt700042773.f1
Method	BLASTX
NCBI GI	g606811
BLAST score	155

E value 1.0e-10
Match length 38
% identity 79
NCBI Description (U08401) carbonic anhydrase [Zea mays]

Seq. No. 301741
Seq. ID clt700042785.f1
Method BLASTX
NCBI GI g1653089
BLAST score 193
E value 4.0e-15
Match length 86
% identity 47
NCBI Description (D90911) hypothetical protein [Synechocystis sp.]

Seq. No. 301742
Seq. ID clt700042807.f1
Method BLASTN
NCBI GI g1906603
BLAST score 152
E value 4.0e-80
Match length 263
% identity 89
NCBI Description Zea mays ACCase gene, intron containing colonist1 and colonist2 retrotransposons and reverse transcriptase pseudogene, complete sequence

Seq. No. 301743
Seq. ID clt700042844.f1
Method BLASTN
NCBI GI g22328
BLAST score 268
E value 1.0e-149
Match length 268
% identity 100
NCBI Description Maize mRNA for a high mobility group protein

Seq. No. 301744
Seq. ID clt700042853.f1
Method BLASTN
NCBI GI g2661765
BLAST score 244
E value 1.0e-135
Match length 280
% identity 97
NCBI Description Zea mays mRNA for putative porphobilinogen deaminase

Seq. No. 301745
Seq. ID clt700042863.f1
Method BLASTX
NCBI GI g119961
BLAST score 176
E value 5.0e-13
Match length 50
% identity 68
NCBI Description FERREDOXIN V PRECURSOR (FD V) >gi_168475 (M73828)
ferredoxin [Zea mays] >gi_444684_prf_1907324A

ferredoxin:ISOTYPE=V [Zea mays]

Seq. No. 301746
Seq. ID clt700042904.f1
Method BLASTN
NCBI GI g2239259
BLAST score 36
E value 2.0e-11
Match length 88
% identity 87
NCBI Description Zea mays mRNA for cinnamoyl CoA reductase

Seq. No. 301747
Seq. ID clt700042989.f1
Method BLASTN
NCBI GI g312289
BLAST score 33
E value 4.0e-09
Match length 33
% identity 100
NCBI Description O.sativa short highly repeated, interspersed DNA

Seq. No. 301748
Seq. ID clt700043027.f1
Method BLASTX
NCBI GI g68029
BLAST score 149
E value 7.0e-10
Match length 64
% identity 48
NCBI Description phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize
>gi_22408_emb_CAA33317_ (X15239) PEP carboxylase [Zea mays]
>gi_228619_prf_1807332A phosphoenolpyruvate carboxylase
[Zea mays]

Seq. No. 301749
Seq. ID clt700043163.f1
Method BLASTN
NCBI GI g4176423
BLAST score 43
E value 4.0e-15
Match length 51
% identity 96
NCBI Description Oryza sativa rpl12-2 gene for chloroplast ribosomal protein
L12, complete cds

Seq. No. 301750
Seq. ID clt700043272.f1
Method BLASTX
NCBI GI g312179
BLAST score 427
E value 1.0e-42
Match length 85
% identity 98
NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase
(phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi_1185554 (U45858) glyceraldehyde-3-phosphate
dehydrogenase [Zea mays]

Seq. No. 301751
Seq. ID clt700043329.f1
Method BLASTX
NCBI GI g2244925
BLAST score 151
E value 4.0e-10
Match length 44
% identity 64
NCBI Description (Z97339) glutaredoxin [Arabidopsis thaliana]

Seq. No. 301752
Seq. ID clt700043330.f1
Method BLASTX
NCBI GI g4107009
BLAST score 233
E value 8.0e-20
Match length 48
% identity 94
NCBI Description (D82039) OSK1 [Oryza sativa]

Seq. No. 301753
Seq. ID clt700043341.f1
Method BLASTX
NCBI GI g1854376
BLAST score 444
E value 2.0e-44
Match length 86
% identity 100
NCBI Description (AB001337) Sucrose-Phosphate Synthase [Saccharum officinarum]

Seq. No. 301754
Seq. ID clt700043358.f1
Method BLASTX
NCBI GI g82080
BLAST score 179
E value 2.0e-13
Match length 53
% identity 70
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
>gi_226872_prf_1609235A chlorophyll a/b binding protein
[Lycopersicon esculentum]

Seq. No. 301755
Seq. ID clt700043362.f1
Method BLASTX
NCBI GI g1673456
BLAST score 336
E value 8.0e-32
Match length 66
% identity 100
NCBI Description (Y09214) rubisco small subunit [Zea mays]

Seq. No. 301756

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Seq. ID clt700043422.f1
Method BLASTX
NCBI GI g1176689
BLAST score 266
E value 1.0e-23
Match length 89
% identity 61
NCBI Description HYPOTHETICAL PROTEIN IN PETB 5'REGION >gi_97579_pir_S18125
hypothetical protein - Synechococcus sp. (PCC 7002)
>gi_38965_emb_CAA44776_(X63049) orf [Synechococcus
PCC7002]

Seq. No. 301757
Seq. ID clt700043431.f1
Method BLASTN
NCBI GI g2326946
BLAST score 241
E value 1.0e-133
Match length 255
% identity 99
NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29

Seq. No. 301758
Seq. ID clt700043447.f1
Method BLASTX
NCBI GI g2326947
BLAST score 228
E value 4.0e-25
Match length 60
% identity 100
NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor
[Zea mays]

Seq. No. 301759
Seq. ID clt700043463.f1
Method BLASTX
NCBI GI g2654226
BLAST score 243
E value 7.0e-21
Match length 61
% identity 77
NCBI Description (AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis
thaliana]

Seq. No. 301760
Seq. ID clt700043468.f1
Method BLASTX
NCBI GI g4538939
BLAST score 210
E value 5.0e-17
Match length 45
% identity 84
NCBI Description (AL049483) Col-0 casein kinase I-like protein [Arabidopsis
thaliana]

Seq. No. 301761
Seq. ID clt700043496.f1

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Method BLASTN
NCBI GI g2326946
BLAST score 153
E value 9.0e-81
Match length 160
% identity 99
NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29

Seq. No. 301762
Seq. ID clt700043623.f1
Method BLASTX
NCBI GI g2500959
BLAST score 248
E value 2.0e-21
Match length 90
% identity 56
NCBI Description ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS)
>gi_1653611_dbj_BAA18523_ (D90915) alanyl-tRNA synthetase
[Synechocystis sp.]

Seq. No. 301763
Seq. ID clt700043633.f1
Method BLASTX
NCBI GI g1076685
BLAST score 160
E value 3.0e-11
Match length 45
% identity 34
NCBI Description SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_
(D30038) SPF1 protein [Ipomoea batatas]

Seq. No. 301764
Seq. ID clt700043642.f1
Method BLASTX
NCBI GI g115772
BLAST score 387
E value 1.0e-37
Match length 89
% identity 84
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
(CAB-1) (LHCP) >gi_82460_pir_S03705 chlorophyll
a/b-binding protein 1R precursor - rice
>gi_20178_emb_CAA32108_ (X13908) chlorophyll a/b-binding
protein (AA -31 to 235) [Oryza sativa].

Seq. No. 301765
Seq. ID clt700043679.f1
Method BLASTX
NCBI GI g4455364
BLAST score 144
E value 2.0e-09
Match length 39
% identity 72
NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis
thaliana]

Seq. No. 301766

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Seq. ID clt700043753.f1
Method BLASTX
NCBI GI g2326947
BLAST score 224
E value 3.0e-31
Match length 70
% identity 100
NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor [Zea mays]

Seq. No. 301767
Seq. ID clt700043761.f1
Method BLASTX
NCBI GI g2130091
BLAST score 356
E value 3.0e-34
Match length 68
% identity 97
NCBI Description aspartate aminotransferase - proso millet
>gi_633095_dbj_BAA08106_ (D45076) plastidic aspartate
aminotransferase [Panicum miliaceum]

Seq. No. 301768
Seq. ID clt700043884.f1
Method BLASTX
NCBI GI g2459411
BLAST score 265
E value 1.0e-23
Match length 83
% identity 59
NCBI Description (AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301769
Seq. ID clt700043901.f1
Method BLASTX
NCBI GI g82080
BLAST score 173
E value 1.0e-12
Match length 52
% identity 69
NCBI Description chlorophyll a/b-binding protein type III precursor - tomato
>gi_226872_prf_1609235A chlorophyll a/b binding protein
[Lycopersicon esculentum]

Seq. No. 301770
Seq. ID clt700043923.f1
Method BLASTX
NCBI GI g4539404
BLAST score 205
E value 2.0e-16
Match length 58
% identity 67
NCBI Description (AL049524) putative protein [Arabidopsis thaliana]

Seq. No. 301771
Seq. ID clt700044039.f1
Method BLASTN

DRAFT BLAST

NCBI GI	g3885895
BLAST score	46
E value	7.0e-17
Match length	182
% identity	81
NCBI Description	Oryza sativa plastocyanin precursor, mRNA, complete cds
Seq. No.	301772
Seq. ID	clt700044109.r1
Method	BLASTX
NCBI GI	g2213632
BLAST score	228
E value	3.0e-19
Match length	72
% identity	60
NCBI Description	(AC000103) F21J9.24 [Arabidopsis thaliana]
Seq. No.	301773
Seq. ID	clt700044167.f1
Method	BLASTX
NCBI GI	g82080
BLAST score	180
E value	1.0e-13
Match length	54
% identity	69
NCBI Description	chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf_1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]
Seq. No.	301774
Seq. ID	clt700044356.f1
Method	BLASTX
NCBI GI	g4581162
BLAST score	208
E value	8.0e-17
Match length	49
% identity	82
NCBI Description	(AC006220) putative symbiosis-related protein [Arabidopsis thaliana]
Seq. No.	301775
Seq. ID	clt700044358.f1
Method	BLASTN
NCBI GI	g2326946
BLAST score	229
E value	1.0e-126
Match length	247
% identity	99
NCBI Description	Z.mays mRNA for chlorophyll a/b-binding protein CP29
Seq. No.	301776
Seq. ID	clt700044368.f1
Method	BLASTX
NCBI GI	g1176505
BLAST score	162
E value	2.0e-11
Match length	80

% identity 42
NCBI Description HYPOTHETICAL 47.8 KD PROTEIN B0280.9 IN CHROMOSOME III
>gi_500770 (U10438) B0280.9 gene product [Caenorhabditis elegans]

Seq. No. 301777
Seq. ID clt700044383.f1
Method BLASTX
NCBI GI g2326352
BLAST score 312
E value 5.0e-29
Match length 89
% identity 71
NCBI Description (Y11156) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301778
Seq. ID clt700044389.f1
Method BLASTX
NCBI GI g3482914
BLAST score 211
E value 3.0e-17
Match length 88
% identity 47
NCBI Description (AC003970) Similar to nodulins and lipase [Arabidopsis thaliana]

Seq. No. 301779
Seq. ID clt700044401.f1
Method BLASTX
NCBI GI g2462833
BLAST score 200
E value 8.0e-16
Match length 82
% identity 49
NCBI Description (AF000657) highly similar to froha and frohb, potential frohc [Arabidopsis thaliana]

Seq. No. 301780
Seq. ID clt700044527.f1
Method BLASTX
NCBI GI g3885896
BLAST score 187
E value 2.0e-14
Match length 73
% identity 53
NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]

Seq. No. 301781
Seq. ID clt700044539.f1
Method BLASTX
NCBI GI g3269291
BLAST score 318
E value 1.0e-29
Match length 82
% identity 74
NCBI Description (AL030978) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 301782
Seq. ID clt700044544.f1
Method BLASTX
NCBI GI g2326947
BLAST score 199
E value 2.0e-28
Match length 66
% identity 100
NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor [Zea mays]

Seq. No. 301783
Seq. ID clt700044557.f1
Method BLASTX
NCBI GI g4585882
BLAST score 221
E value 2.0e-18
Match length 46
% identity 93
NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 301784
Seq. ID clt700044585.f1
Method BLASTX
NCBI GI g3450842
BLAST score 262
E value 2.0e-34
Match length 84
% identity 85
NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No. 301785
Seq. ID clt700044619.f1
Method BLASTX
NCBI GI g2244910
BLAST score 142
E value 2.0e-09
Match length 44
% identity 66
NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No. 301786
Seq. ID clt700044733.f1
Method BLASTX
NCBI GI g2623295
BLAST score 334
E value 1.0e-31
Match length 79
% identity 76
NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301787
Seq. ID clt700044778.f1
Method BLASTX

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NCBI GI g3341648
BLAST score 455
E value 8.0e-46
Match length 84
% identity 100
NCBI Description (AJ005343) DNA directed RNA polymerase [Zea mays]

Seq. No. 301788
Seq. ID clt700044784.f1
Method BLASTN
NCBI GI g22204
BLAST score 46
E value 6.0e-17
Match length 117
% identity 93
NCBI Description Maize Bz-McC gene for UDPglucose flavonoid glycosyl-transferase

Seq. No. 301789
Seq. ID clt700044801.f1
Method BLASTX
NCBI GI g3337361
BLAST score 146
E value 1.0e-09
Match length 52
% identity 48
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 301790
Seq. ID clt700044864.f1
Method BLASTX
NCBI GI g4220517
BLAST score 301
E value 1.0e-27
Match length 89
% identity 63
NCBI Description (AL035356) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301791
Seq. ID clt700044891.f1
Method BLASTX
NCBI GI g1814401
BLAST score 377
E value 1.0e-36
Match length 85
% identity 84
NCBI Description (U84888) phosphoglucomutase [Mesembryanthemum crystallinum]

Seq. No. 301792
Seq. ID clt700044894.f1
Method BLASTX
NCBI GI g4567283
BLAST score 168
E value 3.0e-12
Match length 59
% identity 59
NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

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Seq. No.	301793
Seq. ID	clt700044936.f1
Method	BLASTX
NCBI GI	g100880
BLAST score	190
E value	6.0e-15
Match length	58
% identity	71
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A, chloroplast - maize
Seq. No.	301794
Seq. ID	clt700044960.f1
Method	BLASTX
NCBI GI	g115815
BLAST score	327
E value	9.0e-31
Match length	69
% identity	88
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-M9) (LHCP) >gi_100866_pir_S13098 chlorophyll a/b-binding protein precursor - maize >gi_22355_emb_CAA39376_ (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays]
Seq. No.	301795
Seq. ID	clt700044991.f1
Method	BLASTN
NCBI GI	g2773153
BLAST score	67
E value	2.0e-29
Match length	79
% identity	96
NCBI Description	Oryza sativa abscisic acid- and stress-inducible protein (Asrl) mRNA, complete cds
Seq. No.	301796
Seq. ID	clt700045013.f1
Method	BLASTX
NCBI GI	g3004564
BLAST score	282
E value	1.0e-25
Match length	82
% identity	63
NCBI Description	(AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]
Seq. No.	301797
Seq. ID	clt700045074.f1
Method	BLASTX
NCBI GI	g115786
BLAST score	266
E value	1.0e-23
Match length	68
% identity	81
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays]

Seq. No. 301798
Seq. ID clt700045077.f1
Method BLASTN
NCBI GI g21843
BLAST score 37
E value 1.0e-11
Match length 59
% identity 92
NCBI Description Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II

Seq. No. 301799
Seq. ID clt700045136.f1
Method BLASTX
NCBI GI g1673456
BLAST score 278
E value 4.0e-25
Match length 55
% identity 100
NCBI Description (Y09214) rubisco small subunit [Zea mays]

Seq. No. 301800
Seq. ID clt700045148.f1
Method BLASTN
NCBI GI g168470
BLAST score 172
E value 4.0e-92
Match length 250
% identity 93
NCBI Description Maize ferredoxin I (Fd) isoprotein mRNA, pFD1'

Seq. No. 301801
Seq. ID clt700045162.f1
Method BLASTX
NCBI GI g4006835
BLAST score 177
E value 4.0e-13
Match length 91
% identity 36
NCBI Description (AC005970) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301802
Seq. ID clt700045182.f1
Method BLASTN
NCBI GI g168529
BLAST score 57
E value 2.0e-23
Match length 57
% identity 100
NCBI Description Zea mays opaque2 heterodimerizing protein 1 (OHP1) mRNA, complete cds

Seq. No. 301803

Seq. ID clt700045259.f1
 Method BLASTX
 NCBI GI g131197
 BLAST score 141
 E value 2.0e-15
 Match length 51
 % identity 88
 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
 (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) (GOS5
 PROTEIN) >gi_72679_pir_A1RZH photosystem I protein psaH
 precursor - rice >gi_20240_emb_CAA36191_ (X51911) GOS5
 [Oryza sativa]

Seq. No. 301804
 Seq. ID clt700045263.f1
 Method BLASTX
 NCBI GI g4468984
 BLAST score 213
 E value 1.0e-17
 Match length 73
 % identity 58
 NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 301805
 Seq. ID clt700045305.f1
 Method BLASTN
 NCBI GI g2981206
 BLAST score 198
 E value 1.0e-107
 Match length 220
 % identity 98
 NCBI Description Zea mays photosystem I complex PsaH subunit precursor
 (psaH) mRNA, nuclear gene encoding chloroplast protein,
 complete cds

Seq. No. 301806
 Seq. ID clt700045321.f1
 Method BLASTX
 NCBI GI g2326947
 BLAST score 184
 E value 4.0e-20
 Match length 54
 % identity 98
 NCBI Description (Z50801) Chlorophyll a/b-binding protein CP29 precursor
 [Zea mays]

Seq. No. 301807
 Seq. ID clt700045373.f1
 Method BLASTX
 NCBI GI g4263711
 BLAST score 337
 E value 5.0e-32
 Match length 81
 % identity 79
 NCBI Description (AC006223) putative CCR4-associated transcription factor
 [Arabidopsis thaliana]

Seq. No. 301808
Seq. ID clt700045406.f1
Method BLASTX
NCBI GI g462195
BLAST score 417
E value 3.0e-41
Match length 86
% identity 92
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
>gi_100682_pir_S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950_(AF094774)_ translation initiation factor [Oryza sativa]

Seq. No. 301809
Seq. ID clt700045417.f1
Method BLASTX
NCBI GI g543938
BLAST score 268
E value 5.0e-24
Match length 57
% identity 95
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB48) (LHCP) >gi_82681_pir_S22497 chlorophyll a/b-binding protein precursor (cab-48) - maize
>gi_22228_emb_CAA44888_ (X63205) chlorophyll a /b binding protein [Zea mays]

Seq. No. 301810
Seq. ID clt700045431.f1
Method BLASTN
NCBI GI g2326946
BLAST score 68
E value 2.0e-30
Match length 80
% identity 96
NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29

Seq. No. 301811
Seq. ID clt700045434.f1
Method BLASTX
NCBI GI g115786
BLAST score 277
E value 6.0e-25
Match length 74
% identity 74
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays]

Seq. No. 301812
Seq. ID clt700045462.f1
Method BLASTX
NCBI GI g3913239
BLAST score 504
E value 2.0e-51

Match length 100
% identity 95
NCBI Description PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like protein [Oryza sativa]

Seq. No. 301813
Seq. ID clt700045527.f1
Method BLASTX
NCBI GI g543938
BLAST score 262
E value 4.0e-23
Match length 62
% identity 85
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB48) (LHCP) >gi_82681_pir_S22497 chlorophyll a/b-binding protein precursor (cab-48) - maize >gi_22228_emb_CAA44888_ (X63205) chlorophyll a /b binding protein [Zea mays]

Seq. No. 301814
Seq. ID clt700045543.f1
Method BLASTX
NCBI GI g3789954
BLAST score 398
E value 3.0e-39
Match length 78
% identity 92
NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No. 301815
Seq. ID clt700045579.f1
Method BLASTX
NCBI GI g2446998
BLAST score 219
E value 4.0e-18
Match length 45
% identity 96
NCBI Description (D63954) fatty acid desaturase [Zea mays]

Seq. No. 301816
Seq. ID clt700045586.f1
Method BLASTX
NCBI GI g3093410
BLAST score 323
E value 2.0e-30
Match length 84
% identity 75
NCBI Description (AJ225107) protoporphyrinogen oxidase [Solanum tuberosum]

Seq. No. 301817
Seq. ID clt700045623.f1
Method BLASTN
NCBI GI g2326946
BLAST score 237
E value 1.0e-131

Match length 255
% identity 99
NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29

Seq. No. 301818
Seq. ID clt700045655.f1
Method BLASTX
NCBI GI g534982
BLAST score 155
E value 1.0e-10
Match length 38
% identity 68
NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]

Seq. No. 301819
Seq. ID clt700045658.f1
Method BLASTX
NCBI GI g2914693
BLAST score 159
E value 5.0e-11
Match length 78
% identity 42
NCBI Description (AC003974) putative protein kinase [Arabidopsis thaliana]

Seq. No. 301820
Seq. ID clt700045665.f1
Method BLASTX
NCBI GI g2245087
BLAST score 190
E value 1.0e-14
Match length 50
% identity 64
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301821
Seq. ID clt700045738.f1
Method BLASTX
NCBI GI g115786
BLAST score 198
E value 8.0e-16
Match length 63
% identity 65
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_82680_pir_A29119 chlorophyll a/b-binding protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea mays]

Seq. No. 301822
Seq. ID clt700045842.f1
Method BLASTX
NCBI GI g115815
BLAST score 204
E value 2.0e-16
Match length 62
% identity 66
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-M9) (LHCP) >gi_100866_pir_S13098 chlorophyll

a/b-binding protein precursor - maize
>gi_22355_emb CAA39376 (X55892) light-harvesting
chlorophyll a/b binding protein [Zea mays]

Seq. No. 301823
Seq. ID clt700045910.f1
Method BLASTX
NCBI GI g1673456
BLAST score 376
E value 2.0e-36
Match length 74
% identity 100
NCBI Description (Y09214) rubisco small subunit [Zea mays]

Seq. No. 301824
Seq. ID clt700045928.f1
Method BLASTX
NCBI GI g3885328
BLAST score 180
E value 1.0e-22
Match length 94
% identity 57
NCBI Description (AC005623) putative serine/threonine protein kinase
[Arabidopsis thaliana]

Seq. No. 301825
Seq. ID clt700045986.f1
Method BLASTN
NCBI GI g21843
BLAST score 48
E value 4.0e-18
Match length 106
% identity 88
NCBI Description Wheat PsbO mRNA for 33kDa oxygen evolving protein of
photosystem II

Seq. No. 301826
Seq. ID clt700046012.f1
Method BLASTX
NCBI GI g729478
BLAST score 304
E value 5.0e-28
Match length 61
% identity 97
NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
>gi_442481_dbj_BAA04616 (D17790) ferredoxin-NADP+
reductase [Oryza sativa]

Seq. No. 301827
Seq. ID clt700046014.f1
Method BLASTX
NCBI GI g3421413
BLAST score 226
E value 7.0e-19
Match length 45
% identity 93
NCBI Description (AF081922) protein phosphatase 2A 55 kDa B regulatory

subunit [Oryza sativa] >gi_3421415 (AF081923) protein
phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

Seq. No. 301828
Seq. ID clt700046030.f1
Method BLASTX
NCBI GI g1488043
BLAST score 173
E value 1.0e-12
Match length 47
% identity 70
NCBI Description (U63784) PAPS-reductase-like protein [Catharanthus roseus]

Seq. No. 301829
Seq. ID clt700046032.f1
Method BLASTN
NCBI GI g2326946
BLAST score 237
E value 1.0e-131
Match length 255
% identity 99
NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29

Seq. No. 301830
Seq. ID clt700046060.f1
Method BLASTN
NCBI GI g22292
BLAST score 178
E value 1.0e-95
Match length 279
% identity 98
NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 301831
Seq. ID clt700046066.f1
Method BLASTX
NCBI GI g1673456
BLAST score 239
E value 5.0e-32
Match length 75
% identity 100
NCBI Description (Y09214) rubisco small subunit [Zea mays]

Seq. No. 301832
Seq. ID clt700046073.f1
Method BLASTX
NCBI GI g115815
BLAST score 271
E value 4.0e-24
Match length 65
% identity 77
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
(CAB-M9) (LHCP) >gi_100866_pir_S13098 chlorophyll
a/b-binding protein precursor - maize
>gi_22355_emb_CAA39376_ (X55892) light-harvesting
chlorophyll a/b binding protein [Zea mays]

Seq. No. 301833
Seq. ID clt700046077.f1
Method BLASTN
NCBI GI g3420038
BLAST score 40
E value 3.0e-13
Match length 52
% identity 49
NCBI Description Zea mays gypsy/Ty3-type retrotransposon Tekay, complete sequence

Seq. No. 301834
Seq. ID clt700046241.f1
Method BLASTX
NCBI GI g2739008
BLAST score 191
E value 6.0e-15
Match length 76
% identity 55
NCBI Description (AF022463) CYP78A3p [Glycine max]

Seq. No. 301835
Seq. ID clt700046406.f1
Method BLASTX
NCBI GI g3283026
BLAST score 184
E value 6.0e-14
Match length 92
% identity 38
NCBI Description (AF051562) putative transposase [Arabidopsis thaliana]

Seq. No. 301836
Seq. ID clt700046458.f1
Method BLASTX
NCBI GI g4335735
BLAST score 151
E value 4.0e-10
Match length 35
% identity 74
NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301837
Seq. ID clt700046489.f1
Method BLASTN
NCBI GI g861198
BLAST score 63
E value 2.0e-27
Match length 87
% identity 93
NCBI Description Hordeum vulgare protoporphyrin IX Mg-chelatase subunit precursor (Xantha-f) gene, complete cds

Seq. No. 301838
Seq. ID cyk700047301.f1
Method BLASTX
NCBI GI g2618691
BLAST score 287

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E value 7.0e-26
Match length 107
% identity 56
NCBI Description (AC002510) putative chloroplast envelope Ca²⁺-ATPase [Arabidopsis thaliana]

Seq. No. 301839
Seq. ID cyk700047370.f1
Method BLASTX
NCBI GI g4006915
BLAST score 159
E value 6.0e-11
Match length 74
% identity 41
NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301840
Seq. ID cyk700047402.f1
Method BLASTX
NCBI GI g3023932
BLAST score 211
E value 4.0e-17
Match length 78
% identity 51
NCBI Description HISTONE DEACETYLASE 3 (HD3) >gi_2791688 (AF039753) histone deacetylase-3; HD-3 [Gallus gallus]

Seq. No. 301841
Seq. ID cyk700047429.f1
Method BLASTN
NCBI GI g559535
BLAST score 309
E value 1.0e-174
Match length 335
% identity 99
NCBI Description Z.mays mRNA for metallothionein

Seq. No. 301842
Seq. ID cyk700047456.f1
Method BLASTX
NCBI GI g4039155
BLAST score 169
E value 3.0e-12
Match length 79
% identity 39
NCBI Description (AF104258) putative copper-inducible 35.6 kDa protein [Festuca rubra]

Seq. No. 301843
Seq. ID cyk700047539.f1
Method BLASTX
NCBI GI g2499946
BLAST score 299
E value 2.0e-27
Match length 96
% identity 66
NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE

PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana
tabacum]

Seq. No. 301844
Seq. ID cyk700047591.f1
Method BLASTX
NCBI GI g2213594
BLAST score 378
E value 1.0e-36
Match length 110
% identity 69
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No. 301845
Seq. ID cyk700047652.f1
Method BLASTX
NCBI GI g4008406
BLAST score 200
E value 9.0e-16
Match length 58
% identity 60
NCBI Description (Z82286) predicted using Genefinder [Caenorhabditis elegans]

Seq. No. 301846
Seq. ID cyk700047710.f1
Method BLASTX
NCBI GI g4580398
BLAST score 226
E value 8.0e-19
Match length 52
% identity 77
NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis thaliana]

Seq. No. 301847
Seq. ID cyk700047769.f1
Method BLASTN
NCBI GI g4140643
BLAST score 201
E value 1.0e-109
Match length 310
% identity 92
NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 301848
Seq. ID cyk700047815.f1
Method BLASTX
NCBI GI g3366659
BLAST score 163
E value 2.0e-11
Match length 54
% identity 63
NCBI Description (AF036763) P-ATPase [Emericella nidulans]

Seq. No. 301849
Seq. ID cyk700047828.f1
Method BLASTX
NCBI GI g584861
BLAST score 153
E value 3.0e-10
Match length 56
% identity 50
NCBI Description CYTOCHROME P450 71A2 (CYPLXXIA2) (P-450EG4)
>gi_480396_pir_S36806 cytochrome P450 71A2 - eggplant
>gi_408140_emb_CAA50645 (X71654) P450 hydroxylase [Solanum
melongena] >gi_441185_dbj_BAA03635_ (D14990) Cytochrome
P-450EG4 [Solanum melongena]

Seq. No. 301850
Seq. ID cyk700047850.f1
Method BLASTX
NCBI GI g4206114
BLAST score 389
E value 6.0e-38
Match length 78
% identity 92
NCBI Description (AF097663) cytoplasmic glucose-6-phosphate 1-dehydrogenase
[Mesembryanthemum crystallinum]

Seq. No. 301851
Seq. ID cyk700047889.f1
Method BLASTX
NCBI GI g3168840
BLAST score 183
E value 8.0e-14
Match length 51
% identity 75
NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No. 301852
Seq. ID cyk700047924.f1
Method BLASTN
NCBI GI g2981287
BLAST score 56
E value 9.0e-23
Match length 128
% identity 86
NCBI Description Bos taurus histone H4.1 mRNA, complete cds

Seq. No. 301853
Seq. ID cyk700047958.f1
Method BLASTX
NCBI GI g1351136
BLAST score 439
E value 1.0e-43
Match length 88
% identity 100
NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
>gi_514946 (L22296) UDP-glucose:D-fructose
2-glucosyl-transferase [Zea mays] >gi_533252 (L33244)
sucrose synthase 2 [Zea mays]

Seq. No. 301854
Seq. ID cyk700048174.f1
Method BLASTX
NCBI GI g3025299
BLAST score 291
E value 2.0e-26
Match length 93
% identity 57
NCBI Description HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi_2088660
(AF002109) ABC1 isolog [Arabidopsis thaliana]

Seq. No. 301855
Seq. ID cyk700048179.f1
Method BLASTX
NCBI GI g1620986
BLAST score 154
E value 2.0e-10
Match length 35
% identity 89
NCBI Description (Y08858) 40S ribosomal protein S17 [Nicotiana plumbaginifolia]

Seq. No. 301856
Seq. ID cyk700048210.f1
Method BLASTX
NCBI GI g3121951
BLAST score 168
E value 6.0e-12
Match length 109
% identity 36
NCBI Description CH-TOG PROTEIN (COLONIC AND HEPATIC TUMOR OVER-EXPRESSED PROTEIN) (KIAA0097) >gi_603951_dbj_BAA07892_ (D43948) This gene is novel. [Homo sapiens]

Seq. No. 301857
Seq. ID cyk700048223.f1
Method BLASTX
NCBI GI g3868800
BLAST score 365
E value 5.0e-35
Match length 103
% identity 61
NCBI Description (AB013603) topoisomerase III beta [Mus musculus]

Seq. No. 301858
Seq. ID cyk700048234.f1
Method BLASTX
NCBI GI g3122388
BLAST score 203
E value 5.0e-16
Match length 67
% identity 60
NCBI Description WD-40 REPEAT PROTEIN MSI2 >gi_2394231 (AF016847) WD-40 repeat protein [Arabidopsis thaliana]
>gi_4581121_gb_AAD24611.1_AC005825_18 (AC005825) putative WD-40 protein MSI2 [Arabidopsis thaliana]

Seq. No. 301859
Seq. ID cyk700048266.f1
Method BLASTX
NCBI GI g4539383
BLAST score 169
E value 4.0e-12
Match length 91
% identity 41
NCBI Description (AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No. 301860
Seq. ID cyk700048267.f1
Method BLASTN
NCBI GI g433040
BLAST score 54
E value 1.0e-21
Match length 170
% identity 84
NCBI Description Zea mays W-22 clone PREM-1A retroelement PREM-1, partial sequence

Seq. No. 301861
Seq. ID cyk700048271.f1
Method BLASTX
NCBI GI g1076353
BLAST score 421
E value 9.0e-42
Match length 97
% identity 85
NCBI Description myosin heavy chain PCR11 - Arabidopsis thaliana (fragment)

Seq. No. 301862
Seq. ID cyk700048315.f1
Method BLASTX
NCBI GI g3687469
BLAST score 178
E value 1.0e-13
Match length 51
% identity 67
NCBI Description (AL031798) putative diphthine synthase [Schizosaccharomyces pombe]

Seq. No. 301863
Seq. ID cyk700048318.f1
Method BLASTX
NCBI GI g3176715
BLAST score 241
E value 1.0e-20
Match length 96
% identity 52
NCBI Description (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 301864
Seq. ID cyk700048365.f1

Method BLASTX
NCBI GI g3242783
BLAST score 229
E value 3.0e-19
Match length 67
% identity 60
NCBI Description (AF055354) respiratory burst oxidase protein B [Arabidopsis thaliana]

Seq. No. 301865
Seq. ID cyk700048446.f1
Method BLASTX
NCBI GI g1350595
BLAST score 228
E value 2.0e-19
Match length 49
% identity 84
NCBI Description RHO2 PROTEIN >gi_1076923_pir_JC4045 Rho2 protein - fission yeast (Schizosaccharomyces pombe) >gi_1064858_dbj_BAA07378_(D38181) Rho 2 [Schizosaccharomyces pombe]

Seq. No. 301866
Seq. ID cyk700048453.f1
Method BLASTX
NCBI GI g4377999
BLAST score 393
E value 2.0e-38
Match length 99
% identity 69
NCBI Description (AF076951) Cu-Zn superoxide dismutase [Glomerella cingulata]

Seq. No. 301867
Seq. ID cyk700048471.f1
Method BLASTX
NCBI GI g2129559
BLAST score 228
E value 5.0e-19
Match length 80
% identity 59
NCBI Description cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No. 301868
Seq. ID cyk700048478.f1
Method BLASTX
NCBI GI g2275211
BLAST score 290
E value 2.0e-26
Match length 66
% identity 83
NCBI Description (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. 301869
Seq. ID cyk700048479.f1
Method BLASTX
NCBI GI g3776573
BLAST score 236
E value 2.0e-20
Match length 61
% identity 67
NCBI Description (AC005388) Similar to nodulins and lipase homolog F14J9.5
gi 3482914 from Arabidopsis thaliana BAC gb AC003970.
Alternate first exon from 72258 to 72509. [Arabidopsis
thaliana]

Seq. No. 301870
Seq. ID cyk700048492.f1
Method BLASTX
NCBI GI g585165
BLAST score 291
E value 2.0e-26
Match length 80
% identity 70
NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
(G6PD) >gi_2129985_pir_S60287 glucose-6-phosphate
1-dehydrogenase (EC 1.1.1.49) - potato
>gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate
1-dehydrogenase [Solanum tuberosum]

Seq. No. 301871
Seq. ID cyk700048502.f1
Method BLASTX
NCBI GI g2293566
BLAST score 369
E value 1.0e-35
Match length 73
% identity 100
NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No. 301872
Seq. ID cyk700048605.f1
Method BLASTX
NCBI GI g4455232
BLAST score 262
E value 2.0e-24
Match length 88
% identity 60
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 301873
Seq. ID cyk700048636.f1
Method BLASTX
NCBI GI g2980798
BLAST score 187
E value 3.0e-14
Match length 63
% identity 52
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 301874
Seq. ID cyk700048650.f1
Method BLASTN
NCBI GI g22185
BLAST score 33
E value 4.0e-09
Match length 53
% identity 91
NCBI Description Z.mays mRNA for b-32 protein, putative regulatory factor of zein expression (clone b-32.120)

Seq. No. 301875
Seq. ID cyk700048662.f1
Method BLASTN
NCBI GI g2288968
BLAST score 54
E value 6.0e-22
Match length 85
% identity 91
NCBI Description Zea mays mRNA for glutathione transferase

Seq. No. 301876
Seq. ID cyk700048675.f1
Method BLASTX
NCBI GI g3738308
BLAST score 204
E value 3.0e-16
Match length 100
% identity 47
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 301877
Seq. ID cyk700048691.f1
Method BLASTX
NCBI GI g4138179
BLAST score 263
E value 3.0e-23
Match length 77
% identity 69
NCBI Description (AJ223969) elongation factor 1 alpha subunit [Malus domestica]

Seq. No. 301878
Seq. ID cyk700048747.f1
Method BLASTX
NCBI GI g4105798
BLAST score 229
E value 2.0e-25
Match length 73
% identity 71
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 301879
Seq. ID cyk700048751.f1
Method BLASTX
NCBI GI g2130023
BLAST score 169

E value 5.0e-12
 Match length 82
 % identity 57
 NCBI Description DNA-binding protein ABF1 - wild oat (fragment)
 >gi_1159877_emb_CAA88326_ (Z48429) DNA-binding protein
 [Avena fatua]

 Seq. No. 301880
 Seq. ID cyk700048760.f1
 Method BLASTN
 NCBI GI g3320103
 BLAST score 35
 E value 1.0e-10
 Match length 55
 % identity 91
 NCBI Description Zea mays mRNA for calcium-dependent protein kinase

 Seq. No. 301881
 Seq. ID cyk700048805.f1
 Method BLASTX
 NCBI GI g82696
 BLAST score 283
 E value 5.0e-29
 Match length 80
 % identity 88
 NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_
 (X61121) glycine-rich protein [Zea mays]

 Seq. No. 301882
 Seq. ID cyk700048818.f1
 Method BLASTX
 NCBI GI g542058
 BLAST score 150
 E value 5.0e-10
 Match length 39
 % identity 67
 NCBI Description HSR203J protein - common tobacco >gi_444002_emb_CAA54393_
 (X77136) HSR203J [Nicotiana tabacum]

 Seq. No. 301883
 Seq. ID cyk700048838.f1
 Method BLASTX
 NCBI GI g4454043
 BLAST score 258
 E value 1.0e-22
 Match length 69
 % identity 67
 NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]

 Seq. No. 301884
 Seq. ID cyk700048876.f1
 Method BLASTN
 NCBI GI g998429
 BLAST score 53
 E value 4.0e-21
 Match length 77
 % identity 92

NCBI Description GRF1=general regulatory factor [Zea mays, XL80, Genomic, 5348 nt]

Seq. No. 301885
Seq. ID cyk700048896.f1
Method BLASTX
NCBI GI g2980767
BLAST score 182
E value 6.0e-14
Match length 77
% identity 48
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 301886
Seq. ID cyk700048904.f1
Method BLASTX
NCBI GI g4582461
BLAST score 364
E value 5.0e-35
Match length 101
% identity 71
NCBI Description (AC007071) putative triacylglycerol lipase [Arabidopsis thaliana]

Seq. No. 301887
Seq. ID cyk700048929.f1
Method BLASTX
NCBI GI g2541876
BLAST score 168
E value 5.0e-12
Match length 79
% identity 43
NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No. 301888
Seq. ID cyk700048931.f1
Method BLASTN
NCBI GI g1408221
BLAST score 71
E value 9.0e-32
Match length 201
% identity 91
NCBI Description Sorghum bicolor pathogenesis-related protein (PR-10) mRNA, complete cds

Seq. No. 301889
Seq. ID cyk700048934.f1
Method BLASTN
NCBI GI g4240538
BLAST score 258
E value 1.0e-143
Match length 265
% identity 99
NCBI Description Zea mays knotted class 1 homeodomain protein liguleless3 (lg3) mRNA, complete cds

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Seq. No. 301890
Seq. ID cyk700048973.f1
Method BLASTX
NCBI GI g1353193
BLAST score 176
E value 6.0e-13
Match length 50
% identity 64
NCBI Description O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir_JQ2268
O-methyltransferase (EC 2.1.1.-) - maize >gi_404070
(L14063) O-methyltransferase [Zea mays]

Seq. No. 301891
Seq. ID cyk700048987.f1
Method BLASTX
NCBI GI g4585972
BLAST score 277
E value 8.0e-25
Match length 96
% identity 51
NCBI Description (AC005287) Putative ATPase [Arabidopsis thaliana]

Seq. No. 301892
Seq. ID cyk700049013.f1
Method BLASTX
NCBI GI g2058311
BLAST score 186
E value 4.0e-14
Match length 40
% identity 85
NCBI Description (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii]

Seq. No. 301893
Seq. ID cyk700049102.f1
Method BLASTX
NCBI GI g4588906
BLAST score 305
E value 5.0e-28
Match length 67
% identity 88
NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]

Seq. No. 301894
Seq. ID cyk700049141.f1
Method BLASTN
NCBI GI g559535
BLAST score 252
E value 1.0e-140
Match length 294
% identity 96
NCBI Description Z.mays mRNA for metallothionein

Seq. No. 301895
Seq. ID cyk700049142.f1
Method BLASTN
NCBI GI g603189
BLAST score 38

E value 4.0e-12
Match length 81
% identity 86
NCBI Description Zea mays translation initiation factor eIF-4A mRNA,
complete cds

Seq. No. 301896
Seq. ID cyk700049168.f1
Method BLASTX
NCBI GI g1313909
BLAST score 198
E value 8.0e-16
Match length 76
% identity 61
NCBI Description (D84508) CDPK-related protein kinase [Zea mays]

Seq. No. 301897
Seq. ID cyk700049175.f1
Method BLASTN
NCBI GI g4582786
BLAST score 40
E value 3.0e-13
Match length 40
% identity 100
NCBI Description Zea mays mRNA for adenosine kinase, putative

Seq. No. 301898
Seq. ID cyk700049210.f1
Method BLASTN
NCBI GI g1747295
BLAST score 86
E value 8.0e-41
Match length 165
% identity 89
NCBI Description Oryza sativa mRNA for vacuolar H⁺-pyrophosphatase, complete cds

Seq. No. 301899
Seq. ID cyk700049214.f1
Method BLASTX
NCBI GI q3885334
BLAST score 297
E value 4.0e-27
Match length 88
% identity 67
NCBI Description (AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No. 301900
Seq. ID cyk700049247.f1
Method BLASTX
NCBI GI g1706260
BLAST score 283
E value 1.0e-25
Match length 76
% identity 74
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir_S59597

cysteine proteinase 1 precursor - maize
>gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays]

Seq. No. 301901
Seq. ID cyk700049294.f1
Method BLASTX
NCBI GI g2190553
BLAST score 178
E value 7.0e-18
Match length 97
% identity 47
NCBI Description (AC001229) Strong similarity to Arabidopsis zeta-crystallin-like protein (gb_Z49268). [Arabidopsis thaliana]

Seq. No. 301902
Seq. ID cyk700049352.f1
Method BLASTX
NCBI GI g4115559
BLAST score 229
E value 4.0e-19
Match length 104
% identity 46
NCBI Description (AB013596) UDP-glucose:anthocysnin 5-O-glucosyltransferase [Perilla frutescens]

Seq. No. 301903
Seq. ID cyk700049357.f1
Method BLASTN
NCBI GI g1042260
BLAST score 42
E value 2.0e-14
Match length 54
% identity 94
NCBI Description {Mul element insertion site, clone 10} [maize, Transposon, 285 nt]

Seq. No. 301904
Seq. ID cyk700049422.f1
Method BLASTX
NCBI GI g2130024
BLAST score 155
E value 1.0e-10
Match length 66
% identity 55
NCBI Description DNA-binding protein ABF2 - wild oat
>gi_1159879_emb_CAA88331_ (Z48431) DNA-binding protein [Avena fatua]

Seq. No. 301905
Seq. ID cyk700049454.f1
Method BLASTX
NCBI GI g444344
BLAST score 235
E value 7.0e-24
Match length 70

% identity 74
NCBI Description thaumatin-like protein [Zea mays]

Seq. No. 301906
Seq. ID cyk700049460.f1
Method BLASTX
NCBI GI g3367568
BLAST score 177
E value 5.0e-13
Match length 39
% identity 79
NCBI Description (AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 301907
Seq. ID cyk700049493.f1
Method BLASTX
NCBI GI g3913366
BLAST score 175
E value 7.0e-13
Match length 96
% identity 47
NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR >gi_1597723 (U67422) CRINKLY4 precursor [Zea mays]

Seq. No. 301908
Seq. ID cyk700049530.f1
Method BLASTX
NCBI GI g549597
BLAST score 217
E value 8.0e-18
Match length 88
% identity 48
NCBI Description ATP-DEPENDENT RNA HELICASE DBP7 >gi_539330_pir_S38093 probable purine nucleotide-binding protein YKR024c - yeast (Saccharomyces cerevisiae) >gi_486449_emb_CAA82096_(Z28249) ORF YKR024c [Saccharomyces cerevisiae]

Seq. No. 301909
Seq. ID cyk700049532.f1
Method BLASTX
NCBI GI g3360289
BLAST score 150
E value 5.0e-10
Match length 40
% identity 60
NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No. 301910
Seq. ID cyk700049560.f1
Method BLASTX
NCBI GI g2980781
BLAST score 214
E value 2.0e-17
Match length 53
% identity 62

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 301911
Seq. ID cyk700049654.f1
Method BLASTN
NCBI GI g168654
BLAST score 34
E value 1.0e-09
Match length 94
% identity 84
NCBI Description Zea mays ADP glucose pyrophosphorylase (shrunken-2) gene, complete cds

Seq. No. 301912
Seq. ID cyk700049692.f1
Method BLASTN
NCBI GI g1945282
BLAST score 37
E value 2.0e-11
Match length 61
% identity 90
NCBI Description O.sativa mRNA for myb factor, 1402 bp

Seq. No. 301913
Seq. ID cyk700049694.f1
Method BLASTX
NCBI GI g585876
BLAST score 232
E value 1.0e-19
Match length 81
% identity 62
NCBI Description 60S RIBOSOMAL PROTEIN L23A (L25) >gi_1084424_pir S48026
ribosomal protein L25 - common tobacco >gi_310935 (L18908)
60S ribosomal protein L25 [Nicotiana tabacum]

Seq. No. 301914
Seq. ID cyk700049731.f1
Method BLASTN
NCBI GI g1906603
BLAST score 226
E value 1.0e-124
Match length 277
% identity 96
NCBI Description Zea mays ACCase gene, intron containing colonist1 and colonist2 retrotransposons and reverse transcriptase pseudogene, complete sequence

Seq. No. 301915
Seq. ID cyk700049738.f1
Method BLASTX
NCBI GI g2570047
BLAST score 222
E value 2.0e-18
Match length 87
% identity 41
NCBI Description (Y09234) MSTK2S kinase-like protein [Mus musculus]

Seq. No. 301916
Seq. ID cyk700049749.f1
Method BLASTX
NCBI GI g3805964
BLAST score 306
E value 1.0e-28
Match length 64
% identity 86
NCBI Description (Y13773) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No. 301917
Seq. ID cyk700049772.f1
Method BLASTX
NCBI GI g2244855
BLAST score 261
E value 6.0e-23
Match length 100
% identity 54
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301918
Seq. ID cyk700049805.f1
Method BLASTX
NCBI GI g4378178
BLAST score 181
E value 5.0e-16
Match length 89
% identity 56
NCBI Description (AF102543) unknown [Zymomonas mobilis]

Seq. No. 301919
Seq. ID cyk700049823.f1
Method BLASTX
NCBI GI g128185
BLAST score 235
E value 3.0e-26
Match length 75
% identity 85
NCBI Description NITRATE REDUCTASE (NR) >gi_66208_pir_RDBHNH nitrate reductase (NADH) (EC 1.6.6.1) - barley (cv. Himalaya)
>gi_18994_emb_CAA40976_ (X57845) nitrate reductase [Hordeum vulgare]

Seq. No. 301920
Seq. ID cyk700049824.f1
Method BLASTX
NCBI GI g1491929
BLAST score 415
E value 5.0e-41
Match length 89
% identity 89
NCBI Description (U51272) 1,3-beta-D-glucan synthase catalytic subunit [Emericella nidulans]

Seq. No. 301921
Seq. ID cyk700049833.f1
Method BLASTX

NCBI GI g4467126
BLAST score 226
E value 6.0e-19
Match length 63
% identity 71
NCBI Description (AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]

Seq. No. 301922
Seq. ID cyk700049887.f1
Method BLASTX
NCBI GI g2598037
BLAST score 291
E value 2.0e-26
Match length 98
% identity 54
NCBI Description (AJ001272) manganese resistance 1 protein [Saccharomyces cerevisiae]

Seq. No. 301923
Seq. ID cyk700049888.f1
Method BLASTN
NCBI GI g1657759
BLAST score 80
E value 1.0e-37
Match length 88
% identity 98
NCBI Description Zea mays retrotransposon Fourf 5' LTR and primer binding site DNA sequence

Seq. No. 301924
Seq. ID cyk700049907.f1
Method BLASTX
NCBI GI g2293566
BLAST score 378
E value 9.0e-37
Match length 75
% identity 100
NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No. 301925
Seq. ID cyk700049910.f1
Method BLASTX
NCBI GI g3522929
BLAST score 407
E value 5.0e-40
Match length 80
% identity 96
NCBI Description (AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 301926
Seq. ID cyk700049953.f1
Method BLASTX
NCBI GI g100490
BLAST score 402

E value 2.0e-39
Match length 103
% identity 23
NCBI Description polyubiquitin - garden snapdragon (fragment)
>gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus]

Seq. No. 301927
Seq. ID cyk700049964.f1
Method BLASTX
NCBI GI g1076641
BLAST score 208
E value 8.0e-17
Match length 40
% identity 97
NCBI Description tau-protein kinase (EC 2.7.1.135) homolog - common tobacco
>gi_456356_emb_CAA54803_ (X77763) shaggy like protein kinase [Nicotiana tabacum] >gi_1094395_prf_ 2106142A Ser/Thr protein kinase [Nicotiana tabacum]

Seq. No. 301928
Seq. ID cyk700050015.f1
Method BLASTX
NCBI GI g4539399
BLAST score 184
E value 6.0e-14
Match length 38
% identity 100
NCBI Description (AL035526) ras-like GTP-binding protein [Arabidopsis thaliana]

Seq. No. 301929
Seq. ID cyk700050036.f1
Method BLASTX
NCBI GI g1209756
BLAST score 254
E value 3.0e-22
Match length 91
% identity 55
NCBI Description (U43629) integral membrane protein [Beta vulgaris]

Seq. No. 301930
Seq. ID cyk700050061.f1
Method BLASTX
NCBI GI g1076685
BLAST score 300
E value 2.0e-27
Match length 90
% identity 34
NCBI Description SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_ (D30038) SPF1 protein [Ipomoea batatas]

Seq. No. 301931
Seq. ID cyk700050077.f1
Method BLASTX
NCBI GI g902586
BLAST score 438

E value 8.0e-44
Match length 88
% identity 20
NCBI Description (U29162) ubiquitin [Zea mays]

Seq. No. 301932
Seq. ID cyk700050123.f1
Method BLASTX
NCBI GI g2894569
BLAST score 186
E value 2.0e-14
Match length 50
% identity 64
NCBI Description (AL021890) putative protein [Arabidopsis thaliana]

Seq. No. 301933
Seq. ID cyk700050135.f1
Method BLASTX
NCBI GI g422029
BLAST score 312
E value 6.0e-29
Match length 99
% identity 69
NCBI Description transcription factor OBF3.2, ocs element-binding - maize
>gi_297018_emb_CAA48904_ (X69152) ocs-element binding
factor 3.2 [Zea mays]

Seq. No. 301934
Seq. ID cyk700050162.f1
Method BLASTX
NCBI GI g1708073
BLAST score 242
E value 1.0e-20
Match length 103
% identity 51
NCBI Description GMP SYNTHASE (GLUTAMINE-HYDROLYSING) (GLUTAMINE
AMIDOTRANSFERASE) (GMP SYNTHETASE) >gi_1077145_pir_S55099
GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) - yeast
(Saccharomyces cerevisiae) >gi_854469_emb_CAA89932_
(Z49809) Gualp [Saccharomyces cerevisiae]

Seq. No. 301935
Seq. ID cyk700050189.f1
Method BLASTX
NCBI GI g2129587
BLAST score 187
E value 3.0e-14
Match length 83
% identity 45
NCBI Description gamma-glutamyltransferase (EC 2.3.2.2) - Arabidopsis
thaliana >gi_928934_emb_CAA89206_ (Z49240) gamma-glutamyl
transpeptidase [Arabidopsis thaliana]
>gi_1585436_prf_2124427C gamma-Glu transpeptidase
[Arabidopsis thaliana]

Seq. No. 301936
Seq. ID cyk700050204.f1

Method BLASTX
NCBI GI g542157
BLAST score 177
E value 2.0e-13
Match length 52
% identity 67
NCBI Description ribosomal 5S RNA-binding protein - Rice

Seq. No. 301937
Seq. ID cyk700050222.f1
Method BLASTX
NCBI GI g2702268
BLAST score 161
E value 2.0e-11
Match length 49
% identity 61
NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No. 301938
Seq. ID cyk700050241.f1
Method BLASTX
NCBI GI g4558552
BLAST score 280
E value 3.0e-25
Match length 65
% identity 41
NCBI Description (AC007138) putative P-glycoprotein-like protein [Arabidopsis thaliana]

Seq. No. 301939
Seq. ID cyk700050275.f1
Method BLASTN
NCBI GI g2668743
BLAST score 41
E value 8.0e-14
Match length 73
% identity 89
NCBI Description Zea mays ubiquitin conjugating enzyme (UBC) mRNA, complete cds

Seq. No. 301940
Seq. ID cyk700050285.f1
Method BLASTX
NCBI GI g2281085
BLAST score 215
E value 2.0e-17
Match length 61
% identity 64
NCBI Description (AC002333) CTR1 protein kinase isolog [Arabidopsis thaliana]

Seq. No. 301941
Seq. ID cyk700050290.f1
Method BLASTX
NCBI GI g673433
BLAST score 288
E value 4.0e-26

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Match length 82
% identity 68
NCBI Description (X56953) protein synthesis initiation factor 4A [Mus musculus]

Seq. No. 301942
Seq. ID cyk700050349.f1
Method BLASTN
NCBI GI g4206307
BLAST score 57
E value 1.0e-23
Match length 154
% identity 86
NCBI Description Zea mays retrotransposon Cinful-2

Seq. No. 301943
Seq. ID cyk700050391.f1
Method BLASTN
NCBI GI g499013
BLAST score 82
E value 1.0e-38
Match length 114
% identity 93
NCBI Description T.aestivum (Capitole) mitochondrial orf240 gene

Seq. No. 301944
Seq. ID cyk700050395.f1
Method BLASTX
NCBI GI g1335862
BLAST score 154
E value 1.0e-10
Match length 51
% identity 65
NCBI Description (U42608) clathrin heavy chain [Glycine max]

Seq. No. 301945
Seq. ID cyk700050474.f1
Method BLASTX
NCBI GI g3482915
BLAST score 315
E value 2.0e-29
Match length 77
% identity 71
NCBI Description (AC003970) Similar to 12-oxophytodienoate reductase, gi_2765083 and old-yellow-enzyme homolog, gi_2232254 [Arabidopsis thaliana]

Seq. No. 301946
Seq. ID cyk700050518.f1
Method BLASTX
NCBI GI g266578
BLAST score 244
E value 2.0e-22
Match length 55
% identity 98
NCBI Description METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir_S17560
metallothionein-like protein - maize >gi_236730_bbs_57629

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(S57628) metallothionein homologue [Zea mays, Peptide, 76 aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186)
metallothionein-like protein [Zea mays]
>gi_228095_prf_1717215A metallothionein-like protein [Zea mays]

Seq. No. 301947
Seq. ID cyk700050539.f1
Method BLASTX
NCBI GI g3128218
BLAST score 302
E value 1.0e-27
Match length 64
% identity 91
NCBI Description (AC004077) putative end13 protein [Arabidopsis thaliana]

Seq. No. 301948
Seq. ID cyk700050604.f1
Method BLASTX
NCBI GI g629688
BLAST score 353
E value 1.0e-33
Match length 100
% identity 68
NCBI Description dehydroquinase shikimate dehydrogenase - Common tobacco
>gi_535771 (L32794) dehydroquinate dehydratase/shikimate
dehydrogenase [Nicotiana tabacum]

Seq. No. 301949
Seq. ID cyk700050630.f1
Method BLASTX
NCBI GI g4467359
BLAST score 361
E value 9.0e-35
Match length 87
% identity 76
NCBI Description (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis thaliana]

Seq. No. 301950
Seq. ID cyk700050635.f1
Method BLASTX
NCBI GI g66009
BLAST score 216
E value 3.0e-26
Match length 73
% identity 88
NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,
cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH
(AA 1-337) [Zea mays]

Seq. No. 301951
Seq. ID cyk700050649.f1
Method BLASTX
NCBI GI g4539676
BLAST score 217
E value 9.0e-18

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Match length 101
% identity 53
NCBI Description (AF061282) patatin-like protein [Sorghum bicolor]

Seq. No. 301952
Seq. ID cyk700050660.f1
Method BLASTX
NCBI GI g586324
BLAST score 397
E value 7.0e-39
Match length 101
% identity 67
NCBI Description TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90) >gi_419854_pir_S34023 TATA box-binding protein-associated factor chain TAFII90 - yeast (Saccharomyces cerevisiae) >gi_311674_emb_CAA79685_(Z21487) unknown [Saccharomyces cerevisiae] >gi_536569_emb_CAA85160_(Z36067) ORF YBR198c [Saccharomyces cerevisiae] >gi_1091232_prf_2020425A TATA box-binding protein-associated factor [Saccharomyces cerevisiae]

Seq. No. 301953
Seq. ID cyk700050733.f1
Method BLASTX
NCBI GI g2226329
BLAST score 274
E value 2.0e-24
Match length 71
% identity 72
NCBI Description (AF001634) physical impedance induced protein [Zea mays]

Seq. No. 301954
Seq. ID cyk700050743.f1
Method BLASTX
NCBI GI g3868853
BLAST score 186
E value 5.0e-14
Match length 47
% identity 68
NCBI Description (AB013853) GPI-anchored protein [Vigna radiata]

Seq. No. 301955
Seq. ID cyk700050750.f1
Method BLASTN
NCBI GI g1185553
BLAST score 188
E value 1.0e-101
Match length 287
% identity 99
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2) gene, complete cds

Seq. No. 301956
Seq. ID cyk700050754.f1
Method BLASTX
NCBI GI g1667389

BLAST score 403
E value 1.0e-39
Match length 94
% identity 87
NCBI Description (Y09238) 3-hydroxy-3-methylglutaryl coenzyme A reductase [Zea mays]

Seq. No. 301957
Seq. ID cyk700050762.f1
Method BLASTX
NCBI GI g1277236
BLAST score 228
E value 3.0e-19
Match length 56
% identity 75
NCBI Description (U52430) Sec13p [Pichia pastoris]

Seq. No. 301958
Seq. ID cyk700050787.f1
Method BLASTX
NCBI GI g3885968
BLAST score 307
E value 2.0e-28
Match length 72
% identity 83
NCBI Description (AF100985) phosphopyruvate hydratase [Penaeus monodon]

Seq. No. 301959
Seq. ID cyk700050801.f1
Method BLASTX
NCBI GI g2129552
BLAST score 256
E value 2.0e-22
Match length 76
% identity 64
NCBI Description calcium-dependent protein kinase 19 - Arabidopsis thaliana (fragment)

Seq. No. 301960
Seq. ID cyk700050833.f1
Method BLASTX
NCBI GI g417578
BLAST score 287
E value 4.0e-26
Match length 57
% identity 91
NCBI Description RAS-RELATED PROTEIN RAC1 >gi_345368_pir_A45324 ras-related GTP-binding protein - Caenorhabditis elegans
>gi_6829_emb_CAA48506_ (X68492) small ras-related protein [Caenorhabditis elegans] >gi_156424 (L03711) rac1 protein [Caenorhabditis elegans] >gi_156426 (L04287) rac1 protein [Caenorhabditis elegans]

Seq. No. 301961
Seq. ID cyk700050885.f1
Method BLASTN
NCBI GI g4115614

BLAST score 61
E value 8.0e-26
Match length 250
% identity 86
NCBI Description Zea mays mRNA for root cap-specific glycine-rich protein, complete cds

Seq. No. 301962
Seq. ID cyk700050896.f1
Method BLASTN
NCBI GI g3294466
BLAST score 106
E value 8.0e-53
Match length 210
% identity 89
NCBI Description Zea mays phosphoglucomutase 1 mRNA, complete cds

Seq. No. 301963
Seq. ID cyk700050923.f1
Method BLASTX
NCBI GI g1706956
BLAST score 442
E value 3.0e-44
Match length 90
% identity 91
NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]

Seq. No. 301964
Seq. ID cyk700050989.f1
Method BLASTX
NCBI GI g1723440
BLAST score 189
E value 4.0e-19
Match length 89
% identity 54
NCBI Description HYPOTHETICAL 35.9 KD PROTEIN C56F8.08 IN CHROMOSOME I
>gi_1204230_emb_CAA93579_ (Z69728) unknown
[Schizosaccharomyces pombe]

Seq. No. 301965
Seq. ID cyk700051004.f1
Method BLASTX
NCBI GI g1255728
BLAST score 249
E value 1.0e-21
Match length 94
% identity 49
NCBI Description (U33265) complement fixation antigen [Coccidioides immitis]
>gi_1256769 (U51271) complement-fixation antigen
[Coccidioides immitis]

Seq. No. 301966
Seq. ID cyk700051023.f1
Method BLASTX
NCBI GI g1170092
BLAST score 327
E value 9.0e-31

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Match length	75
% identity	88
NCBI Description	GLUTATHIONE S-TRANSFERASE IV (GST-IV) (GST-27) (CLASS PHI) >gi_1076807_pir_S52037 glutathione transferase (EC 2.5.1.18) 27K chain - maize >gi_529015 (U12679) glutathione S-transferase IV [Zea mays] >gi_695789_emb_CAA56047_ (X79515) glutathione transferase [Zea mays] >gi_1094866_prf_2106424A glutathione S-transferase:ISOTYPE=IV [Zea mays]
Seq. No.	301967
Seq. ID	cyk700051056.f1
Method	BLASTX
NCBI GI	g3695403
BLAST score	188
E value	2.0e-14
Match length	51
% identity	82
NCBI Description	(AF096373) contains similarity to the pfkB family of carbohydrate kinases (Pfam: PF00294, E=1.6e-75) [Arabidopsis thaliana] >gi_4538955_emb_CAB39779.1_ (AL049488) fructokinase-like protein [Arabidopsis thaliana]
Seq. No.	301968
Seq. ID	cyk700051060.f1
Method	BLASTX
NCBI GI	g4006920
BLAST score	223
E value	2.0e-18
Match length	62
% identity	69
NCBI Description	(Z99708) actin interacting protein [Arabidopsis thaliana]
Seq. No.	301969
Seq. ID	cyk700051071.f1
Method	BLASTX
NCBI GI	g4204259
BLAST score	167
E value	6.0e-12
Match length	90
% identity	39
NCBI Description	(AC005223) 18074 [Arabidopsis thaliana]
Seq. No.	301970
Seq. ID	cyk700051096.f1
Method	BLASTX
NCBI GI	g1621465
BLAST score	354
E value	8.0e-34
Match length	70
% identity	87
NCBI Description	(U73105) laccase [Liriodendron tulipifera]
Seq. No.	301971
Seq. ID	cyk700051130.f1
Method	BLASTX
NCBI GI	g1172836

BLAST score 301
E value 1.0e-27
Match length 65
% identity 86
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787)
small ras-related protein [Nicotiana tabacum]

Seq. No. 301972
Seq. ID cyk700051155.f1
Method BLASTX
NCBI GI g4588012
BLAST score 235
E value 2.0e-20
Match length 101
% identity 46
NCBI Description (AF085717) putative callose synthase catalytic subunit
[Gossypium hirsutum]

Seq. No. 301973
Seq. ID cyk700051203.f1
Method BLASTX
NCBI GI g3292826
BLAST score 377
E value 2.0e-36
Match length 95
% identity 72
NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301974
Seq. ID cyk700051224.f1
Method BLASTX
NCBI GI g1346485
BLAST score 253
E value 5.0e-22
Match length 55
% identity 89
NCBI Description MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT
MALIC ENZYME) (NADP-ME) >gi_20469_emb_CAA39690_ (X56233)
malic enzyme [Populus balsamifera subsp. trichocarpa]

Seq. No. 301975
Seq. ID cyk700051225.f1
Method BLASTX
NCBI GI g2252830
BLAST score 383
E value 3.0e-37
Match length 101
% identity 81
NCBI Description (AF013293) weak similarity to receptor protein kinase
[Arabidopsis thaliana]

Seq. No. 301976
Seq. ID cyk700051236.f1
Method BLASTX
NCBI GI g2344899
BLAST score 194
E value 3.0e-18

Match length 95
% identity 52
NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 301977
Seq. ID cyk700051237.f1
Method BLASTX
NCBI GI g4406766
BLAST score 226
E value 5.0e-19
Match length 82
% identity 49
NCBI Description (AC006836) putative flavonol sulfotransferase [Arabidopsis thaliana]

Seq. No. 301978
Seq. ID cyk700051250.f1
Method BLASTX
NCBI GI g3258570
BLAST score 159
E value 4.0e-11
Match length 38
% identity 68
NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]

Seq. No. 301979
Seq. ID cyk700051256.f1
Method BLASTN
NCBI GI g22312
BLAST score 179
E value 3.0e-96
Match length 206
% identity 98
NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid)

Seq. No. 301980
Seq. ID cyk700051271.f1
Method BLASTX
NCBI GI g3293031
BLAST score 377
E value 1.0e-36
Match length 89
% identity 72
NCBI Description (AJ007574) amino acid carrier [Ricinus communis]

Seq. No. 301981
Seq. ID cyk700051295.f1
Method BLASTX
NCBI GI g1888357
BLAST score 219
E value 4.0e-18
Match length 68
% identity 59
NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]
>gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	301982
Seq. ID	cyk700051321.f1
Method	BLASTX
NCBI GI	g3445397
BLAST score	179
E value	1.0e-13
Match length	67
% identity	42
NCBI Description	(AJ010166) S-domain receptor-like protein kinase [Zea mays]
Seq. No.	301983
Seq. ID	cyk700051334.f1
Method	BLASTX
NCBI GI	g122772
BLAST score	149
E value	6.0e-10
Match length	44
% identity	59
NCBI Description	TRANSCRIPTION FACTOR HBP-1B >gi_100809_pir_S15347 transcription factor HBP-1b - wheat >gi_21635_emb_CAA40102_(X56782) HBP-1b [Triticum aestivum]
Seq. No.	301984
Seq. ID	cyk700051341.f1
Method	BLASTX
NCBI GI	g2501024
BLAST score	196
E value	2.0e-15
Match length	42
% identity	81
NCBI Description	PROBABLE LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS) >gi_1086773 (U41105) coded for by C. elegans cDNA yk124d11.3; coded for by C. elegans cDNA yk48a4.3; coded for by C. elegans cDNA yk124d11.5; coded for by C. elegans cDNA cm7h5; coded for by C. elegans cDNA cm7a10; similar to class II aminoacyl-tRNA sy
Seq. No.	301985
Seq. ID	cyk700051379.f1
Method	BLASTX
NCBI GI	g3859548
BLAST score	225
E value	1.0e-18
Match length	49
% identity	84
NCBI Description	(AF097182) protein phosphatase 2A catalytic subunit [Oryza sativa]
Seq. No.	301986
Seq. ID	cyk700051414.f1
Method	BLASTX
NCBI GI	g3335359
BLAST score	227
E value	5.0e-19
Match length	61
% identity	66

NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No. 301987
Seq. ID cyk700051439.f1
Method BLASTX
NCBI GI g3451075
BLAST score 208
E value 7.0e-17
Match length 85
% identity 40

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 301988
Seq. ID cyk700051460.f1
Method BLASTX
NCBI GI g4587987
BLAST score 239
E value 1.0e-20
Match length 78
% identity 56

NCBI Description (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana]

Seq. No. 301989
Seq. ID cyk700051516.f1
Method BLASTX
NCBI GI g461532
BLAST score 346
E value 4.0e-35
Match length 80
% identity 89

NCBI Description ADP-RIBOSYLATION FACTOR >gi_1362500_pir_D49993
ADP-ribosylation factor - Ajellomyces capsulata >gi_407693
(L25117) ADP-ribosylation factor [Histoplasma capsulatum]

Seq. No. 301990
Seq. ID cyk700051517.f1
Method BLASTX
NCBI GI g4371280
BLAST score 383
E value 3.0e-37
Match length 101
% identity 76

NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 301991
Seq. ID cyk700051610.f1
Method BLASTX
NCBI GI g2582381
BLAST score 318
E value 1.0e-29
Match length 87
% identity 72

NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana tabacum]

Seq. No. 301992

Seq. ID cyk700051640.f1
Method BLASTN
NCBI GI g169818
BLAST score 98
E value 5.0e-48
Match length 138
% identity 93
NCBI Description Rice 25S ribosomal RNA gene

Seq. No. 301993
Seq. ID cyk700051658.f1
Method BLASTX
NCBI GI g730461
BLAST score 216
E value 1.0e-17
Match length 56
% identity 68
NCBI Description 40S RIBOSOMAL PROTEIN YS29A >gi_626904_pir_S48503
ribosomal protein S29.e.A, cytosolic - yeast (Saccharomyces
cerevisiae) >gi_287628_dbj_BAA03507 (D14676) ribosomal
protein YS29 [Saccharomyces cerevisiae] >gi_625108 (U19729)
Ylr388wp [Saccharomyces cerevisiae]

Seq. No. 301994
Seq. ID cyk700051718.f1
Method BLASTX
NCBI GI g3876501
BLAST score 178
E value 3.0e-13
Match length 75
% identity 39
NCBI Description (Z92784) F31C3.5 [Caenorhabditis elegans]

Seq. No. 301995
Seq. ID cyk700051732.f1
Method BLASTX
NCBI GI g3334140
BLAST score 315
E value 7.0e-30
Match length 92
% identity 74
NCBI Description CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5
(CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5)
>gi_2737888 (U59148) nucleolar protein AnCbf5p [Emericella
nidulans]

Seq. No. 301996
Seq. ID cyk700051764.f1
Method BLASTX
NCBI GI g1237250
BLAST score 141
E value 3.0e-09
Match length 36
% identity 64
NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum]

Seq. No. 301997

Seq. ID cyk700051768.f1
Method BLASTX
NCBI GI g4101564
BLAST score 179
E value 2.0e-13
Match length 77
% identity 52
NCBI Description (AF004556) IFA-binding protein [Arabidopsis thaliana]

Seq. No. 301998
Seq. ID cyk700051804.f1
Method BLASTX
NCBI GI g3236261
BLAST score 192
E value 7.0e-15
Match length 63
% identity 60
NCBI Description (AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No. 301999
Seq. ID cyk700051808.f1
Method BLASTN
NCBI GI g3386564
BLAST score 35
E value 2.0e-10
Match length 35
% identity 100
NCBI Description Sorghum bicolor 1-aminocyclopropane-1-carboxylate oxidase (AC01) mRNA, complete cds

Seq. No. 302000
Seq. ID cyk700051834.f1
Method BLASTX
NCBI GI g3559805
BLAST score 295
E value 5.0e-27
Match length 69
% identity 70
NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No. 302001
Seq. ID cyk700051842.f1
Method BLASTX
NCBI GI g1402902
BLAST score 206
E value 1.0e-16
Match length 85
% identity 46
NCBI Description (X98323) peroxidase [Arabidopsis thaliana]
>gi_1419386_emb_CAA67428_ (X98928) peroxidase ATP10a [Arabidopsis thaliana]

Seq. No. 302002
Seq. ID cyk700051849.f1
Method BLASTX

NCBI GI g2980793
BLAST score 280
E value 3.0e-25
Match length 97
% identity 57
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 302003
Seq. ID cyk700051863.f1
Method BLASTN
NCBI GI g3746898
BLAST score 38
E value 4.0e-12
Match length 62
% identity 90
NCBI Description Neurospora crassa clock-controlled gene-6 protein (ccg-6) gene, complete cds

Seq. No. 302004
Seq. ID cyk700051872.f1
Method BLASTX
NCBI GI g3451071
BLAST score 383
E value 3.0e-37
Match length 96
% identity 78
NCBI Description (AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No. 302005
Seq. ID cyk700051885.f1
Method BLASTX
NCBI GI g3420801
BLAST score 324
E value 2.0e-30
Match length 90
% identity 66
NCBI Description (AF081066) IAA-amino acid hydrolase homolog ILL3 [Arabidopsis thaliana]

Seq. No. 302006
Seq. ID cyk700051887.f1
Method BLASTX
NCBI GI g2979544
BLAST score 181
E value 6.0e-24
Match length 82
% identity 68
NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No. 302007
Seq. ID cyk700051888.f1
Method BLASTN
NCBI GI g473602
BLAST score 77
E value 2.0e-35
Match length 173

% identity 86
NCBI Description Zea mays W-22 histone H2A mRNA, complete cds

Seq. No. 302008
Seq. ID cyk700051902.f1
Method BLASTX
NCBI GI g3355480
BLAST score 154
E value 2.0e-10
Match length 88
% identity 35
NCBI Description (AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No. 302009
Seq. ID cyk700051916.f1
Method BLASTX
NCBI GI g730464
BLAST score 196
E value 3.0e-15
Match length 55
% identity 69
NCBI Description 40S RIBOSOMAL PROTEIN RS16 HOMOLOG (RP61R HOMOLOG)
>gi_2119075_pir_S67619 ribosomal protein S16.e.B - yeast
(Saccharomyces cerevisiae) >gi_606441_emb_CAA87357_
(Z47071) putative ribosomal protein [Saccharomyces cerevisiae] >gi_1431106_emb_CAA98649_ (Z74131) ORF YDL083c [Saccharomyces cerevisiae]

Seq. No. 302010
Seq. ID cyk700051948.f1
Method BLASTN
NCBI GI g1617324
BLAST score 37
E value 6.0e-12
Match length 69
% identity 88
NCBI Description H.vulgare mRNA for myb4 transcription factor

Seq. No. 302011
Seq. ID cyk700051969.f1
Method BLASTX
NCBI GI g119136
BLAST score 485
E value 3.0e-49
Match length 99
% identity 92
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
>gi_84946_pir_S01193 translation elongation factor eEF-1 alpha chain (gene F2) - fruit fly (Drosophila melanogaster)
>gi_7917_emb_CAA29994_ (X06870) EF-1-alpha [Drosophila melanogaster]

Seq. No. 302012
Seq. ID cyk700051980.f1
Method BLASTX
NCBI GI g4510361

BLAST score 245
E value 3.0e-21
Match length 77
% identity 65
NCBI Description (AC007017) putative DNA-binding protein RAV2 [Arabidopsis thaliana]

Seq. No. 302013
Seq. ID cyk700052047.f1
Method BLASTX
NCBI GI g4388728
BLAST score 153
E value 3.0e-10
Match length 59
% identity 58
NCBI Description (AC006413) putative grrl-like protein [Arabidopsis thaliana]

Seq. No. 302014
Seq. ID cyk700052061.f1
Method BLASTX
NCBI GI g1617398
BLAST score 163
E value 2.0e-11
Match length 84
% identity 40
NCBI Description (X96737) synaptobrevin-like protein [Mus musculus]

Seq. No. 302015
Seq. ID cyk700052119.f1
Method BLASTN
NCBI GI g726477
BLAST score 46
E value 7.0e-17
Match length 74
% identity 91
NCBI Description Avena fatua nondormancy-associated clone AFN3 putative ORF1 mRNA, partial cds

Seq. No. 302016
Seq. ID cyk700052143.f1
Method BLASTX
NCBI GI g2129754
BLAST score 161
E value 3.0e-11
Match length 33
% identity 91
NCBI Description translation elongation factor Tu precursor - Arabidopsis thaliana >gi_1149571_emb_CAA61511_ (X89227) mitochondrial elongation factor Tu [Arabidopsis thaliana]

Seq. No. 302017
Seq. ID cyk700052148.f1
Method BLASTX
NCBI GI g4454012
BLAST score 156
E value 1.0e-10

Match length 46
% identity 57
NCBI Description (AL035396) Pollen-specific protein precursor like [Arabidopsis thaliana]

Seq. No. 302018
Seq. ID cyk700052158.f1
Method BLASTX
NCBI GI g1002796
BLAST score 228
E value 5.0e-19
Match length 49
% identity 82
NCBI Description (U33915) Cpm10 [Craterostigma plantagineum]

Seq. No. 302019
Seq. ID cyk700052174.f1
Method BLASTX
NCBI GI g543752
BLAST score 153
E value 2.0e-16
Match length 72
% identity 68
NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) (ETHYLENE-FORMING ENZYME) (EFE) >gi_281612_pir_JQ1656 ethylene-forming enzyme - Pseudomonas syringae pv. phaseolicola plasmid pPSP1 >gi_216878_dbj_BAA02477 (D13182) 'Ethylene-forming enzyme' [Pseudomonas syringae] >gi_4323597_gb_AAD16440_ (AF101058) ethylene-forming enzyme [Pseudomonas syringae pv. phaseolicola]

Seq. No. 302020
Seq. ID cyk700052213.f1
Method BLASTX
NCBI GI g1346735
BLAST score 273
E value 3.0e-24
Match length 73
% identity 67
NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_1076562_pir_S49647 phosphoglycerate mutase (EC 5.4.2.1) - castor bean >gi_474170_emb_CAA49995_ (X70652) phosphoglycerate mutase [Ricinus communis]

Seq. No. 302021
Seq. ID cyk700052230.f1
Method BLASTX
NCBI GI g399334
BLAST score 199
E value 5.0e-16
Match length 51
% identity 84
NCBI Description CYSTATIN I PRECURSOR (CORN KERNEL CYSTEINE PROTEINASE INHIBITOR) >gi_322868_pir_S27239 cysteine proteinase inhibitor - maize >gi_217962_dbj_BAA01472_ (D10622) corn cystatin I [Zea mays]

Seq. No. 302022
Seq. ID cyk700052253.f1
Method BLASTX
NCBI GI g2245039
BLAST score 146
E value 2.0e-09
Match length 59
% identity 42
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302023
Seq. ID cyk700052335.f1
Method BLASTX
NCBI GI g4104939
BLAST score 206
E value 2.0e-16
Match length 98
% identity 41
NCBI Description (AF042382) vetispiradiene synthase [Solanum tuberosum]

Seq. No. 302024
Seq. ID cyk700052342.f1
Method BLASTX
NCBI GI g2809250
BLAST score 336
E value 9.0e-32
Match length 92
% identity 67
NCBI Description (AC002560) F21B7.19 [Arabidopsis thaliana]

Seq. No. 302025
Seq. ID cyk700052364.f1
Method BLASTX
NCBI GI g4558828
BLAST score 173
E value 1.0e-12
Match length 76
% identity 45
NCBI Description (AF076692) aureobasidin-resistance protein; Aurl homolog; Aurl [Aspergillus fumigatus]

Seq. No. 302026
Seq. ID cyk700052387.f1
Method BLASTN
NCBI GI g6598431
BLAST score 36
E value 7.0e-11
Match length 68
% identity 88
NCBI Description Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 302027
Seq. ID cyk700052459.f1
Method BLASTX
NCBI GI g4321762

BLAST score 258
E value 5.0e-24
Match length 68
% identity 85
NCBI Description (AF061107) transcription factor MYC7E [Zea mays]

Seq. No. 302028
Seq. ID cyk700052470.f1
Method BLASTX
NCBI GI g1546692
BLAST score 149
E value 3.0e-14
Match length 77
% identity 57
NCBI Description (X98805) peroxidase ATP19a [Arabidopsis thaliana]

Seq. No. 302029
Seq. ID cyk700052476.f1
Method BLASTX
NCBI GI g2493935
BLAST score 249
E value 2.0e-21
Match length 92
% identity 47
NCBI Description CYTOCHROME B >gi_542522_pir_S40619 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - migratory locust mitochondrion (SGC4) >gi_1182025_emb_CAA56537_ (X80245) Cytochrome B [Locusta migratoria]

Seq. No. 302030
Seq. ID cyk700052483.f1
Method BLASTX
NCBI GI g2943792
BLAST score 330
E value 5.0e-31
Match length 98
% identity 56
NCBI Description (AB006809) PV72 [Cucurbita sp.]

Seq. No. 302031
Seq. ID cyk700052490.f1
Method BLASTX
NCBI GI g100347
BLAST score 170
E value 3.0e-12
Match length 47
% identity 70
NCBI Description monosaccharide transport protein MST1 - common tobacco >gi_19885_emb_CAA47324_ (X66856) monosaccharide transporter [Nicotiana tabacum]

Seq. No. 302032
Seq. ID dhd700197930.h1
Method BLASTX
NCBI GI g2505874
BLAST score 197
E value 2.0e-21

Match length 68
% identity 75
NCBI Description (Y12776) putative kinase [Arabidopsis thaliana]

Seq. No. 302033
Seq. ID dhd700197969.h1
Method BLASTX
NCBI GI g633110
BLAST score 162
E value 1.0e-11
Match length 38
% identity 87
NCBI Description (D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No. 302034
Seq. ID dhd700197995.h1
Method BLASTX
NCBI GI g3135543
BLAST score 233
E value 6.0e-20
Match length 49
% identity 90
NCBI Description (AF062393) aquaporin [Oryza sativa]

Seq. No. 302035
Seq. ID dhd700198003.h1
Method BLASTX
NCBI GI g2492519
BLAST score 263
E value 1.0e-25
Match length 63
% identity 95
NCBI Description 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_(D86121) 26S proteasome ATPase subunit [Spinacia oleracea]

Seq. No. 302036
Seq. ID dhd700198020.h1
Method BLASTN
NCBI GI g1498052
BLAST score 156
E value 1.0e-82
Match length 189
% identity 95
NCBI Description Zea mays ribosomal protein S8 mRNA, complete cds

Seq. No. 302037
Seq. ID dhd700198040.h1
Method BLASTX
NCBI GI g1491931
BLAST score 245
E value 2.0e-21
Match length 57
% identity 88
NCBI Description (U52078) kinesin-like protein [Nicotiana tabacum]

Seq. No. 302038

Seq. ID dhd700198046.h1
Method BLASTN
NCBI GI g3885891
BLAST score 42
E value 1.0e-14
Match length 54
% identity 94
NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
mRNA, complete cds

Seq. No. 302039
Seq. ID dyk700102007.h1
Method BLASTX
NCBI GI g4514635
BLAST score 191
E value 1.0e-14
Match length 47
% identity 74
NCBI Description (AB021175) root cap protein 1 [Zea mays]

Seq. No. 302040
Seq. ID dyk700102021.h1
Method BLASTX
NCBI GI g3913517
BLAST score 225
E value 1.0e-18
Match length 51
% identity 86
NCBI Description 3' (2'),5'-BISPHOSPHATE NUCLEOTIDASE
(3' (2'),5-BISPHOSPHONUCLEOSIDE 3' (2')-PHOSPHOHYDROLASE)
(DPNPASE) >gi_1109672 (U33283) 3' (2'),5-diphosphonucleoside
3' (2') phosphohydrolase [Oryza sativa]
>gi_1586671_prf_2204308A diphosphonucleoside
phosphohydrolase [Oryza sativa]

Seq. No. 302041
Seq. ID dyk700102055.h1
Method BLASTX
NCBI GI g2150000
BLAST score 322
E value 5.0e-30
Match length 89
% identity 62
NCBI Description (AF000939) aleurone ribonuclease [Hordeum vulgare]

Seq. No. 302042
Seq. ID dyk700102086.h1
Method BLASTX
NCBI GI g4530126
BLAST score 264
E value 3.0e-23
Match length 96
% identity 50
NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1
[Phaseolus vulgaris]

Seq. No. 302043

Seq. ID dyk700102137.h1
Method BLASTX
NCBI GI g549063
BLAST score 158
E value 8.0e-11
Match length 35
% identity 83
NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
>gi_1072464_pir_A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
21kd polypeptide [Oryza sativa]

Seq. No. 302044
Seq. ID dyk700102167.h1
Method BLASTN
NCBI GI g2668741
BLAST score 136
E value 1.0e-70
Match length 148
% identity 98
NCBI Description Zea mays glycine-rich RNA binding protein (GRP) mRNA,
complete cds

Seq. No. 302045
Seq. ID dyk700102170.h1
Method BLASTX
NCBI GI g1091678
BLAST score 193
E value 8.0e-15
Match length 80
% identity 42
NCBI Description activator-like transposable element [Pennisetum glaucum]

Seq. No. 302046
Seq. ID dyk700102178.h1
Method BLASTX
NCBI GI g112994
BLAST score 319
E value 1.0e-29
Match length 71
% identity 87
NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
>gi_82685_pir_S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
ABA-inducible gene protein [Zea mays]
>gi_226091_prf_1410284A abscisic acid inducible gene [Zea
mays]

Seq. No. 302047
Seq. ID dyk700102188.h1
Method BLASTX
NCBI GI g4218535
BLAST score 233
E value 1.0e-19
Match length 49
% identity 90
NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]

Seq. No. 302048
Seq. ID dyk700102210.h1
Method BLASTX
NCBI GI g729775
BLAST score 359
E value 2.0e-34
Match length 73
% identity 86
NCBI Description HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR)
>gi_100264_pir_S25481 heat shock transcription factor 8 -
Peruvian tomato >gi_19492_emb_CAA47869_ (X67600) heat shock transcription factor 8 [Lycopersicon peruvianum]

Seq. No. 302049
Seq. ID dyk700102227.h1
Method BLASTX
NCBI GI g3309066
BLAST score 406
E value 5.0e-40
Match length 78
% identity 94
NCBI Description (AF073488) bifunctional dihydrofolate reductase-thymidylate synthase [Zea mays]

Seq. No. 302050
Seq. ID dyk700102231.h1
Method BLASTX
NCBI GI g3953479
BLAST score 414
E value 7.0e-41
Match length 98
% identity 81
NCBI Description (AC002328) F22O2.24 [Arabidopsis thaliana]

Seq. No. 302051
Seq. ID dyk700102233.h1
Method BLASTX
NCBI GI g2995321
BLAST score 325
E value 1.0e-30
Match length 93
% identity 72
NCBI Description (Z68759) amino acid carrier [Ricinus communis]

Seq. No. 302052
Seq. ID dyk700102243.h1
Method BLASTN
NCBI GI g433039
BLAST score 34
E value 1.0e-09
Match length 34
% identity 100
NCBI Description Zea mays W-22 clone PREM-1 retroelement PREM-1, partial sequence

Seq. No. 302053
Seq. ID dyk700102313.h1
Method BLASTX
NCBI GI g112697
BLAST score 204
E value 3.0e-16
Match length 48
% identity 79
NCBI Description 14 KD PROLINE-RICH PROTEIN DC2.15 PRECURSOR
>gi_486809_pir_S35714 proline-rich protein, 14K, embryonic
- carrot >gi_18316_emb_CAA33476_ (X15436) 14 kD protein (AA
1-137) [Daucus carota]

Seq. No. 302054
Seq. ID dyk700102330.h1
Method BLASTN
NCBI GI g4115614
BLAST score 192
E value 1.0e-104
Match length 304
% identity 91
NCBI Description Zea mays mRNA for root cap-specific glycine-rich protein,
complete cds

Seq. No. 302055
Seq. ID dyk700102332.h1
Method BLASTX
NCBI GI g1402910
BLAST score 210
E value 6.0e-17
Match length 61
% identity 59
NCBI Description (X98316) peroxidase [Arabidopsis thaliana]
>gi_1429223_emb_CAA67550_ (X99096) peroxidase [Arabidopsis
thaliana]

Seq. No. 302056
Seq. ID dyk700102348.h1
Method BLASTX
NCBI GI g4371279
BLAST score 329
E value 6.0e-31
Match length 102
% identity 61
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302057
Seq. ID dyk700102404.h1
Method BLASTX
NCBI GI g3334661
BLAST score 222
E value 2.0e-18
Match length 96
% identity 46
NCBI Description (Y10490) putative cytochrome P450 [Glycine max]

Seq. No. 302058

Seq. ID dyk700102406.h1
Method BLASTX
NCBI GI g1353193
BLAST score 315
E value 3.0e-29
Match length 91
% identity 62
NCBI Description O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir_JQ2268
O-methyltransferase (EC 2.1.1.-) - maize >gi_404070
(L14063) O-methyltransferase [Zea mays]

Seq. No. 302059
Seq. ID dyk700102415.h1
Method BLASTX
NCBI GI g2832661
BLAST score 383
E value 4.0e-37
Match length 106
% identity 78
NCBI Description (AL021710) pherophorin - like protein [Arabidopsis thaliana]

Seq. No. 302060
Seq. ID dyk700102428.h1
Method BLASTX
NCBI GI g4539301
BLAST score 343
E value 2.0e-32
Match length 99
% identity 61
NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No. 302061
Seq. ID dyk700102481.h1
Method BLASTX
NCBI GI g2914700
BLAST score 251
E value 1.0e-21
Match length 68
% identity 79
NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No. 302062
Seq. ID dyk700102511.h1
Method BLASTX
NCBI GI g1170937
BLAST score 357
E value 3.0e-34
Match length 75
% identity 91
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No. 302063
Seq. ID dyk700102549.h1
Method BLASTN
NCBI GI g393183
BLAST score 96
E value 5.0e-47
Match length 100
% identity 99
NCBI Description Zea mays alcohol dehydrogenase (tasselseed 2) mRNA,
complete cds

Seq. No. 302064
Seq. ID dyk700102582.h1
Method BLASTN
NCBI GI g3821780
BLAST score 38
E value 3.0e-12
Match length 38
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 302065
Seq. ID dyk700102621.h1
Method BLASTX
NCBI GI g3510249
BLAST score 312
E value 7.0e-29
Match length 73
% identity 68
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Seq. No. 302066
Seq. ID dyk700102668.h1
Method BLASTX
NCBI GI g2673914
BLAST score 224
E value 2.0e-18
Match length 105
% identity 43
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302067
Seq. ID dyk700102670.h1
Method BLASTN
NCBI GI g2668739
BLAST score 175
E value 8.0e-94
Match length 233
% identity 94
NCBI Description Zea mays translation initiation factor GOS2 (TIF) mRNA,
complete cds

Seq. No. 302068
Seq. ID dyk700102703.h1
Method BLASTN
NCBI GI g6598558
BLAST score 36

E value 7.0e-11
Match length 68
% identity 88
NCBI Description Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 302069
Seq. ID dyk700102725.h1
Method BLASTX
NCBI GI g3482921
BLAST score 219
E value 5.0e-18
Match length 80
% identity 55
NCBI Description (AC003970) Unknown protein [Arabidopsis thaliana]

Seq. No. 302070
Seq. ID dyk700102734.h1
Method BLASTX
NCBI GI g4530126
BLAST score 223
E value 1.0e-18
Match length 75
% identity 60
NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No. 302071
Seq. ID dyk700102740.h1
Method BLASTX
NCBI GI g3355465
BLAST score 350
E value 2.0e-33
Match length 95
% identity 65
NCBI Description (AC004218) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 302072
Seq. ID dyk700102743.h1
Method BLASTX
NCBI GI g1754997
BLAST score 325
E value 2.0e-30
Match length 80
% identity 85
NCBI Description (U48690) calmodulin TaCaM2-1 [Triticum aestivum]

Seq. No. 302073
Seq. ID dyk700102751.h1
Method BLASTN
NCBI GI g2224845
BLAST score 38
E value 5.0e-12
Match length 50
% identity 94
NCBI Description Zea mays mRNA for anionic peroxidase

Seq. No. 302074
Seq. ID dyk700102753.h1
Method BLASTX
NCBI GI g2129733
BLAST score 231
E value 5.0e-21
Match length 75
% identity 72
NCBI Description serine O-acetyltransferase (EC 2.3.1.30) SAT1 precursor - Arabidopsis thaliana >gi_1184048 (U22964) serine acetyltransferase [Arabidopsis thaliana]

Seq. No. 302075
Seq. ID dyk700102796.h1
Method BLASTX
NCBI GI g2809246
BLAST score 222
E value 2.0e-18
Match length 68
% identity 60
NCBI Description (AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No. 302076
Seq. ID dyk700102802.h1
Method BLASTX
NCBI GI g2160167
BLAST score 267
E value 2.0e-37
Match length 102
% identity 81
NCBI Description (AC000132) Identical to A. thaliana Myb-like protein (gb_D58424). [Arabidopsis thaliana]

Seq. No. 302077
Seq. ID dyk700102820.h1
Method BLASTX
NCBI GI g1181331
BLAST score 223
E value 2.0e-18
Match length 74
% identity 59
NCBI Description (X77569) calnexin [Zea mays]

Seq. No. 302078
Seq. ID dyk700102828.h1
Method BLASTX
NCBI GI g4220514
BLAST score 391
E value 3.0e-38
Match length 92
% identity 79
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 302079
Seq. ID dyk700102876.h1
Method BLASTX

NCBI GI g4510376
BLAST score 233
E value 1.0e-19
Match length 81
% identity 56
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 302080
Seq. ID dyk700102915.h1
Method BLASTX
NCBI GI g417828
BLAST score 205
E value 2.0e-16
Match length 69
% identity 62
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 >gi_320775_pir_S31245 translation initiation factor eIF-2A - yeast (Saccharomyces cerevisiae) >gi_172787 (M77514) SUI1 protein [Saccharomyces cerevisiae] >gi_1255973_emb_CAA65499_ (X96722) ORF N0905 [Saccharomyces cerevisiae] >gi_1302282_emb_CAA96150_ (Z71520) ORF YNL244c [Saccharomyces cerevisiae]

Seq. No. 302081
Seq. ID dyk700102919.h1
Method BLASTN
NCBI GI g557681
BLAST score 59
E value 1.0e-24
Match length 63
% identity 98
NCBI Description Z.mays mRNA for ribosomal protein S28

Seq. No. 302082
Seq. ID dyk700102931.h1
Method BLASTX
NCBI GI g3043415
BLAST score 365
E value 4.0e-35
Match length 70
% identity 99
NCBI Description (Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No. 302083
Seq. ID dyk700102947.h1
Method BLASTX
NCBI GI g4376203
BLAST score 251
E value 9.0e-22
Match length 79
% identity 59
NCBI Description (U35226) putative cytochrome P-450 [Nicotiana plumbaginifolia]

Seq. No. 302084
Seq. ID dyk700103083.h1
Method BLASTX
NCBI GI g3024500

BLAST score 310
E value 1.0e-28
Match length 68
% identity 90
NCBI Description RAS-RELATED PROTEIN RAB11A >gi_1370142_emb_CAA98177_(Z73949) RAB11A [Lotus japonicus]

Seq. No. 302085
Seq. ID dyk700103093.h1
Method BLASTX
NCBI GI g4584345
BLAST score 380
E value 8.0e-37
Match length 102
% identity 70
NCBI Description (AC007127) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 302086
Seq. ID dyk700103094.h1
Method BLASTX
NCBI GI g4467097
BLAST score 368
E value 2.0e-35
Match length 82
% identity 89
NCBI Description (AL035538) heat shock protein 70 like protein [Arabidopsis thaliana]

Seq. No. 302087
Seq. ID dyk700103104.h1
Method BLASTX
NCBI GI g3695019
BLAST score 303
E value 8.0e-28
Match length 89
% identity 62
NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 302088
Seq. ID dyk700103145.h1
Method BLASTX
NCBI GI g122007
BLAST score 160
E value 4.0e-11
Match length 34
% identity 94
NCBI Description HISTONE H2A >gi_100161_pir_S11498 histone H2A - parsley >gi_20448_emb_CAA37828_(X53831) H2A histone protein (AA 1 - 149) [Petroselinum crispum]

Seq. No. 302089
Seq. ID dyk700103188.h1
Method BLASTX
NCBI GI g3954807
BLAST score 312
E value 7.0e-29

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Match length 90
% identity 60
NCBI Description (AJ011862) flavonoid 3',5'-hydroxylase [Catharanthus roseus]

Seq. No. 302090
Seq. ID dyk700103236.h1
Method BLASTX
NCBI GI g2246442
BLAST score 224
E value 1.0e-18
Match length 93
% identity 44
NCBI Description (U63298) farnesyltransferase alpha subunit [Pisum sativum]

Seq. No. 302091
Seq. ID dyk700103257.h1
Method BLASTX
NCBI GI g3355308
BLAST score 236
E value 5.0e-20
Match length 91
% identity 54
NCBI Description (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]

Seq. No. 302092
Seq. ID dyk700103272.h1
Method BLASTX
NCBI GI g2459445
BLAST score 145
E value 3.0e-09
Match length 60
% identity 53
NCBI Description (AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No. 302093
Seq. ID dyk700103316.h1
Method BLASTX
NCBI GI g2213594
BLAST score 211
E value 5.0e-17
Match length 53
% identity 70
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No. 302094
Seq. ID dyk700103336.h1
Method BLASTX
NCBI GI g2384675
BLAST score 236
E value 2.0e-20
Match length 82
% identity 72
NCBI Description (AF012659) putative potassium transporter AtKT4p [Arabidopsis thaliana]

Seq. No. 302095
Seq. ID dyk700103353.h1
Method BLASTN
NCBI GI g498743
BLAST score 55
E value 3.0e-22
Match length 245
% identity 46
NCBI Description O.sativa (var. IR36) PIR7a and PIR7b genes

Seq. No. 302096
Seq. ID dyk700103368.h1
Method BLASTX
NCBI GI g4581164
BLAST score 183
E value 1.0e-16
Match length 87
% identity 55
NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No. 302097
Seq. ID dyk700103394.h1
Method BLASTX
NCBI GI g2851508
BLAST score 245
E value 4.0e-21
Match length 64
% identity 69
NCBI Description 60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs
gb_AA395597, gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No. 302098
Seq. ID dyk700103406.h1
Method BLASTX
NCBI GI g2244994
BLAST score 246
E value 2.0e-21
Match length 63
% identity 76
NCBI Description (Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]

Seq. No. 302099
Seq. ID dyk700103414.h1
Method BLASTX
NCBI GI g100907
BLAST score 146
E value 2.0e-09
Match length 34
% identity 74
NCBI Description pathogenesis-related protein 1 - maize
>gi_228409_prf_1803521A pathogenesis-related protein 1 [Zea mays]

Seq. No. 302100
Seq. ID dyk700103442.h1
Method BLASTX
NCBI GI g2058311
BLAST score 144
E value 3.0e-09
Match length 42
% identity 62
NCBI Description (X79566) cinnamoyl-CoA reductase [Eucalyptus gunnii]

Seq. No. 302101
Seq. ID dyk700103478.h1
Method BLASTX
NCBI GI g3152559
BLAST score 256
E value 2.0e-22
Match length 54
% identity 80
NCBI Description (AC002986) Similarity to A. thaliana gene product F21M12.20, gb_AC000132. EST gb_Z25651 comes from this gene. [Arabidopsis thaliana]

Seq. No. 302102
Seq. ID dyk700103532.h1
Method BLASTX
NCBI GI g2286153
BLAST score 193
E value 3.0e-17
Match length 56
% identity 93
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 302103
Seq. ID dyk700103575.h1
Method BLASTX
NCBI GI g2501572
BLAST score 189
E value 1.0e-14
Match length 79
% identity 41
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545 (L47118) EMB8 gene product [Picea glauca]

Seq. No. 302104
Seq. ID dyk700103584.h1
Method BLASTX
NCBI GI g1170937
BLAST score 222
E value 2.0e-18
Match length 70
% identity 99
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481 (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No. 302105

Seq. ID dyk700103589.h1
Method BLASTX
NCBI GI g1778145
BLAST score 299
E value 2.0e-27
Match length 82
% identity 72
NCBI Description (U66402) phosphate/phosphoenolpyruvate translocator precursor [Nicotiana tabacum]

Seq. No. 302106
Seq. ID dyk700103632.h1
Method BLASTX
NCBI GI g1172836
BLAST score 378
E value 1.0e-36
Match length 71
% identity 97
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787)
small ras-related protein [Nicotiana tabacum]

Seq. No. 302107
Seq. ID dyk700103715.h1
Method BLASTN
NCBI GI g3420038
BLAST score 35
E value 3.0e-10
Match length 51
% identity 92
NCBI Description Zea mays gypsy/Ty3-type retrotransposon Tekay, complete sequence

Seq. No. 302108
Seq. ID dyk700103723.h1
Method BLASTX
NCBI GI g2827711
BLAST score 490
E value 9.0e-50
Match length 100
% identity 91
NCBI Description (AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No. 302109
Seq. ID dyk700103724.h1
Method BLASTX
NCBI GI g2244749
BLAST score 155
E value 9.0e-11
Match length 78
% identity 48
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 302110
Seq. ID dyk700103735.h1
Method BLASTX
NCBI GI g2827143

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BLAST score 250
E value 1.0e-21
Match length 74
% identity 62
NCBI Description (AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No. 302111
Seq. ID dyk700103772.h1
Method BLASTX
NCBI GI g1657382
BLAST score 390
E value 4.0e-38
Match length 87
% identity 85
NCBI Description (Y09101) cholinephosphate cytidylyltransferase [Pisum sativum]

Seq. No. 302112
Seq. ID dyk700103776.h1
Method BLASTX
NCBI GI g1362406
BLAST score 208
E value 8.0e-17
Match length 85
% identity 54
NCBI Description probable membrane protein YPR011c - yeast (Saccharomyces cerevisiae) >gi_887588_emb_CAA90155_ (Z49919) unknown [Saccharomyces cerevisiae] >gi_939745_ (U31900) Lpz11p [Saccharomyces cerevisiae] >gi_1314086_emb_CAA95008_ (Z71255) unknown [Saccharomyces cerevisiae]

Seq. No. 302113
Seq. ID dyk700103815.h1
Method BLASTX
NCBI GI g3643611
BLAST score 199
E value 1.0e-15
Match length 58
% identity 60
NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No. 302114
Seq. ID dyk700103851.h1
Method BLASTX
NCBI GI g4508073
BLAST score 173
E value 1.0e-12
Match length 101
% identity 39
NCBI Description (AC005882) 43220 [Arabidopsis thaliana]

Seq. No. 302115
Seq. ID dyk700103861.h1
Method BLASTX
NCBI GI g3876615
BLAST score 229

E value 3.0e-19
Match length 93
% identity 49
NCBI Description (Z74031) Similarity to Yeast D-lactate dehydrogenase
(SW:DLD1_YEAST); cDNA EST EMBL:C12235 comes from this gene;
cDNA EST EMBL:C12916 comes from this gene; cDNA EST
EMBL:C10532 comes from this gene; cDNA EST EMBL:C10979
comes f

Seq. No. 302116
Seq. ID dyk700103877.h1
Method BLASTX
NCBI GI g1706260
BLAST score 362
E value 8.0e-35
Match length 90
% identity 79
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
cysteine proteinase 1 precursor - maize
>gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
mays]

Seq. No. 302117
Seq. ID dyk700103896.h1
Method BLASTX
NCBI GI g1330254
BLAST score 388
E value 7.0e-38
Match length 75
% identity 99
NCBI Description (D85039) calcium-dependent protein kinase [Zea mays]

Seq. No. 302118
Seq. ID dyk700103906.h1
Method BLASTN
NCBI GI g22430
BLAST score 71
E value 8.0e-32
Match length 134
% identity 89
NCBI Description Maize pseudo-Gpa2 pseudogene for glyceraldehyde-3-phosphate
dehydrogenase subunit A

Seq. No. 302119
Seq. ID dyk700103908.h1
Method BLASTN
NCBI GI g4160401
BLAST score 157
E value 4.0e-83
Match length 172
% identity 98
NCBI Description Zea mays eIF-5 gene, exons 1-2

Seq. No. 302120
Seq. ID dyk700103946.h1
Method BLASTX
NCBI GI g4008008

BLAST score 149
E value 7.0e-10
Match length 57
% identity 51
NCBI Description (AF084035) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No. 302121
Seq. ID dyk700103956.h1
Method BLASTX
NCBI GI g399854
BLAST score 161
E value 4.0e-11
Match length 57
% identity 63
NCBI Description HISTONE H2B.2 >gi_283042_pir_S28049 histone H2B - maize >gi_22325_emb_CAA40565_ (X57313) H2B histone [Zea mays]

Seq. No. 302122
Seq. ID dyk700103983.h1
Method BLASTX
NCBI GI g3882355
BLAST score 143
E value 5.0e-18
Match length 60
% identity 80
NCBI Description (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis thaliana]

Seq. No. 302123
Seq. ID dyk700103988.h1
Method BLASTX
NCBI GI g4371296
BLAST score 389
E value 7.0e-38
Match length 100
% identity 75
NCBI Description (AC006260) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 302124
Seq. ID dyk700103989.h1
Method BLASTX
NCBI GI g1279206
BLAST score 310
E value 1.0e-28
Match length 64
% identity 98
NCBI Description (X97446) alpha-tubulin [Avena sativa]

Seq. No. 302125
Seq. ID dyk700103991.h1
Method BLASTX
NCBI GI g2160156
BLAST score 364
E value 5.0e-35
Match length 104

% identity 71
NCBI Description (AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb_Z73100). [Arabidopsis thaliana]

Seq. No. 302126
Seq. ID dyk700104013.h1
Method BLASTX
NCBI GI g4508073
BLAST score 201
E value 6.0e-16
Match length 97
% identity 36
NCBI Description (AC005882) 43220 [Arabidopsis thaliana]

Seq. No. 302127
Seq. ID dyk700104071.h1
Method BLASTX
NCBI GI g1172836
BLAST score 432
E value 6.0e-43
Match length 81
% identity 98
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787)
small ras-related protein [Nicotiana tabacum]

Seq. No. 302128
Seq. ID dyk700104115.h1
Method BLASTX
NCBI GI g4204697
BLAST score 238
E value 5.0e-21
Match length 93
% identity 55
NCBI Description (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]

Seq. No. 302129
Seq. ID dyk700104327.h1
Method BLASTX
NCBI GI g1705585
BLAST score 359
E value 2.0e-34
Match length 82
% identity 85
NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE 2 (PEPCASE)
>gi_82710_pir_JH0667 phosphoenolpyruvate carboxylase (EC
4.1.1.31) C3-form - maize >gi_429149_emb_CAA43709_ (X61489)
phosphoenolpyruvate carboxylase [Zea mays]

Seq. No. 302130
Seq. ID dyk700104345.h1
Method BLASTX
NCBI GI g2738996
BLAST score 198
E value 2.0e-17
Match length 86
% identity 52

NCBI Description (AF022457) CYP97B2p [Glycine max]

Seq. No. 302131
Seq. ID dyk700104350.h1
Method BLASTX
NCBI GI g1706260
BLAST score 253
E value 4.0e-41
Match length 100
% identity 98
NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir_S59597
cysteine proteinase 1 precursor - maize
>gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays]

Seq. No. 302132
Seq. ID dyk700104373.h1
Method BLASTX
NCBI GI g122106
BLAST score 203
E value 9.0e-28
Match length 69
% identity 85
NCBI Description HISTONE H4 >gi_70771_pir_HSZM4 histone H4 - maize
>gi_81642_pir_S06904 histone H4 - Arabidopsis thaliana
>gi_2119028_pir_S60475 histone H4 - garden pea
>gi_21795_emb_CAA24924 (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]
>gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata]
>gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
>gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_225838_prf_1314298A histone H4 [Arabidopsis thaliana]

Seq. No. 302133
Seq. ID dyk700104442.h1
Method BLASTX
NCBI GI g2459446
BLAST score 234
E value 8.0e-20
Match length 89
% identity 52
NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No. 302134
Seq. ID dyk700104452.h1
Method BLASTX
NCBI GI g2894598
BLAST score 220
E value 4.0e-18
Match length 99

% identity 42
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 302135
Seq. ID dyk700104502.h1
Method BLASTN
NCBI GI g397395
BLAST score 193
E value 1.0e-104
Match length 193
% identity 100
NCBI Description Z.mays MNB1b mRNA for DNA-binding protein

Seq. No. 302136
Seq. ID dyk700104509.h1
Method BLASTX
NCBI GI g3386600
BLAST score 453
E value 2.0e-45
Match length 102
% identity 83
NCBI Description (AC004665) putative glycoprotein [Arabidopsis thaliana]

Seq. No. 302137
Seq. ID dyk700104522.h1
Method BLASTN
NCBI GI g2226328
BLAST score 49
E value 1.0e-18
Match length 61
% identity 95
NCBI Description Zea mays physical impedance induced protein (IIG1) mRNA, complete cds

Seq. No. 302138
Seq. ID dyk700104649.h1
Method BLASTX
NCBI GI g2924777
BLAST score 217
E value 2.0e-24
Match length 104
% identity 10
NCBI Description (AC002334) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 302139
Seq. ID dyk700104657.h1
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 302140
Seq. ID dyk700104663.h1

Method BLASTX
NCBI GI g584706
BLAST score 354
E value 3.0e-37
Match length 86
% identity 80
NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
>gi_2130066_pir_JC5124 aspartate transaminase (EC
2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_
(D14673) aspartate aminotransferase [Oryza sativa]

Seq. No. 302141
Seq. ID dyk700104711.h1
Method BLASTX
NCBI GI g3618220
BLAST score 298
E value 3.0e-27
Match length 68
% identity 81
NCBI Description (AL031579) chorismate synthase [Schizosaccharomyces pombe]

Seq. No. 302142
Seq. ID dyk700104721.h1
Method BLASTN
NCBI GI g312178
BLAST score 60
E value 4.0e-25
Match length 92
% identity 91
NCBI Description Z.mays GapC2 gene

Seq. No. 302143
Seq. ID dyk700104764.h1
Method BLASTN
NCBI GI g786131
BLAST score 78
E value 7.0e-36
Match length 137
% identity 90
NCBI Description Oryza sativa root-specific RCc3 mRNA, complete cds

Seq. No. 302144
Seq. ID dyk700104785.h1
Method BLASTX
NCBI GI g2578033
BLAST score 204
E value 3.0e-16
Match length 77
% identity 51
NCBI Description (X97016) omega-6 desaturase [Gossypium hirsutum]

Seq. No. 302145
Seq. ID dyk700104812.h1
Method BLASTX
NCBI GI g1076289
BLAST score 247
E value 6.0e-24

Match length 88
% identity 62
NCBI Description amino acid permease AAP5 - Arabidopsis thaliana
>gi_608673_emb_CAA54632_ (X77501) amino acid permease
[Arabidopsis thaliana]

Seq. No. 302146
Seq. ID dyk700104829.h1
Method BLASTX
NCBI GI g4490306
BLAST score 201
E value 7.0e-16
Match length 102
% identity 48
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 302147
Seq. ID dyk700104836.h1
Method BLASTX
NCBI GI g4063750
BLAST score 175
E value 1.0e-12
Match length 46
% identity 63
NCBI Description (AC005851) putative indole-3-acetate
beta-glucosyltransferase synthetase [Arabidopsis thaliana]

Seq. No. 302148
Seq. ID dyk700104903.h1
Method BLASTX
NCBI GI g2570505
BLAST score 430
E value 1.0e-42
Match length 95
% identity 92
NCBI Description (AF022735) proteasome component [Oryza sativa]

Seq. No. 302149
Seq. ID dyk700104937.h1
Method BLASTX
NCBI GI g4468813
BLAST score 145
E value 2.0e-09
Match length 51
% identity 53
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 302150
Seq. ID dyk700104942.h1
Method BLASTN
NCBI GI g1063665
BLAST score 189
E value 1.0e-102
Match length 239
% identity 95
NCBI Description Zea mays unknown protein mRNA, complete cds

Seq. No. 302151
Seq. ID dyk700104960.h1
Method BLASTN
NCBI GI g2331140
BLAST score 33
E value 5.0e-09
Match length 45
% identity 93
NCBI Description Oryza sativa water-stress inducible protein (WSI) mRNA, complete cds

Seq. No. 302152
Seq. ID dyk700104967.h1
Method BLASTX
NCBI GI g4559358
BLAST score 199
E value 1.0e-15
Match length 50
% identity 70
NCBI Description (AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No. 302153
Seq. ID dyk700104982.h1
Method BLASTX
NCBI GI g4263777
BLAST score 469
E value 3.0e-47
Match length 113
% identity 73
NCBI Description (AC006068) putative serine carboxypeptidase II [Arabidopsis thaliana] >gi_4510391_gb_AAD21479.1 (AC007017) putative serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No. 302154
Seq. ID dyk700105046.h1
Method BLASTX
NCBI GI g4558591
BLAST score 230
E value 3.0e-19
Match length 70
% identity 60
NCBI Description (AC006555) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No. 302155
Seq. ID dyk700105060.h1
Method BLASTX
NCBI GI g2062169
BLAST score 188
E value 2.0e-22
Match length 75
% identity 68
NCBI Description (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No. 302156

Seq. ID dyk700105068.h1
Method BLASTX
NCBI GI g2388571
BLAST score 219
E value 5.0e-18
Match length 87
% identity 54
NCBI Description (AC000098) Strong similarity to Arabidopsis peroxidase ATPEROX7A (gb_X98321). [Arabidopsis thaliana] >gi_2738254 (U97684) peroxidase precursor [Arabidopsis thaliana]

Seq. No. 302157
Seq. ID dyk700105088.h1
Method BLASTX
NCBI GI g2827548
BLAST score 183
E value 9.0e-14
Match length 101
% identity 40
NCBI Description (AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No. 302158
Seq. ID dyk700105089.h1
Method BLASTX
NCBI GI g3810596
BLAST score 234
E value 9.0e-20
Match length 63
% identity 68
NCBI Description (AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq. No. 302159
Seq. ID dyk700105135.h1
Method BLASTX
NCBI GI g2464915
BLAST score 266
E value 1.0e-23
Match length 87
% identity 68
NCBI Description (Z99708) transcription initiation factor like protein [Arabidopsis thaliana]

Seq. No. 302160
Seq. ID dyk700105142.h1
Method BLASTX
NCBI GI g4519671
BLAST score 178
E value 3.0e-13
Match length 63
% identity 56
NCBI Description (AB017693) transfactor [Nicotiana tabacum]

Seq. No. 302161
Seq. ID dyk700105144.h1
Method BLASTX

NCBI GI g3297818
BLAST score 196
E value 2.0e-15
Match length 67
% identity 57
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 302162
Seq. ID dyk700105172.h1
Method BLASTX
NCBI GI g2618731
BLAST score 344
E value 9.0e-33
Match length 89
% identity 71
NCBI Description (U49077) IAA21 [Arabidopsis thaliana]

Seq. No. 302163
Seq. ID dyk700105185.h1
Method BLASTX
NCBI GI g3757521
BLAST score 200
E value 7.0e-16
Match length 69
% identity 52
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 302164
Seq. ID dyk700105243.h1
Method BLASTX
NCBI GI g4454026
BLAST score 147
E value 1.0e-09
Match length 42
% identity 64
NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No. 302165
Seq. ID dyk700105250.h1
Method BLASTX
NCBI GI g3434986
BLAST score 296
E value 4.0e-27
Match length 82
% identity 63
NCBI Description (AB016895) Pop3 [Schizosaccharomyces pombe]

Seq. No. 302166
Seq. ID dyk700105273.h1
Method BLASTX
NCBI GI g2982452
BLAST score 239
E value 2.0e-20
Match length 74
% identity 22
NCBI Description (AL022223) receptor protein kinase-like protein [Arabidopsis thaliana]

Seq. No. 302167
Seq. ID dyk700105309.h1
Method BLASTX
NCBI GI g1710511
BLAST score 321
E value 6.0e-30
Match length 89
% identity 70
NCBI Description 60S RIBOSOMAL PROTEIN L1 (L4) >gi_1165139_emb_CAA57671_(X82180) ribosomal protein L4 [Rattus norvegicus]

Seq. No. 302168
Seq. ID dyk700105327.h1
Method BLASTX
NCBI GI g3024018
BLAST score 397
E value 7.0e-39
Match length 75
% identity 100
NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
>gi_1546919_emb_CAA69225_(Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation initiation factor 5A [Zea mays]

Seq. No. 302169
Seq. ID dyk700105423.h1
Method BLASTX
NCBI GI g2160692
BLAST score 203
E value 3.0e-16
Match length 72
% identity 54
NCBI Description (U73527) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No. 302170
Seq. ID dyk700105434.h1
Method BLASTX
NCBI GI g2052094
BLAST score 410
E value 2.0e-40
Match length 96
% identity 80
NCBI Description (Z49147) phenylalanine ammonia-lyase [Hordeum vulgare]

Seq. No. 302171
Seq. ID dyk700105453.h1
Method BLASTX
NCBI GI g4262148
BLAST score 287
E value 5.0e-26
Match length 76
% identity 71
NCBI Description (AC005275) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No. 302172
Seq. ID dyk700105504.h1
Method BLASTN
NCBI GI g22292
BLAST score 80
E value 3.0e-37
Match length 180
% identity 86
NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 302173
Seq. ID dyk700105511.h1
Method BLASTX
NCBI GI g2129581
BLAST score 325
E value 2.0e-30
Match length 92
% identity 70
NCBI Description envelope Ca2+-ATPase precursor - Arabidopsis thaliana
>gi_471089_dbj_BAA03091 (D13984) chloroplast envelope
Ca2+-ATPase precursor [Arabidopsis thaliana]
>gi_4165448_emb_CAA49558 (X69940) envelope Ca2+-ATPase
[Arabidopsis thaliana]

Seq. No. 302174
Seq. ID dyk700105526.h1
Method BLASTX
NCBI GI g3776579
BLAST score 239
E value 2.0e-20
Match length 96
% identity 53
NCBI Description (AC005388) Strong similarity to F22013.22 gi_3063460 myosin
homolog from A. thaliana BAC gb_AC003981. [Arabidopsis
thaliana]

Seq. No. 302175
Seq. ID dyk700105605.h1
Method BLASTX
NCBI GI g3128172
BLAST score 245
E value 1.0e-31
Match length 100
% identity 65
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302176
Seq. ID dyk700105612.h1
Method BLASTX
NCBI GI g4371280
BLAST score 197
E value 2.0e-15
Match length 42
% identity 88
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302177

Seq. ID dyk700105629.h1
Method BLASTX
NCBI GI g3033390
BLAST score 401
E value 2.0e-39
Match length 98
% identity 64
NCBI Description (AC004238) putative vacuolar sorting receptor [Arabidopsis thaliana]

Seq. No. 302178
Seq. ID dyk700105630.h1
Method BLASTX
NCBI GI g1206013
BLAST score 174
E value 1.0e-27
Match length 99
% identity 69
NCBI Description (U44087) beta-D-glucosidase precursor [Zea mays]

Seq. No. 302179
Seq. ID dyk700105690.h1
Method BLASTX
NCBI GI g1707642
BLAST score 266
E value 2.0e-23
Match length 91
% identity 55
NCBI Description (Y07748) TMK [Oryza sativa]

Seq. No. 302180
Seq. ID dyk700105704.h1
Method BLASTX
NCBI GI g82696
BLAST score 145
E value 2.0e-15
Match length 58
% identity 79
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]

Seq. No. 302181
Seq. ID dyk700105720.h1
Method BLASTN
NCBI GI g485815
BLAST score 33
E value 4.0e-09
Match length 69
% identity 87
NCBI Description Wheat mRNA for WZF1, complete cds

Seq. No. 302182
Seq. ID dyk700105732.h1
Method BLASTX
NCBI GI g3128228
BLAST score 386
E value 1.0e-37

Match length 82
% identity 88
NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No. 302183
Seq. ID dyk700105737.h1
Method BLASTX
NCBI GI g3341697
BLAST score 326
E value 1.0e-30
Match length 96
% identity 65
NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302184
Seq. ID dyk700105802.h1
Method BLASTX
NCBI GI g4263791
BLAST score 241
E value 1.0e-20
Match length 96
% identity 50
NCBI Description (AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 302185
Seq. ID dyk700105819.h1
Method BLASTX
NCBI GI g82696
BLAST score 249
E value 6.0e-22
Match length 60
% identity 82
NCBI Description glycine-rich protein - maize >gi_22293_emb_CAA43431_(X61121) glycine-rich protein [Zea mays]

Seq. No. 302186
Seq. ID dyk700105829.h1
Method BLASTX
NCBI GI g4455301
BLAST score 162
E value 2.0e-11
Match length 45
% identity 84
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 302187
Seq. ID dyk700105933.h1
Method BLASTX
NCBI GI g3337367
BLAST score 245
E value 4.0e-21
Match length 93
% identity 51
NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302188
Seq. ID dyk700105937.h1
Method BLASTX
NCBI GI g3549626
BLAST score 153
E value 2.0e-10
Match length 90
% identity 37
NCBI Description (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

Seq. No. 302189
Seq. ID dyk700105941.h1
Method BLASTX
NCBI GI g66009
BLAST score 396
E value 8.0e-39
Match length 75
% identity 100
NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C, cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH (AA 1-337) [Zea mays]

Seq. No. 302190
Seq. ID dyk700105965.h1
Method BLASTX
NCBI GI g1370603
BLAST score 358
E value 2.0e-36
Match length 86
% identity 93
NCBI Description (X98245) annexin p35 [Zea mays]

Seq. No. 302191
Seq. ID dyk700105968.h1
Method BLASTX
NCBI GI g128185
BLAST score 141
E value 8.0e-09
Match length 44
% identity 64
NCBI Description NITRATE REDUCTASE (NR) >gi_66208_pir_RDBHNH nitrate reductase (NADH) (EC 1.6.6.1) - barley (cv. Himalaya) >gi_18994_emb_CAA40976_ (X57845) nitrate reductase [Hordeum vulgare]

Seq. No. 302192
Seq. ID dyk700105982.h1
Method BLASTX
NCBI GI g3810596
BLAST score 290
E value 2.0e-26
Match length 90
% identity 54
NCBI Description (AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq. No. 302193
Seq. ID dyk700105993.h1
Method BLASTX
NCBI GI g1839188
BLAST score 297
E value 4.0e-27
Match length 82
% identity 68
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 302194
Seq. ID dyk700105996.h1
Method BLASTX
NCBI GI g2924784
BLAST score 274
E value 2.0e-24
Match length 99
% identity 51
NCBI Description (AC002334) similar to jasmonate inducible protein [Arabidopsis thaliana]

Seq. No. 302195
Seq. ID dyk700106034.h1
Method BLASTX
NCBI GI g549063
BLAST score 142
E value 4.0e-09
Match length 30
% identity 80
NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
>gi_1072464_pir_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
21kd polypeptide [Oryza sativa]

Seq. No. 302196
Seq. ID dyk700106093.h1
Method BLASTX
NCBI GI g4335745
BLAST score 280
E value 4.0e-25
Match length 100
% identity 47
NCBI Description (AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 302197
Seq. ID dyk700106139.h1
Method BLASTX
NCBI GI g2501555
BLAST score 171
E value 2.0e-12
Match length 51
% identity 63
NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148)
possible apospory-associated protein [Pennisetum ciliare]

Seq. No. 302198
Seq. ID dyk700106210.h1
Method BLASTX
NCBI GI g2959767
BLAST score 212
E value 2.0e-20
Match length 92
% identity 60
NCBI Description (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292
(AC005309) glutathione-conjugate transporter AtMRP4
[Arabidopsis thaliana]

Seq. No. 302199
Seq. ID dyk700106266.h1
Method BLASTN
NCBI GI g1550813
BLAST score 161
E value 2.0e-85
Match length 216
% identity 94
NCBI Description Z.mays mRNA for acidic ribosomal protein P0

Seq. No. 302200
Seq. ID dyk700106293.h1
Method BLASTN
NCBI GI g4416300
BLAST score 129
E value 2.0e-66
Match length 141
% identity 98
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster
region, complete sequence

Seq. No. 302201
Seq. ID dyk700106340.h1
Method BLASTN
NCBI GI g1848280
BLAST score 44
E value 1.0e-15
Match length 44
% identity 100
NCBI Description Sorghum bicolor membrane intrinsic protein (Mip1) mRNA,
partial cds

Seq. No. 302202
Seq. ID dyk700106349.h1
Method BLASTX
NCBI GI g404690
BLAST score 233
E value 1.0e-19
Match length 102
% identity 50
NCBI Description (L19075) cytochrome P450 [Catharanthus roseus]

Seq. No. 302203
Seq. ID dyk700106353.h1
Method BLASTX

NCBI GI g1523800
BLAST score 150
E value 3.0e-10
Match length 39
% identity 69
NCBI Description (Y07694) MAP kinase kinase alpha protein kinase [Arabidopsis thaliana]

Seq. No. 302204
Seq. ID dyk700106429.h1
Method BLASTX
NCBI GI g1747310
BLAST score 140
E value 5.0e-09
Match length 25
% identity 100
NCBI Description (D58424) Myb-like DNA binding protein [Arabidopsis thaliana]

Seq. No. 302205
Seq. ID dyk700106434.h1
Method BLASTX
NCBI GI g3056725
BLAST score 185
E value 3.0e-14
Match length 68
% identity 51
NCBI Description (AF034774) ent-kaurene synthase [Arabidopsis thaliana]

Seq. No. 302206
Seq. ID dyk700106468.h1
Method BLASTX
NCBI GI g3292829
BLAST score 145
E value 4.0e-14
Match length 93
% identity 47
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 302207
Seq. ID dyk700106518.h1
Method BLASTX
NCBI GI g2665890
BLAST score 309
E value 2.0e-32
Match length 97
% identity 73
NCBI Description (AF035944) calcium-dependent protein kinase [Fragaria x ananassa]

Seq. No. 302208
Seq. ID dyk700106532.h1
Method BLASTN
NCBI GI g559535
BLAST score 69
E value 1.0e-30
Match length 178

% identity 91
NCBI Description Z.mays mRNA for metallothionein

Seq. No. 302209
Seq. ID dyk700106538.h1
Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 36
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 302210
Seq. ID dyk700106570.h1
Method BLASTN
NCBI GI g433871
BLAST score 38
E value 4.0e-12
Match length 90
% identity 86
NCBI Description C.roseus mRNA for HMG protein

Seq. No. 302211
Seq. ID dyk700106587.h1
Method BLASTX
NCBI GI g4263048
BLAST score 185
E value 5.0e-14
Match length 46
% identity 72
NCBI Description (AC005142) putative hydrolase [Arabidopsis thaliana]

Seq. No. 302212
Seq. ID dyk700106627.h1
Method BLASTN
NCBI GI g2062705
BLAST score 36
E value 6.0e-11
Match length 36
% identity 100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 302213
Seq. ID dyk700106660.h1
Method BLASTX
NCBI GI g1352186
BLAST score 251
E value 2.0e-27
Match length 87
% identity 69
NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)
(CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide
synthase [Linum usitatissimum]

Seq. No. 302214
Seq. ID dyk700106670.h1

Method BLASTX
NCBI GI g4581164
BLAST score 253
E value 7.0e-25
Match length 96
% identity 61
NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No. 302215
Seq. ID dyk700106681.h1
Method BLASTX
NCBI GI g2257756
BLAST score 340
E value 4.0e-32
Match length 77
% identity 82
NCBI Description (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]
>gi_3650466 (AF026917) histone deacetylase HD2-p39 [Zea mays]

Seq. No. 302216
Seq. ID dyk700106683.h1
Method BLASTX
NCBI GI g3193296
BLAST score 142
E value 6.0e-09
Match length 51
% identity 49
NCBI Description (AF069298) similar to pectinesterase [Arabidopsis thaliana]

Seq. No. 302217
Seq. ID dyk700106710.h1
Method BLASTX
NCBI GI g3892051
BLAST score 215
E value 5.0e-20
Match length 63
% identity 79
NCBI Description (AC002330) predicted NADH dehydrogenase 24 kD subunit
[Arabidopsis thaliana]

Seq. No. 302218
Seq. ID dyk700106731.h1
Method BLASTX
NCBI GI g3255943
BLAST score 153
E value 3.0e-10
Match length 28
% identity 96
NCBI Description (AJ007333) PP2A1 protein [Catharanthus roseus]

Seq. No. 302219
Seq. ID dyk700106733.h1
Method BLASTN
NCBI GI g1129083
BLAST score 93
E value 6.0e-45

Match length 152
% identity 91
NCBI Description Wheat mRNA for protein H2A, complete cds, clone wCH2A-2

Seq. No. 302220
Seq. ID dyk700106842.h1
Method BLASTX
NCBI GI g4115388
BLAST score 263
E value 3.0e-23
Match length 82
% identity 63
NCBI Description (AC005967) putative prolylcarboxypeptidase [Arabidopsis thaliana]

Seq. No. 302221
Seq. ID dyk700106850.h1
Method BLASTX
NCBI GI g1161167
BLAST score 181
E value 1.0e-13
Match length 88
% identity 34
NCBI Description (L42466) ethylene-forming enzyme [Picea glauca]

Seq. No. 302222
Seq. ID dyk700106862.h1
Method BLASTX
NCBI GI g3860277
BLAST score 256
E value 2.0e-22
Match length 73
% identity 63
NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604 (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 302223
Seq. ID dyk700106901.h1
Method BLASTN
NCBI GI g577818
BLAST score 98
E value 3.0e-48
Match length 121
% identity 98
NCBI Description Z.mays gene for H2B histone (gH2B4)

Seq. No. 302224
Seq. ID dyk700106911.h1
Method BLASTX
NCBI GI g347855
BLAST score 156
E value 1.0e-10
Match length 78
% identity 41
NCBI Description (L21753) glucose transporter [Saccharum hybrid cultivar H65-7052]

Seq. No. 302225
Seq. ID dyk700106927.h1
Method BLASTX
NCBI GI g3176687
BLAST score 392
E value 3.0e-38
Match length 99
% identity 73
NCBI Description (AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No. 302226
Seq. ID dyk700106945.h1
Method BLASTX
NCBI GI g3176673
BLAST score 229
E value 3.0e-19
Match length 86
% identity 51
NCBI Description (AC003671) Similar to serine/threonine kinase gb_Y12531 from Brassica oleracea. [Arabidopsis thaliana]

Seq. No. 302227
Seq. ID dyk700106946.h1
Method BLASTX
NCBI GI g4056615
BLAST score 161
E value 3.0e-11
Match length 60
% identity 62
NCBI Description (AF067401) Scl1 protein [Oryza sativa]

Seq. No. 302228
Seq. ID dyk700106955.h1
Method BLASTX
NCBI GI g4056506
BLAST score 319
E value 1.0e-29
Match length 100
% identity 61
NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 302229
Seq. ID fC-zmf1700337353a5
Method BLASTN
NCBI GI g56539
BLAST score 87
E value 3.0e-41
Match length 301
% identity 94
NCBI Description R.norvegicus gene encoding prolactin, exon 5
>gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
: exon v and flanks

Q32000

Seq. No.	302230
Seq. ID	fc-zmf1700342888g1
Method	BLASTX
NCBI GI	g4098521
BLAST score	324
E value	2.0e-30
Match length	76
% identity	76
NCBI Description	(U79160) HMG-CoA synthase [Arabidopsis thaliana] >gi_4098523 (U79161) HMG-CoA synthase [Arabidopsis thaliana]
Seq. No.	302231
Seq. ID	fc-zmf1700344603g1
Method	BLASTX
NCBI GI	g267196
BLAST score	621
E value	9.0e-65
Match length	168
% identity	74
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_66574_pir__YUPOY ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - potato >gi_21471_emb_CAA41359 (X58453) glycogen (starch) synthase [Solanum tuberosum]
Seq. No.	302232
Seq. ID	fc-zmf1700345831g1
Method	BLASTX
NCBI GI	g2879792
BLAST score	172
E value	4.0e-12
Match length	78
% identity	44
NCBI Description	(AL021813) SPAC23A1.04c, possible glycosyl hydrolase, len:756aa, similar eg. to C. elegans Q18679, (586aa), fasta scores, opt:566, E():0, (48.0% identity in 452 aa overlap), also similar to YHR204W, YH04_YEAST, P38888, hypothet
Seq. No.	302233
Seq. ID	fc-zmf1700345831z1
Method	BLASTX
NCBI GI	g1504008
BLAST score	178
E value	5.0e-28
Match length	166
% identity	45
NCBI Description	(D86967) Containing ATP/GTP-binding site motif A(P-loop): Similar to C.elegans protein(P1:CEC47E128);Similar to Mouse alpha-mannosidase(P1:B54407) [Homo sapiens]
Seq. No.	302234
Seq. ID	fc-zmf1700348376y2
Method	BLASTN
NCBI GI	g304040
BLAST score	169
E value	2.0e-90
Match length	185

% identity 98
NCBI Description Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene

Seq. No. 302235
Seq. ID fC-zmf1700349776g1
Method BLASTX
NCBI GI g3021270
BLAST score 424
E value 8.0e-42
Match length 141
% identity 57
NCBI Description (AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]

Seq. No. 302236
Seq. ID fC-zmf1700350656f5
Method BLASTX
NCBI GI g2104675
BLAST score 337
E value 9.0e-32
Match length 100
% identity 67
NCBI Description (X97903) transcription factor [Vicia faba]

Seq. No. 302237
Seq. ID fC-zmf1700350656f6
Method BLASTX
NCBI GI g4587989
BLAST score 211
E value 5.0e-17
Match length 110
% identity 43
NCBI Description (AF085279) hypothetical Cys-3-His zinc finger protein [Arabidopsis thaliana]

Seq. No. 302238
Seq. ID fC-zmf1700350815d4
Method BLASTX
NCBI GI g542395
BLAST score 190
E value 2.0e-14
Match length 50
% identity 80
NCBI Description ubiquitin - basidiomycete (Phanerochaete chrysosporium) (fragment) >gi_467696_emb_CAA83244_ (Z31373) ubiquitin [Phanerochaete chrysosporium]

Seq. No. 302239
Seq. ID fC-zmf1700352166b1
Method BLASTX
NCBI GI g4510395
BLAST score 207
E value 2.0e-16
Match length 76
% identity 51
NCBI Description (AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana]

DRAFT

Seq. No. 302240
Seq. ID fC-zmf1700352582f2
Method BLASTX
NCBI GI g3924611
BLAST score 601
E value 2.0e-62
Match length 128
% identity 89
NCBI Description (AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No. 302241
Seq. ID fC-zmf1700354921g1
Method BLASTX
NCBI GI g2459435
BLAST score 421
E value 2.0e-41
Match length 154
% identity 56
NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No. 302242
Seq. ID fC-zmf1700382985h1
Method BLASTX
NCBI GI g4210330
BLAST score 658
E value 4.0e-69
Match length 158
% identity 78
NCBI Description (AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No. 302243
Seq. ID fC-zmf1700464505b1
Method BLASTX
NCBI GI g3033400
BLAST score 371
E value 2.0e-35
Match length 83
% identity 80
NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No. 302244
Seq. ID fC-zmf1700465148f2
Method BLASTN
NCBI GI g2832689
BLAST score 162
E value 5.0e-86
Match length 285
% identity 100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21 (ESSAI project)

Seq. No. 302245
Seq. ID fC-zmf1700465406b1

Method BLASTX
NCBI GI g1707642
BLAST score 215
E value 3.0e-17
Match length 84
% identity 54
NCBI Description (Y07748) TMK [Oryza sativa]

Seq. No. 302246
Seq. ID fC-zmf1700466204d4
Method BLASTX
NCBI GI g1710124
BLAST score 256
E value 3.0e-22
Match length 74
% identity 72
NCBI Description (U62279) leucine-rich repeat-containing extracellular glycoprotein; contains six N-glycosylation sites [NX(S/T)] [Sorghum bicolor]

Seq. No. 302247
Seq. ID fC-zmf1700467207b1
Method BLASTX
NCBI GI g3256035
BLAST score 187
E value 6.0e-14
Match length 52
% identity 62
NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No. 302248
Seq. ID fC-zmf1700467236b1
Method BLASTX
NCBI GI g3249072
BLAST score 185
E value 1.0e-13
Match length 66
% identity 53
NCBI Description (AC004473) Contains similarity to hypothetical 43.1 KD protein in NDK-GCPE intergenic region gb_493519 from E. coli sequence gb_U02965. [Arabidopsis thaliana]

Seq. No. 302249
Seq. ID fC-zmf1700467533b1
Method BLASTX
NCBI GI g3337361
BLAST score 387
E value 3.0e-37
Match length 105
% identity 64
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 302250
Seq. ID fC-zmf1700467714b1
Method BLASTX
NCBI GI g1223926

BLAST score 311
E value 2.0e-28
Match length 64
% identity 92
NCBI Description (U49741) Vigna radiata carboxypeptidase II mRNA, partial cds [Vigna radiata]

Seq. No. 302251
Seq. ID fC-zmf1700467776b1
Method BLASTX
NCBI GI g3024362
BLAST score 436
E value 3.0e-43
Match length 88
% identity 91
NCBI Description PHENYLALANINE AMMONIA-LYASE G2B >gi_2118317_pir_S60042 phenylalanine ammonia-lyase (EC 4.3.1.5) 2b - Japanese aspen x large-toothed aspen >gi_1109641_dbj_BAA07860_(D43802) phenylalanine ammonia-lyase [Populus kitakamiensis]

Seq. No. 302252
Seq. ID fC-zmf1700467803b1
Method BLASTX
NCBI GI g1403522
BLAST score 461
E value 5.0e-46
Match length 96
% identity 85
NCBI Description (X57187) chitinase [Phaseolus vulgaris]

Seq. No. 302253
Seq. ID fC-zmf1700468004b1
Method BLASTX
NCBI GI g4432830
BLAST score 333
E value 5.0e-31
Match length 111
% identity 58
NCBI Description (AC006283) similar to pheromone receptor deficient mutant [Arabidopsis thaliana]

Seq. No. 302254
Seq. ID fC-zmf1700468053b1
Method BLASTN
NCBI GI g3769285
BLAST score 63
E value 8.0e-27
Match length 239
% identity 87
NCBI Description Vigna radiata gene for 1-aminocyclopropane-1-carboxylate synthase, complete cds

Seq. No. 302255
Seq. ID fC-zmf1700468133b1
Method BLASTX
NCBI GI g2493495

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BLAST score	166
E value	1.0e-11
Match length	48
% identity	62
NCBI Description	SERINE CARBOXYPEPTIDASE-LIKE >gi_2129878_pir_S72370 carboxypeptidase - garden pea (fragment) >gi_1089904_emb_CAA92216_ (Z68130) carboxypeptidase [Pisum sativum] >gi_1587217_prf_ 2206338A Ser carboxypeptidase [Pisum sativum]
Seq. No.	302256
Seq. ID	fC-zmf1700468226b1
Method	BLASTX
NCBI GI	g114947
BLAST score	201
E value	1.0e-15
Match length	104
% identity	50
NCBI Description	BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR >gi_105434_pir_B32688 beta-galactosidase-related protein - human >gi_179421 (M27508) beta-galactosidase related protein precursor [Homo sapiens]
Seq. No.	302257
Seq. ID	fC-zmf1700468226f2
Method	BLASTX
NCBI GI	g2501021
BLAST score	159
E value	7.0e-11
Match length	56
% identity	59
NCBI Description	LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS) >gi_1652562_dbj_BAA17483_ (D90906) lysyl-tRNA synthetase [Synechocystis sp.]
Seq. No.	302258
Seq. ID	fC-zmf1700468289b1
Method	BLASTX
NCBI GI	g4455369
BLAST score	178
E value	6.0e-13
Match length	46
% identity	78
NCBI Description	(AL035524) hypothetical protein [Arabidopsis thaliana]
Seq. No.	302259
Seq. ID	fC-zmf1700468444f2
Method	BLASTN
NCBI GI	g6598508
BLAST score	81
E value	7.0e-38
Match length	153
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T13P21 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	302260

Seq. ID	fC-zmf1700468704f2
Method	BLASTX
NCBI GI	g466190
BLAST score	299
E value	3.0e-27
Match length	109
% identity	52
NCBI Description	RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE B (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE) >gi_629120_pir_S45555 hypothetical protein X13 - Bacillus subtilis >gi_410137 (L09228) ORFX13 [Bacillus subtilis] >gi_2634751_emb CAB14248 (Z99116) similar to hypothetical proteins [Bacillus subtilis]
Seq. No.	302261
Seq. ID	fC-zmf1700468993b1
Method	BLASTX
NCBI GI	g1935019
BLAST score	719
E value	3.0e-76
Match length	169
% identity	85
NCBI Description	(Z93774) sucrose transport protein [Vicia faba]
Seq. No.	302262
Seq. ID	fC-zmf1700469527b1
Method	BLASTX
NCBI GI	g2494174
BLAST score	305
E value	1.0e-27
Match length	100
% identity	64
NCBI Description	GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi_497979 (U10034) glutamate decarboxylase [Arabidopsis thaliana]
Seq. No.	302263
Seq. ID	fC-zmf1700469527f2
Method	BLASTN
NCBI GI	g2618677
BLAST score	325
E value	0.0e+00
Match length	329
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	302264
Seq. ID	fC-zmf1700469566b1
Method	BLASTX
NCBI GI	g114167
BLAST score	508
E value	1.0e-51
Match length	104
% identity	89
NCBI Description	3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE 2 (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE 2) (EPSP SYNTHASE 2) >gi_100297_pir_S18354 3-phosphoshikimate

1-carboxyvinyltransferase (EC 2.5.1.19) - common tobacco
>gi_170231 (M61905) 5-enolpyruvylshikimate-3-phosphate
synthase [Nicotiana tabacum]

Seq. No. 302265
Seq. ID fc-zmf1700469566f2
Method BLASTX
NCBI GI g1418331
BLAST score 300
E value 2.0e-27
Match length 106
% identity 57
NCBI Description (X95909) receptor like protein kinase [Arabidopsis thaliana]

Seq. No. 302266
Seq. ID fc-zmf1700469777b1
Method BLASTX
NCBI GI g3367516
BLAST score 207
E value 2.0e-16
Match length 68
% identity 50
NCBI Description (AC004392) Similar to beta-glucosidase BGQ60 precursor
gb_L41869 from Hordeum vulgare. [Arabidopsis thaliana]

Seq. No. 302267
Seq. ID fc-zmf1700470006b1
Method BLASTX
NCBI GI g2244867
BLAST score 246
E value 6.0e-21
Match length 73
% identity 59
NCBI Description (Z97337) hydroxynitrile lyase [Arabidopsis thaliana]

Seq. No. 302268
Seq. ID fc-zmf1700470273f2
Method BLASTX
NCBI GI g4335736
BLAST score 219
E value 7.0e-18
Match length 108
% identity 40
NCBI Description (AC006248) putative copia polyprotein [Arabidopsis thaliana]

Seq. No. 302269
Seq. ID fc-zmf1700470673b1
Method BLASTX
NCBI GI g1931655
BLAST score 171
E value 4.0e-12
Match length 44
% identity 75
NCBI Description (U95973) receptor-kinase isolog [Arabidopsis thaliana]

Seq. No. 302270
Seq. ID fC-zmf1700471493b1
Method BLASTX
NCBI GI g1706110
BLAST score 325
E value 4.0e-30
Match length 82
% identity 80
NCBI Description NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT) >gi_1143713 (U13632) non-green plastid phosphate/triose-phosphate translocator precursor [Brassica oleracea]

Seq. No. 302271
Seq. ID fC-zmf1700471493f2
Method BLASTN
NCBI GI g6598653
BLAST score 228
E value 1.0e-125
Match length 259
% identity 97
NCBI Description Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence

Seq. No. 302272
Seq. ID fC-zmf1700471593b1
Method BLASTX
NCBI GI g1754522
BLAST score 193
E value 1.0e-14
Match length 60
% identity 65
NCBI Description (D89984) ornithine decarboxylase [Nicotiana tabacum]

Seq. No. 302273
Seq. ID fC-zmf1700472059b1
Method BLASTX
NCBI GI g4538667
BLAST score 193
E value 9.0e-15
Match length 58
% identity 66
NCBI Description (AL049474) clathrin coat assembly protein [Schizosaccharomyces pombe]

Seq. No. 302274
Seq. ID fC-zmf1700472168b1
Method BLASTX
NCBI GI g3122389
BLAST score 182
E value 7.0e-14
Match length 50
% identity 78
NCBI Description WD-40 REPEAT PROTEIN MSI3 >gi_2394233 (AF016848) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No. 302275

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Seq. ID	fC-zmf1700472661b1
Method	BLASTN
NCBI GI	g2606080
BLAST score	194
E value	1.0e-105
Match length	277
% identity	100
NCBI Description	Glycine max sucrose synthase (SS) mRNA, complete cds
Seq. No.	302276
Seq. ID	fC-zmf1700472710b1
Method	BLASTX
NCBI GI	g2501231
BLAST score	385
E value	3.0e-37
Match length	88
% identity	76
NCBI Description	HYPOTHETICAL 38.1 KD PROTEIN >gi_99505_pir_S24930 hypothetical protein - pink corydalis >gi_18258_emb_CAA45139_ (X63595) protein of unknown function [Corydalis sempervirens] >gi_444333_prf_1906382A pCSC71 protein [Corydalis sempervirens]
Seq. No.	302277
Seq. ID	fC-zmf1700472751b1
Method	BLASTX
NCBI GI	g4098129
BLAST score	369
E value	3.0e-35
Match length	74
% identity	92
NCBI Description	(U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.	302278
Seq. ID	fC-zmf1700474549b1
Method	BLASTX
NCBI GI	g4115936
BLAST score	335
E value	2.0e-31
Match length	78
% identity	82
NCBI Description	(AF118223) No definition line found [Arabidopsis thaliana]
Seq. No.	302279
Seq. ID	fC-zmf1700475620b1
Method	BLASTX
NCBI GI	g1155255
BLAST score	279
E value	1.0e-24
Match length	105
% identity	55
NCBI Description	(U39228) beta-glucosidase [Prunus avium]
Seq. No.	302280
Seq. ID	fC-zmf1700548428f3
Method	BLASTX
NCBI GI	g535454

BLAST score 377
E value 2.0e-36
Match length 109
% identity 61
NCBI Description (U13940) cysteine proteinase [Alnus glutinosa]

Seq. No. 302281
Seq. ID fC-zmf1700549125f3
Method BLASTX
NCBI GI g2388574
BLAST score 548
E value 3.0e-56
Match length 122
% identity 87
NCBI Description (AC000098) Strong similarity to Phalaenopsis homeobox protein (gb_U34743). [Arabidopsis thaliana]

Seq. No. 302282
Seq. ID fC-zmf1700549863r3
Method BLASTX
NCBI GI g1236949
BLAST score 257
E value 3.0e-22
Match length 68
% identity 76
NCBI Description (U50075) lipoxygenase L-5 [Glycine max]

Seq. No. 302283
Seq. ID fC-zmf1700552735f3
Method BLASTX
NCBI GI g1076531
BLAST score 481
E value 2.0e-48
Match length 123
% identity 73
NCBI Description hypothetical protein, pollen allergen homolog - garden pea >gi_2129891_pir_S65056 pollen allergen homolog precursor (clone PPA1) - garden pea >gi_732905_emb_CAA59470_ (X85187) homology with pollen allergens [Pisum sativum]

Seq. No. 302284
Seq. ID fC-zmf1700610957h2
Method BLASTX
NCBI GI g310580
BLAST score 259
E value 3.0e-22
Match length 54
% identity 94
NCBI Description (L19360) protein kinase 2 [Glycine max]

Seq. No. 302285
Seq. ID fC-zmf1700611201a1
Method BLASTX
NCBI GI g3063691
BLAST score 534
E value 1.0e-54
Match length 156

% identity 62
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 302286
Seq. ID fC-zmf1700903880z1
Method BLASTX
NCBI GI g4335745
BLAST score 259
E value 2.0e-22
Match length 148
% identity 41
NCBI Description (AC006284) putative hydrolase (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 302287
Seq. ID fC-zmf1700903946z1
Method BLASTX
NCBI GI g4102600
BLAST score 502
E value 7.0e-51
Match length 142
% identity 75
NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]

Seq. No. 302288
Seq. ID fC-zmf1700904260g1
Method BLASTX
NCBI GI g2809262
BLAST score 352
E value 3.0e-33
Match length 165
% identity 44
NCBI Description (AC002560) F21B7.31 [Arabidopsis thaliana]

Seq. No. 302289
Seq. ID fC-zmf1700905073g1
Method BLASTX
NCBI GI g4510375
BLAST score 198
E value 4.0e-15
Match length 131
% identity 45
NCBI Description (AC007017) putative homeotic protein BEL1 [Arabidopsis thaliana]

Seq. No. 302290
Seq. ID fC-zmf1700906621a1
Method BLASTX
NCBI GI g4335763
BLAST score 301
E value 2.0e-27
Match length 116
% identity 47
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 302291

Seq. ID fC-zmle700423591r3
Method BLASTX
NCBI GI g3639087
BLAST score 352
E value 2.0e-33
Match length 113
% identity 64
NCBI Description (AF090444) phospholipase D2 [Brassica oleracea] >gi_3924621
(U85482) phospholipase D [Brassica oleracea var. capitata]
>gi_4324971_gb_AAD17209_ (AF113919) phospholipase D2
[Brassica oleracea var. capitata]

Seq. No. 302292
Seq. ID fC-zmle700427538b1
Method BLASTX
NCBI GI g1781348
BLAST score 156
E value 1.0e-10
Match length 34
% identity 88
NCBI Description (Y10380) homologous to plastidic aldolases [Solanum
tuberosum]

Seq. No. 302293
Seq. ID fC-zmle700428142a4
Method BLASTX
NCBI GI g1632822
BLAST score 408
E value 5.0e-40
Match length 87
% identity 89
NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi_1667594
(U77297) transmembrane protein [Oryza sativa]

Seq. No. 302294
Seq. ID fC-zmle700428946d3
Method BLASTN
NCBI GI g3342803
BLAST score 94
E value 2.0e-45
Match length 178
% identity 88
NCBI Description Zea mays strain B73 putative 6-phosphogluconate
dehydrogenase mRNA, nuclear gene encoding putative plastid
protein, partial cds

Seq. No. 302295
Seq. ID fC-zmle700429434f3
Method BLASTN
NCBI GI g3342031
BLAST score 52
E value 3.0e-20
Match length 60
% identity 98
NCBI Description Oryza sativa 18S small subunit ribosomal RNA gene, complete
sequence

Seq. No. 302296
Seq. ID fC-zmle700431670f4
Method BLASTX
NCBI GI g4033424
BLAST score 186
E value 2.0e-14
Match length 41
% identity 85
NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic pyrophosphatase [Zea mays]

Seq. No. 302297
Seq. ID fC-zmle700433471d3
Method BLASTN
NCBI GI g553071
BLAST score 189
E value 1.0e-102
Match length 261
% identity 93
NCBI Description Maize catalase (Cat2) mRNA, 3' end

Seq. No. 302298
Seq. ID fC-zmle700434174z1
Method BLASTX
NCBI GI g488571
BLAST score 202
E value 1.0e-15
Match length 41
% identity 98
NCBI Description (U09462) histone H3.2 [Medicago sativa]

Seq. No. 302299
Seq. ID fC-zmle700434272g1
Method BLASTX
NCBI GI g1076755
BLAST score 693
E value 4.0e-73
Match length 183
% identity 72
NCBI Description protein kinase - rice >gi_450300 (L27821) protein kinase [Oryza sativa]

Seq. No. 302300
Seq. ID fC-zmle700441222d3
Method BLASTX
NCBI GI g1345559
BLAST score 170
E value 2.0e-12
Match length 46
% identity 72
NCBI Description (Z15024) hsp82 [Oryza sativa]

Seq. No. 302301
Seq. ID fC-zmle700442391d5
Method BLASTX
NCBI GI g113987

BLAST score 173
E value 2.0e-12
Match length 45
% identity 71
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P0 (DEOXYRIBONUCLEASE (APURINIC OR APYRIMIDINIC)) (APURINIC- APYRIMIDINIC ENDONUCLEASE) >gi_71140_pir_R5FFP0 acidic ribosomal protein P0 - fruit fly (*Drosophila melanogaster*) >gi_576817 (M25772) DNA repair protein [*Drosophila melanogaster*]

Seq. No. 302302
Seq. ID fC-zmle700443787d6
Method BLASTX
NCBI GI g731806
BLAST score 218
E value 4.0e-22
Match length 79
% identity 70
NCBI Description PROBABLE CALCIUM-TRANSPORTING ATPASE 7
>gi_626344_pir_S48431 probable membrane protein YIL048w - yeast (*Saccharomyces cerevisiae*) >gi_557820_emb CAA86174_ (Z38060) orf, len: 1151, CAI: 0.17, similar to S30768
S30768 PROBABLE ATPASE - YEAST (*SACCHAROMYCES CEREVISIAE*) [*Saccharomyces cerevisiae*]

Seq. No. 302303
Seq. ID fC-zmle700444043b1
Method BLASTX
NCBI GI g2081612
BLAST score 151
E value 9.0e-10
Match length 41
% identity 80
NCBI Description (D49714) delta-pyrroline-5-carboxylate synthetase [*Oryza sativa*]

Seq. No. 302304
Seq. ID fC-zmle700445373f5
Method BLASTX
NCBI GI g3402758
BLAST score 372
E value 9.0e-36
Match length 128
% identity 56
NCBI Description (AL031187) serine/threonine kinase - like protein [*Arabidopsis thaliana*]

Seq. No. 302305
Seq. ID fC-zmle700445890d4
Method BLASTX
NCBI GI g4008006
BLAST score 151
E value 2.0e-10
Match length 59
% identity 46
NCBI Description (AF084034) receptor-like protein kinase [*Arabidopsis thaliana*]

Seq. No. 302306
Seq. ID fc-zmle700447121a1
Method BLASTX
NCBI GI g2842478
BLAST score 149
E value 1.0e-09
Match length 80
% identity 39
NCBI Description (AL021749) receptor protein kinase like protein [Arabidopsis thaliana]

Seq. No. 302307
Seq. ID fc-zmle700447833a1
Method BLASTN
NCBI GI g296593
BLAST score 55
E value 4.0e-22
Match length 75
% identity 93
NCBI Description H. vulgare pZE40 gene

Seq. No. 302308
Seq. ID fc-zmle700448273a1
Method BLASTX
NCBI GI g3540182
BLAST score 360
E value 3.0e-34
Match length 125
% identity 54
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No. 302309
Seq. ID fc-zmle700577059a2
Method BLASTX
NCBI GI g2687358
BLAST score 286
E value 4.0e-51
Match length 120
% identity 89
NCBI Description (AF033263) nonphototropic hypocotyl 1 [Zea mays]

Seq. No. 302310
Seq. ID fc-zmle700577234r1
Method BLASTX
NCBI GI g585421
BLAST score 265
E value 3.0e-23
Match length 57
% identity 77
NCBI Description LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi_541879_pir_JQ2391
lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana
>gi_431258 (L23968) lipoxygenase [Arabidopsis thaliana]

Seq. No. 302311
Seq. ID fc-zmle700582195a2
Method BLASTX

NCBI GI g1364161
BLAST score 269
E value 7.0e-24
Match length 93
% identity 63
NCBI Description thiolase precursor, peroxisomal - ripe mango

Seq. No. 302312
Seq. ID fC-zmle700583812a2
Method BLASTN
NCBI GI g3318610
BLAST score 110
E value 3.0e-55
Match length 176
% identity 92
NCBI Description Glycine max mRNA for mitochondrial phosphate transporter, complete cds

Seq. No. 302313
Seq. ID fC-zmle700870829a1
Method BLASTX
NCBI GI g2459435
BLAST score 473
E value 1.0e-47
Match length 125
% identity 71
NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No. 302314
Seq. ID fC-zmle700870829d1
Method BLASTX
NCBI GI g2459435
BLAST score 320
E value 2.0e-29
Match length 76
% identity 78
NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No. 302315
Seq. ID fC-zmle700870883a1
Method BLASTX
NCBI GI g4105772
BLAST score 444
E value 4.0e-44
Match length 107
% identity 43
NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 302316
Seq. ID fC-zmle700871883a1
Method BLASTX
NCBI GI g3204134
BLAST score 871
E value 4.0e-94
Match length 166

% identity 92
NCBI Description (AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No. 302317
Seq. ID fC-zmle700871981d1
Method BLASTX
NCBI GI g2623300
BLAST score 447
E value 2.0e-44
Match length 112
% identity 79
NCBI Description (AC002409) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 302318
Seq. ID fC-zmle700889290a1
Method BLASTX
NCBI GI g1168493
BLAST score 557
E value 3.0e-57
Match length 131
% identity 85
NCBI Description ARGINASE >gi_602422 (U15019) arginase [Arabidopsis thaliana] >gi_4325373_gb_AAD17369_ (AF128396) Arabidopsis thaliana arginase (SW:P46637) (Pfam: PF00491, Score=419.6, E=3.7e-142 N=1) [Arabidopsis thaliana]

Seq. No. 302319
Seq. ID fC-zmro700448758a1
Method BLASTX
NCBI GI g2239260
BLAST score 618
E value 2.0e-64
Match length 136
% identity 88
NCBI Description (Y13734) cinnamoyl CoA reductase [Zea mays]

Seq. No. 302320
Seq. ID fC-zmro700569244f1
Method BLASTX
NCBI GI g4165488
BLAST score 385
E value 3.0e-49
Match length 97
% identity 97
NCBI Description (AJ132399) alpha-tubulin 3 [Hordeum vulgare]

Seq. No. 302321
Seq. ID fC-zmro700570531r1
Method BLASTX
NCBI GI g3913194
BLAST score 171
E value 5.0e-12
Match length 81
% identity 40
NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 3 (CAD) >gi_548323 (L36456) cinnamyl-alcohol dehydrogenase [Stylosanthes humilis]

Seq. No. 302322
Seq. ID fC-zmro700570954a1
Method BLASTX
NCBI GI g2244771
BLAST score 324
E value 5.0e-30
Match length 76
% identity 89
NCBI Description (Z97335) kinesin homolog [Arabidopsis thaliana]

Seq. No. 302323
Seq. ID fC-zmro700570954d1
Method BLASTX
NCBI GI g4093169
BLAST score 248
E value 4.0e-21
Match length 63
% identity 70
NCBI Description (AF095933) p20-Arc [Dictyostelium discoideum]

Seq. No. 302324
Seq. ID fC-zmro700571730a1
Method BLASTX
NCBI GI g3046815
BLAST score 190
E value 2.0e-23
Match length 72
% identity 76
NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 302325
Seq. ID fC-zmro700571850a1
Method BLASTX
NCBI GI g4587525
BLAST score 258
E value 3.0e-22
Match length 117
% identity 42
NCBI Description (AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No. 302326
Seq. ID fC-zmro700572286a1
Method BLASTX
NCBI GI g2739279
BLAST score 332
E value 6.0e-31
Match length 137
% identity 49
NCBI Description (AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi_2791348 emb CAA11154 (AJ223178) short chain alcohol dehydrogenase [Nicotiana tabacum]

Seq. No. 302327

Seq. ID fC-zmro700572681a1
Method BLASTX
NCBI GI g3193316
BLAST score 358
E value 5.0e-34
Match length 103
% identity 68
NCBI Description (AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No. 302328
Seq. ID fC-zmro700573051a1
Method BLASTX
NCBI GI g1352186
BLAST score 453
E value 4.0e-45
Match length 140
% identity 56
NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) (CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide synthase [Linum usitatissimum]

Seq. No. 302329
Seq. ID fC-zmro700573209a1
Method BLASTX
NCBI GI g2980785
BLAST score 514
E value 3.0e-52
Match length 137
% identity 64
NCBI Description (AL022198) SERINE CARBOXYPEPTIDASE II - like protein [Arabidopsis thaliana]

Seq. No. 302330
Seq. ID fC-zmro700573209d1
Method BLASTX
NCBI GI g2493494
BLAST score 290
E value 5.0e-26
Match length 84
% identity 69
NCBI Description SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) >gi_619351_bbs_153537 CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa]

Seq. No. 302331
Seq. ID fC-zmro700573388d1
Method BLASTN
NCBI GI g2446999
BLAST score 121
E value 2.0e-61
Match length 223
% identity 95
NCBI Description Zea mays FAD8 gene for fatty acid desaturase, partial cds

Seq. No. 302332

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Seq. ID	fC-zmro700573489g1
Method	BLASTX
NCBI GI	g1709000
BLAST score	612
E value	8.0e-64
Match length	142
% identity	82
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine synthetase [Hordeum vulgare]
Seq. No.	302333
Seq. ID	fC-zmro700573489z1
Method	BLASTX
NCBI GI	g3024122
BLAST score	722
E value	1.0e-76
Match length	162
% identity	86
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
Seq. No.	302334
Seq. ID	fC-zmro700573673a1
Method	BLASTX
NCBI GI	g123620
BLAST score	620
E value	9.0e-65
Match length	141
% identity	87
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir_S14950 heat shock cognate protein 70 - tomato >gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate 70 [Lycopersicon esculentum]
Seq. No.	302335
Seq. ID	fC-zmro700573673d1
Method	BLASTX
NCBI GI	g1430887
BLAST score	295
E value	1.0e-26
Match length	91
% identity	69
NCBI Description	(X99197) 70 kd heatshockprotein [Medicago sativa]
Seq. No.	302336
Seq. ID	fC-zmro700574787a1
Method	BLASTX
NCBI GI	g4165488
BLAST score	257
E value	6.0e-33
Match length	77
% identity	86
NCBI Description	(AJ132399) alpha-tubulin 3 [Hordeum vulgare]

Seq. No. 302337
Seq. ID fC-zmro700574919a3
Method BLASTX
NCBI GI g1236949
BLAST score 907
E value 3.0e-98
Match length 174
% identity 99
NCBI Description (U50075) lipoxygenase L-5 [Glycine max]

Seq. No. 302338
Seq. ID fC-zmro700575714f1
Method BLASTX
NCBI GI g2522210
BLAST score 305
E value 6.0e-28
Match length 101
% identity 53
NCBI Description (AF023132) choline monooxygenase [Beta vulgaris]

Seq. No. 302339
Seq. ID fC-zmro700576307a2
Method BLASTX
NCBI GI g3482919
BLAST score 141
E value 4.0e-09
Match length 33
% identity 73
NCBI Description (AC003970) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 302340
Seq. ID fC-zmro700807549a1
Method BLASTX
NCBI GI g4457221
BLAST score 381
E value 1.0e-36
Match length 114
% identity 68
NCBI Description (AF127797) putative bZIP DNA-binding protein [Capsicum chinense]

Seq. No. 302341
Seq. ID fC-zmro700807584a1
Method BLASTX
NCBI GI g3218410
BLAST score 516
E value 1.0e-52
Match length 127
% identity 76
NCBI Description (AL023859) putative prolyl-trna synthetase [Schizosaccharomyces pombe]

Seq. No. 302342
Seq. ID fC-zmro700807584r1
Method BLASTX
NCBI GI g731640
BLAST score 172

E value 3.0e-12
 Match length 78
 % identity 47
 NCBI Description PUTATIVE PROLYL-TRNA SYNTHETASE YHR020W (PROLINE--TRNA LIGASE) (PRORS) >gi_626755_pir_S46774 multifunctional amino acid--tRNA ligase homolog - yeast (Saccharomyces cerevisiae) >gi_500692 (U10399) Yhr020wp [Saccharomyces cerevisiae]

 Seq. No. 302343
 Seq. ID fc-zmro700807612a1
 Method BLASTX
 NCBI GI g3402758
 BLAST score 521
 E value 4.0e-53
 Match length 153
 % identity 65
 NCBI Description (AL031187) serine/threonine kinase - like protein [Arabidopsis thaliana]

 Seq. No. 302344
 Seq. ID fc-zmro700829628a1
 Method BLASTX
 NCBI GI g4567246
 BLAST score 362
 E value 2.0e-34
 Match length 112
 % identity 65
 NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

 Seq. No. 302345
 Seq. ID fc-zmro700829706a1
 Method BLASTX
 NCBI GI g3687240
 BLAST score 580
 E value 5.0e-60
 Match length 156
 % identity 70
 NCBI Description (AC005169) extensin-like protein [Arabidopsis thaliana]

 Seq. No. 302346
 Seq. ID fc-zmro700829731a1
 Method BLASTX
 NCBI GI g2492952
 BLAST score 544
 E value 9.0e-56
 Match length 114
 % identity 85
 NCBI Description CHORISMATE SYNTHASE 1 PRECURSOR
 (5-ENOLPYRUVYL SHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1)
 >gi_542026_pir_S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi_410482_emb_CAA79859_ (Z21796) chorismate synthase 1 [Lycopersicon esculentum]

 Seq. No. 302347
 Seq. ID fc-zmro700829816d3
 Method BLASTX

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NCBI GI	g1730168
BLAST score	199
E value	2.0e-15
Match length	52
% identity	75
NCBI Description	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 1 (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi_1370053_emb_CAA61576 (X89396) glucose-6-phosphate isomerase [Clarkia franciscana]
Seq. No.	302348
Seq. ID	fC-zmro700829944d1
Method	BLASTN
NCBI GI	g1143318
BLAST score	68
E value	6.0e-30
Match length	285
% identity	86
NCBI Description	Glycine max biotin carboxyl carrier protein precursor (accB-1) mRNA, complete cds
Seq. No.	302349
Seq. ID	fC-zmro700830015a2
Method	BLASTX
NCBI GI	g2507455
BLAST score	494
E value	5.0e-50
Match length	111
% identity	86
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLtetrahydrofolate SYNTETASE) (FHS) (FTHFS) >gi_322401_pir_A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]
Seq. No.	302350
Seq. ID	fC-zmro700830180d1
Method	BLASTX
NCBI GI	g478809
BLAST score	591
E value	2.0e-61
Match length	107
% identity	100
NCBI Description	protein kinase 6 (EC 2.7.1.-) - soybean >gi_170047 (M67449) protein kinase [Glycine max] >gi_444789_prf_1908223A protein kinase [Glycine max]
Seq. No.	302351
Seq. ID	fC-zmro700830314d4
Method	BLASTX
NCBI GI	g4249391
BLAST score	143
E value	4.0e-09
Match length	51
% identity	53
NCBI Description	(AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase from Arabidopsis thaliana BAC gb_AC004473. [Arabidopsis

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thaliana]

Seq. No. 302352
Seq. ID fC-zmro700830732d1
Method BLASTX
NCBI GI g2980806
BLAST score 286
E value 2.0e-25
Match length 133
% identity 45
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 302353
Seq. ID fC-zmro700830845d1
Method BLASTX
NCBI GI g139780
BLAST score 166
E value 2.0e-11
Match length 61
% identity 61
NCBI Description WOUND-INDUCED PROTEIN 1 >gi_82293_pir_JQ0398 wun1 protein - potato

Seq. No. 302354
Seq. ID fC-zmro700830845f1
Method BLASTX
NCBI GI g130188
BLAST score 465
E value 3.0e-47
Match length 113
% identity 80
NCBI Description PHYTOCHROME A >gi_81937_pir_S06856 phytochrome - garden pea >gi_169132 (M37217) phytochrome [Pisum sativum] >gi_295830_emb_CAA32242 (X14077) phytochrome apoprotein [Pisum sativum] >gi_226757_prf_1604466A phytochrome [Pisum sativum]

Seq. No. 302355
Seq. ID fC-zmro700831185a2
Method BLASTX
NCBI GI g3402758
BLAST score 511
E value 5.0e-52
Match length 135
% identity 72
NCBI Description (AL031187) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No. 302356
Seq. ID fC-zmro700831219d1
Method BLASTX
NCBI GI g4262242
BLAST score 147
E value 3.0e-09
Match length 61
% identity 61
NCBI Description (AC006200) NADC homolog [Arabidopsis thaliana]

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Seq. No.	302357
Seq. ID	fC-zmro700831372d1
Method	BLASTX
NCBI GI	g4490297
BLAST score	144
E value	6.0e-09
Match length	73
% identity	38
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]
Seq. No.	302358
Seq. ID	fC-zmro700831977a2
Method	BLASTX
NCBI GI	g2499488
BLAST score	698
E value	7.0e-74
Match length	150
% identity	90
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]
Seq. No.	302359
Seq. ID	fC-zmro700833740g1
Method	BLASTX
NCBI GI	g2160191
BLAST score	139
E value	6.0e-09
Match length	32
% identity	72
NCBI Description	(AC000132) Identical to A. thaliana AtK-1 (gb_X79279). [Arabidopsis thaliana]
Seq. No.	302360
Seq. ID	fC-zmro700833775r1
Method	BLASTX
NCBI GI	g4455274
BLAST score	358
E value	6.0e-34
Match length	164
% identity	41
NCBI Description	(AL035527) spliceosome associated protein-like [Arabidopsis thaliana]
Seq. No.	302361
Seq. ID	fC-zmro700834080f1
Method	BLASTX
NCBI GI	g2109275
BLAST score	176
E value	8.0e-13
Match length	105
% identity	40
NCBI Description	(U97106) downy mildew resistance protein RPP5 [Arabidopsis thaliana]

thaliana]

Seq. No. 302362
Seq. ID fC-zmro700834281f1
Method BLASTX
NCBI GI g4490310
BLAST score 387
E value 1.0e-37
Match length 96
% identity 78
NCBI Description (AL035678) somatic embryogenesis receptor-like kinase-like protein [Arabidopsis thaliana]

Seq. No. 302363
Seq. ID fC-zmro700834335f1
Method BLASTX
NCBI GI g2598579
BLAST score 515
E value 2.0e-52
Match length 120
% identity 82
NCBI Description (Y15295) L-ascorbate oxidase [Medicago truncatula]

Seq. No. 302364
Seq. ID fC-zmro700834346f1
Method BLASTX
NCBI GI g1709267
BLAST score 351
E value 2.0e-33
Match length 103
% identity 69
NCBI Description INDUCIBLE NITRATE REDUCTASE 1 (NR) >gi_1262166 (L23854)
nitrate reductase [Glycine max]

Seq. No. 302365
Seq. ID fC-zmro700834346r1
Method BLASTN
NCBI GI g409368
BLAST score 70
E value 5.0e-31
Match length 109
% identity 92
NCBI Description Glycine max mutant nitrate reductase mRNA, 3' end

Seq. No. 302366
Seq. ID fC-zmro700834406f1
Method BLASTX
NCBI GI g2506470
BLAST score 389
E value 1.0e-37
Match length 150
% identity 61
NCBI Description ALPHA-1,4 GLUCAN PHOSPHORYLASE, L ISOFORM PRECURSOR (STARCH PHOSPHORYLASE L) >gi_1616637_emb_CAA85354 (Z36880)
alpha-1,4 Glucan Phosphorylase, L isoform precursor [Vicia faba]

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Seq. No.	302367
Seq. ID	fC-zmro700834515a1
Method	BLASTX
NCBI GI	g2246450
BLAST score	169
E value	5.0e-12
Match length	54
% identity	61
NCBI Description	(U68072) 3-hydroxy-3-methylglutaryl CoA reductase 2 [Lycopersicon esculentum]
Seq. No.	302368
Seq. ID	fC-zmro700834515d1
Method	BLASTX
NCBI GI	g322669
BLAST score	216
E value	3.0e-34
Match length	95
% identity	87
NCBI Description	hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) - radish >gi_21102_emb_CAA48610_ (X68651) hydroxymethylglutaryl-CoA reductase (NADPH) [Raphanus sativus]
Seq. No.	302369
Seq. ID	fC-zmro700834529f1
Method	BLASTX
NCBI GI	g1168189
BLAST score	434
E value	3.0e-43
Match length	94
% identity	91
NCBI Description	14-3-3-LIKE PROTEIN A (VFA-1433A) >gi_1076542_pir_S52899 14-3-3 brain protein homolog - fava bean >gi_695765_emb_CAA88415_ (Z48504) 14-3-3 brain protein homolog [Vicia faba]
Seq. No.	302370
Seq. ID	fC-zmro700834529r1
Method	BLASTX
NCBI GI	g1168196
BLAST score	445
E value	4.0e-44
Match length	90
% identity	96
NCBI Description	14-3-3-LIKE PROTEIN >gi_555974 (U15036) 14-3-3-like protein [Pisum sativum]
Seq. No.	302371
Seq. ID	fC-zmro700834608r1
Method	BLASTX
NCBI GI	g2244899
BLAST score	456
E value	7.0e-50
Match length	119
% identity	72
NCBI Description	(Z97338) similar to UFD1 protein [Arabidopsis thaliana]

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Seq. No. 302372
Seq. ID fC-zmro700834677f1
Method BLASTX
NCBI GI g2459435
BLAST score 409
E value 6.0e-40
Match length 122
% identity 60
NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No. 302373
Seq. ID fC-zmro700834677r1
Method BLASTX
NCBI GI g2459435
BLAST score 249
E value 3.0e-21
Match length 62
% identity 73
NCBI Description (AC002332) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No. 302374
Seq. ID fC-zmro700834772f1
Method BLASTX
NCBI GI g4206122
BLAST score 346
E value 8.0e-33
Match length 89
% identity 75
NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No. 302375
Seq. ID fC-zmro700834861f1
Method BLASTN
NCBI GI g1143318
BLAST score 52
E value 3.0e-20
Match length 52
% identity 100
NCBI Description Glycine max biotin carboxyl carrier protein precursor (accB-1) mRNA, complete cds

Seq. No. 302376
Seq. ID fC-zmro700834891f1
Method BLASTX
NCBI GI g1769891
BLAST score 155
E value 1.0e-10
Match length 46
% identity 67
NCBI Description (X99747) bZIP transcription factor [Arabidopsis thaliana] >gi_1865679_emb_CAB04795_ (Z82043) ATB2 [Arabidopsis thaliana]

D E C O D E R
S O U R C E

Seq. No. 302377
Seq. ID fC-zmro700834955f1
Method BLASTX
NCBI GI g3335351
BLAST score 311
E value 1.0e-28
Match length 116
% identity 53
NCBI Description (AC004512) Similar to ERECTA receptor protein kinase
gb_D83257 from A. thaliana. ESTs gb_T41629 and gb_AA586072
come from this gene. [Arabidopsis thaliana]

Seq. No. 302378
Seq. ID fC-zmro700835422f1
Method BLASTX
NCBI GI g4490721
BLAST score 205
E value 1.0e-16
Match length 41
% identity 95
NCBI Description (AL035709) squalene epoxidase-like protein [Arabidopsis
thaliana]

Seq. No. 302379
Seq. ID fC-zmro700835511f1
Method BLASTX
NCBI GI g1086263
BLAST score 199
E value 1.0e-15
Match length 73
% identity 58
NCBI Description TMV resistance protein N - tobacco (Nicotiana glutinosa)
>gi_558887 (U15605) N [Nicotiana glutinosa]

Seq. No. 302380
Seq. ID fC-zmro700835640f1
Method BLASTX
NCBI GI g2129933
BLAST score 227
E value 5.0e-19
Match length 43
% identity 93
NCBI Description myb-related transcription factor TMH27 - tomato
>gi_1167484_emb_CAA64614 (X95296) transcription factor
[Lycopersicon esculentum]

Seq. No. 302381
Seq. ID fC-zmro700835753f1
Method BLASTX
NCBI GI g2182029
BLAST score 395
E value 7.0e-39
Match length 80
% identity 89
NCBI Description (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]

Seq. No. 302382

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Seq. ID	fC-zmro700835753rl
Method	BLASTX
NCBI GI	g2129738
BLAST score	283
E value	3.0e-25
Match length	65
% identity	80
NCBI Description	shaggy-like kinase dzeta - <i>Arabidopsis thaliana</i> >gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta [<i>Arabidopsis thaliana</i>] >gi_1669653_emb_CAA70483_ (Y09300) serine/threonine kinase [<i>Arabidopsis thaliana</i>]
Seq. No.	302383
Seq. ID	fC-zmro700835781a1
Method	BLASTX
NCBI GI	g4512659
BLAST score	339
E value	1.0e-40
Match length	106
% identity	83
NCBI Description	(AC006931) putative protein kinase [<i>Arabidopsis thaliana</i>] >gi_4544465_gb_AAD22372.1_AC006580_4 (AC006580) putative protein kinase [<i>Arabidopsis thaliana</i>]
Seq. No.	302384
Seq. ID	fC-zmro700835853f1
Method	BLASTX
NCBI GI	g3152599
BLAST score	509
E value	1.0e-51
Match length	151
% identity	32
NCBI Description	(AC002986) Strong similarity to lupeol synthase gb_U49919 and cycloartenol synthase gb_U02555 from <i>A. thaliana</i> (the third gene with similar homology). [<i>Arabidopsis thaliana</i>]
Seq. No.	302385
Seq. ID	fC-zmro700835853rl
Method	BLASTX
NCBI GI	g3688600
BLAST score	271
E value	7.0e-24
Match length	58
% identity	84
NCBI Description	(AB009030) beta-Amyrin Synthase [<i>Panax ginseng</i>]
Seq. No.	302386
Seq. ID	fC-zmro700835903f1
Method	BLASTX
NCBI GI	g322794
BLAST score	170
E value	7.0e-25
Match length	85
% identity	74
NCBI Description	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_21599_emb_CAA79357_ (Z18924) UTP--glucose-1-phosphate uridylyltransferase [<i>Solanum</i>

tuberosum]

Seq. No. 302387
Seq. ID fC-zmro700836164f1
Method BLASTX
NCBI GI g4138853
BLAST score 558
E value 1.0e-57
Match length 108
% identity 98
NCBI Description (AF098272) ethylene response sensor [Vigna radiata]

Seq. No. 302388
Seq. ID fC-zmro700836189f1
Method BLASTX
NCBI GI g1351856
BLAST score 629
E value 7.0e-66
Match length 139
% identity 83
NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
(ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase
[Cucurbita sp.]

Seq. No. 302389
Seq. ID fC-zmse700613632y1
Method BLASTX
NCBI GI g1708025
BLAST score 300
E value 3.0e-27
Match length 121
% identity 54
NCBI Description GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD⁺]
>gi_840731_emb_CAA56125_ (X79677) glycerol-3-phosphate
dehydrogenase (NAD⁺) [Cuphea lanceolata]

Seq. No. 302390
Seq. ID fC-zmse700617823a1
Method BLASTX
NCBI GI g3660471
BLAST score 363
E value 5.0e-35
Match length 92
% identity 82
NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha
subunit [Arabidopsis thaliana]

Seq. No. 302391
Seq. ID fC-zmse700673147a1
Method BLASTX
NCBI GI g4585879
BLAST score 695
E value 2.0e-73
Match length 166
% identity 80
NCBI Description (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis
thaliana]

Seq. No. 302392
Seq. ID fC-zmse700673642a1
Method BLASTX
NCBI GI g1001379
BLAST score 428
E value 4.0e-42
Match length 166
% identity 48
NCBI Description (D64006) aspartate beta-semialdehyde dehydrogenase [Synechocystis sp.]

Seq. No. 302393
Seq. ID fC-zmse700799143b1
Method BLASTX
NCBI GI g2065531
BLAST score 670
E value 2.0e-70
Match length 178
% identity 73
NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]

Seq. No. 302394
Seq. ID fC-zmse700806251b1
Method BLASTX
NCBI GI g2852449
BLAST score 775
E value 8.0e-83
Match length 173
% identity 86
NCBI Description (D88207) protein kinase [Arabidopsis thaliana] >gi_2947061
(AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No. 302395
Seq. ID fC-zmse700806251c1
Method BLASTX
NCBI GI g2852447
BLAST score 243
E value 1.0e-20
Match length 92
% identity 60
NCBI Description (D88206) protein kinase [Arabidopsis thaliana]

Seq. No. 302396
Seq. ID fC-zmse700806549b1
Method BLASTX
NCBI GI g2499115
BLAST score 495
E value 4.0e-50
Match length 133
% identity 73
NCBI Description VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi_1835788
(U86662) VPS41 [Lycopersicon esculentum]

Seq. No. 302397
Seq. ID fC-zmse700836372f1
Method BLASTN